

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
7689	38057	A	7743	18	1108	CSGIPRFRDSQSTRAACFFPAWT RMRAPSMDRAAVARVGAVAS ASVCALVAGVVLQAQYIFTLKR KTGRKTKIEMMPEFQKSSVRK NPTRVVEIICGLIKGGAAKLQIIT DFDMTSLRSFSYKGKRCPTCHNI IDNCKRLQMNVEKSVCQLKEK YYAIEVDPLTVEEKVPPYMVE WYTKSHGLLVQQALPKAKLKE IVAESDVMLKEGYENIFFDKLQ QHSIPVFISAGIGDVLVEEIRQA GVYHPNVKVVSNFMDFDETGV LKGFKGELIHVFNKHDGALRN TEYFQSN*KTNSNIILLGDSQG DLRMADGVANVEHILKIGYLN DRSGMSF*EKYMDSYDIVLVQ DESLEVANSILQKIL
7690	38058	A	7744	105	548	PQTPLRKQSYYHVSPLPSSWWDHIP VAGKRA*HAA*FYIMAQLFLPA ASPGPTPASQQPLWTOCLPISW RPWSAHFSFLKPSSPGPPTPASQ QGLWTQLPRSFQRWPWKSSSR PGNGPGRASRPRAQLRPLGG LSRFDNDGHGNFLAQ
7691	38059	A	7745	186	650	RCPGCPPTTASARESREAESRGR GSSGASWGAQWEEPQPRLLL RGTDDCMIFWAPHGSSTWRRR CVHSRSTAADPVLTTPSPA/STPS SNCSGSGTSLAALPLPQLTGP *QPQGWKGTPQPCPLNTWGVITS TGRWATPKIPGLTVPPENMDS MWG
7692	38060	C	7746	212	556	
7693	38061	A	7747	2	312	PDLK*STCLGLPKCWDYR/W/ATMPGWENIFSSMNHTNLALTG AVTSTRDNS*LHRVCSISPWCCL CLSPCPCRVSAGTGRVPSCLCNSGAWNRLLDQDINRNNSC
7694	38062	A	7748	2	366	FLHTKYLLFCGIKAPHKYFIRSII FFFFLRQS/LYSIAQGGVQWGN LGSLQPPSPGFKQLSCLSLPSSW NYRACPPCPANFVFLVEMGFH WIKPG*SRN*PRDPPASASQSG ITGVSHHAQP
7695	38063	A	7749	I	446	MPILFITVSSALSQGAQHIADAQ CDRKGHRTTIQGSRVNLVQPSV GPKVEETQCWGPGGRGMPGAPE APRERRVRSGSRSGDPGVA/PR AASGVGGRYAITGRGRASAAPV CRSGGARRGGAGGQAADCGPG H*KESESRGPEGPAEGSQPL

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7696	38064	A	7750	1	744	GGLIPRAQRESKRRSRGRARA SGV/VWALCYHPRSECCGTL* KWRSSPRCWRTSG(DCGPH* KESESRGPEGPAEGISASLKM* WFASGTCISRCLTLRQRK*LKK IKIIWIKK/SEK/PAEAT*SEGQP F*GPRQTGAEGF*LEPPQPGMSL KLKVILKG*DSRTKMGDQQPP RVHGRTHGPLQPLTPVKQGS CPVKGPSPGIWP*KPLL*CLAT L*WQEGTFSLSGLLGPGTGTGAS VGHKIIY
7697	38065	A	7751	316	650	SYNTHGITFHVPTANVLVVDL MCHLEKLAKYDDIKKMKVQQA LEGLPLKGILDYTEQQVVSNSFT SDTHSFTFDAGAGTAFNNHHFK LIF*YDNEFGYSNRVVELMFHP ASKG
7698	38066	A	7752	2	775	QARRRSRSNRSGLSQSAARPLA AKTAWRVTAVAPPQWPAAAPR*R SSCPHSSCSATSPGPARACQSSA HSPSPRLQAPPPTSSISGSSVPE AATAPLAASARRGTPRPTGRP SWAGTRQGSWAGTQRPWVVA PAPAGPFPRAAAAAR*GRDKS QLTCPYRHSTPPGSAGASRHR RRGLAGPAPSPPGCRAARPWP SAAAALGLGGRGPDLVALHCEI HWPLEFQSLCCCLTSRGGEAS CHPEFHLMHDFLPGSF
7699	38067	A	7753	1	552	MQLTFLLQPSSQTPGIPQPIVC CVYAESGARDSGQP/PSKVPVPS FCTPAATQRG*REPQGCSHAGD CSAQQCS*PGQ/RIS/RGDKV ASNTYLPGPPGLPGQQGPPGTW MKVETITQQINTGTENRNFVLS LYMTISKQYLSEEQGSHWLSC INALQAFFSNAAIWLVTFWELS RVLDGAEND
7700	38068	A	7754	2	538	LGKYITGDKVLASNTYLPGPPG LPGGQGPPGSPGPKGSPGPFRY AIGLLGQPGSRGSIGTHGTIS*S/ G/LPTKQGRRGPVGPPGP PERD GSKGERGAPGPRGSPGPSPGSFD FLLLMLADIRNDITELQEKFVFG HRTHSSAEEFPLPQEFPSPYETM DLGSGDDHPRRTETRDLRAPRD
7701	38069	A	7755	146	373	

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7702	38070	A	7756	678	1582	CQGNNSPLSGVWPSPGDWEDKHS Q*CPVVCSPQNILSQTSRHNDR DYRLPRAETHSSYAQYSTPSN LVVHPTATPSTVPSSPFTLQSD\ YQPKKSFIDANGASTLSKLPTPT SSVPAQKTERKESTS GDKPVSH SCTTPSTSSASATE/S/TTSAPPITS ASAGPCFCSCSTARQVLPYFRDP NLLRTIAVLLCKATVAALINS*C GTYLKIK*SSYSSCDTSLTA VYN S*VSYCWTICFQHNVSDFSSCSA PTQAQPSNQSPMSLTDASSPR IICFSKE*GTPQTNTVPIQTFGFS TPPVSSQAKG
7703	38071	A	7757	1	1365	MHLIPPA TNCDTLVECCLPGL TRDLVCTAFTGFGTSYSPQENS HNHSALHSSNSHSSNPNSNNPSK TSDANILSQTSRHNDRDYRLPR AETHSSSTPVQHPIKPVVVHPTAT PSTVPSSPFTLQSDHQPKKSFDA NGASTLSKLPTPTSSVPAQKTE RKVLQQLSKHNRKV MIRSLAT SIIDLLYIEKDLRYQKNIESTSG DKPVSHSCTTPSTSSASGLNPTS APPTSASA VPVSPVPQSP/PSLT SGPKSS*TIA/PALQATLQLNNS NVDISKINEAQPSNQSPMSLTD ASSPRSYVSPRISTPQTNTVPIKP LISTPPCFITAKG*LLQ*LSQGTS VHSQPHTAACNC*/PSK/SHEP VSPRSILQRSSSSQRSPSPGSQFILL NSSNGIQMATVVVPQEFFF LARFH VFHLTPGTRRPPFQWKISLKHV SRDGPADSWQEEGRASRFTAE GRRH

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7704	38072	A	7758	2	1256	CHCGPP/VKVEAYGSQVLKGVL AQVQLTVGPVGPRTHPVVIFPV PECIIGIDMLSSRQNPHGTSLTG RVWTIMVRKAKWKPLEPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPYCNPIWPVQK TDGSWRMTVGYCKLNQVVTPI AAA VPDVVSLLQEINTTPGTWY AAIDLANDFFPIPVPHKAHQKQF AFRWQGRQYTTFLPQGRWEI NMTKIQGPSTSVKFLGVQWC ACQDIPSKVKDLLLHLPPTTK K/EAQCLSGFRRREHIPHLPIYRV SRKAANFEWSPEQEKAHQVQ AAVQAAWPLGPYDPADPMVLE VSVADRDADWSCWQASI/GHK VGHAAQQHSIJKWKWYIRDWAR ADPEGTTKGQQGQRWWQLAE RQDSRDRDREAIGERQETAVGK ARDGEAVCD
7705	38073	B	7759	56	3476	
7706	38074	A	7760	3	591	DPADPMVLEVSEADRAIVPIS ESQQRPLGFWSKALPSSANNYS FFKRQLACYWVVLVEIEHTM GHQVTRMRPELPINCVLSDPCSH KVGHAQHSIJKWRWYIHDW EGTSKLHEEV.AQIPMVSTPSLP QPAPMASWEVPYDQLTEEKT RAWFTDGSARHAGATQKWTA VALQLPLSGTSLQDSSEEKSSQW
7707	38075	A	7761	1	558	
7708	38076	B	7762	1	1189	
7709	38077	A	7763	604	1760	NSWCRWFNFY*YPTFYWES* NT*IPLREWFG*NHDASCP*TLD SKSFSETRTGSPCSSSLQTAYC GTLWIVQGV
7710	38078	B	7764	1	474	
7711	38079	C	7765	1	3384	
7712	38080	C	7766	1	333	
7713	38081	A	7767	1	390	
7714	38082	A	7768	3	728	
7715	38083	C	7769	184	529	

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7716	38084	A	7770	2	837	CHCGPP/VKVEAYGSQVLKGVL AQVQLTVGPGVGPRTVHPVIVFV PECIGIDMLSSRQNPHGSLTG RVWTIMVRKAKWKPLEPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVPIPTTSPFNPIWPVQK TDGSWRMTVGYCKLNQVVTPI AAAVIDPVVSLLQINTPPGTWY AAIDLANDFFPIPVPVKAHQKQF AFRWQGRQYTTFTVLPQGRWEI NMTKIQGPSTSVKFLGVQWC ACQDIPSKVKDKLHLVPPPTK K/EAQCLSGFRREHIPHL
7717	38085	A	7771	2	469	
7718	38086	A	7772	3	587	YPASAGLMLQNFVGIGRLYHF AIHSPAAGGLDGLHAAVAAIQG ITKIETTPNHQRPAHWTLTQ QAHLQPSPLHFNLPLTLCLMH PTAIPHCFADARTWVN1.PTSSLI GHKKENLKEFISGSLIVHEILEE VLQAEQDFQPFPTRVTVHWGKG NDQTFRGLLDTGSELTLIPGDP KHHYGPPVKVGAYGAQLL
7719	38087	A	7773	I	633	MTVDYRKFNQVVTPMMA/APV DAVSLLEQINTFPCTWYAAIDL ANAFFSIPVHEAHQKQFAFLPQ GYINFPALCHNLIRRELDFFLLL QDITLVHYIDDILLIGSSEQEVV NTLDLIIHKRSKEAEHTAASRIR VSCLPEQKSHEQTLPWEQVPPSS GDIKEYFPNAFVLLTASLQQGQ DNTSQLLTWKAPEDIKMSKT DADADEEIEALRG
7720	38088	B	7774	I	1431	
7721	38089	B	7775	75	947	
7722	38090	A	7776	6107	6706	MVVVFHKCLHYFHSTQLVISR YNSPTEYFQALDLTWRALGT VGSAPPILPDGGTNRRQPFIL SHSGLHRNVLQPETDSQSEDRL PVTWLAWSACCQQQMVGGNP TRSKL*RTGSHYHLPGWEP*RP HFPHAGSLAWQWLLCSSLEHSF GA*ELPCNPCKGWCLCPCHFIF YIFFNSFLSNCPQLCNWHSSYFI

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7723	38091	A	7777	1	3179	MAEGKEEQVLSYTDGSRQREN EEDAKAETPDKTIRSHETYSLPR EWYEGNRPHDSITSQWVPPTR GNYGSTIQDFEWVGDIHSGYVRP VPVPRSLNSDISYFGVGGKQAV FFVCGSARMISKPADSQDVHEL VLSKEDFEKKEKNKEAIYSGYI RNRKDDYDNHTGIDLVGTIIATI KGSNEEDTDTPLFIGKVRLTEFP FVNNGSAEIMLMPSNQQHKTDE KGRANLGVFSVFAPRGHEHTLQ VKAIYNKSIIEGP
7724	38092	A	7778	281	1531	VRVLSPVEKEKLWKNTHKLL SYPTVGAAVTQLQNLTTAMGV GSHGARGQVVALNQRQRQGD QPFTRTVTHWGKG/NMQIFGGL LDTGSELTLPQDPKHHCGPPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHIGSLTGRVRAIMVGKA KWKPLEPLPDKIVNQKQYCIP GGTEISATIKELKDAQEVIPI TFPLNSPIWPVRKTDDCWRMT VDYCELNQVVTPTAATVPDV SLLEQINTSPGTWYADIDLNA VFSIPVHKAHQKQFAFSWQQ QYTFTVLPQEYINSLGLCHNL WRDLDGFLLLQNTLHVYVD DIMLIGSSEQEVANALDLLVSM ASSRVPYDOLTEEEKARFTDGS ARYAGTTRKWTAALQPLSRIS

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7725	38093	A	7779	332	2159	RGYVFCSWKKT DGS/WRMTVD YCKLNQVVIPIAAVSDVVSLL EQINTSPGTWYAAIDL ANAFFSI PVHKAQQKQF AFSWQGQQYTF TVLPQWYINSPALCHNLIRRLD DCFSLPLDITLVH YIDDIMLIGP RQLLACYW ALVETECLTLGHQ VTI*PELPIMNWVLSDPSSHKVG HEQQHSIIKW KWKWYVHDWARA GPEGITT PVISQWPHEQCQGHGG RDGGYAWAQ QCRPLTKADL NTATAKRPI CQQQRPTLSPQYG TIPQGDQPATWWV DYM GSL PSWKQORFVLTGIDTYSGYGFA YPACNASAKTAICGLTECLIH HDIPHISIASDQGTHFM AKEV RQ WAHDHGHIHW SYHVSHIPEAA GLIEWWNGLKSQLQ CQLGDN TWQGWGKV LQKV VYALNQIJP IYGT SPIAKI HRSRNQ OGLEVAP LTITPRDPLAKFLLPFATLQSA GLEVLVPEEGTLP PGDTMIPLN WKLRLPPRHFG LLLPLNQQAK KGVTLAGVTLDYKDEITLLL HNGGKEEYA WNTGDP LGILLI LPCPMIKVN GKLQLKPEALVP KG VFP DTTMLSL SWKLRLP SGHVGLL MPLSQQVQ KGTVL
7726	38094	A	7780	84	202	
7727	38095	A	7781	1	551	RWGSH TVAQAGVQWCDHGS QPRSPGVK *SSHLSLLGSWNHR HATITPG *FCFSRIRSHCVAQA GL *LLTSNHPPALASQT VGTG VSHWTWPNTGSVLTATNKNL KFFHYAISKCLVRAK LSSRLLK EERNKALSAPVVS VSI FDRVLR LLGYSASDWQPEF VETAVSNFV IYGI FRGQ
7728	38096	A	7782	1	678	MPACRLGLLATALIISLLFGFTI VSGTGA EKTGVCP ELOQADQNC TQE CVSD SECADNLKCCSAGC ATFC SLPNGQ LAE *FESEESSL DTVSPFVV FQSISSTL RIE *ARA GDSSQ \DKEGSCPPGV T*LFPS GLC\ RDQVPGGTAQCPGQ\IMK CCR\ NGCGKVSCVTAQFLSSSH HQAEQVR RDSFLPGPASGFOAH LPS PFF GTL YSLFGLT TSFSLSQP

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7729	38097	A	7783	1	1972	MAVNGCLEGPSSNFLSCLFIVA LVGSESTHPLCQLEPATQETRY QLQLQRLPAQRASWIGYIAIAYHI. LEDYEMAAKILEEFRKTQQTSP DKVDYEESELLLYQNQVLREA GLYREALEHLCTYEKQICDKLA VEETKGELLQLCRLEDAADV YRGLQERNPENWAYKGGLEKA LKPANMLERLK1YEEAWTKYP RGLVPRRLPLNFSLGKEFKCECL DKFLRMNFNSKGCPPVFTLRSV YQDKEKC1AIIKLVVGYETSLK SCRLFNPNDGKEEPPTLLWV QY YLAQHYDKIGQPSIALEYIN TAIESTPTLIELFLVKAKIYKHA GNIKEARWMDEAQALDTAD RFINSQCAKYMALKANIKEADED MSSKFTRGGTSAVENLNEIQCWM WFHTECAQAYKAMNKGFEAL QKCHEIERHFIEITDDQDFDHTY CMRKITLRSYV DLLKLEDVLRQ HPFYFK/EQARIAIEIYLKAS*QP PYR*GIKGTRRLDTAKLSDKEL KKLRNKQRRAQKKAQIEEEKK NAEK EKQQRNQKKKKDDDE EIGGPKEELIPEKLAKVETPLEE AIKFLTPLKNLVKNKIETHLFAF EIYFRKAAKMVYYLDPSSQKR AIELATTLDLSLTNRNLQTCME VLEALYDGSLGDCKEAAEIYRA
7730	38098	A	7784	264	429	HRAAPATSQTQE*HRSNAFGE EEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEETLFSN
7731	38099	A	7785	1	681	
7732	38100	A	7786	415	692	
7733	38101	B	7787	1	2204	
7734	38102	A	7788	1	615	MPVDHPP1KAFAKSEKRTSQSVNM LAKTHPYNPLWAQLEWFKLLEI SPKSPINTDKFLLKRLSVPGSDS CRVRMENVLASQVLHPG1QLM M*EGSGWAEARITV/C\$*AANP *KWHPSLPLPW*CRVRMENV LASQVLHPGHADDVGKWLG RSKDHRapeQQTRESGIRLPSLF PGSAEQPWRGNAQWHLWSWKA LRGVFGMIPDSL1YEFHQSAKK SSHFKPPQPLLYWTLVNFIPFS LHSSTWFMWSSNQGIMCKEEV

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7735	38103	A	7789	3129	3197	TQNRRACSPDTEQLARQSGTYP VSLCQATVLEDKAAALPGLGPT LMAVTVVTEAAVAIGCEAAH SSRDEFTNHQLWRRTEVGKKG EGKNKFMGGVNNTVPLLKT RKGSPPDSPHLREKPSLEKVTFQI GSFASPPESDFESRMKKMMEERVK ACGPSEASEAADVQAQDPQVS RSPFKPGFQENVCCPQNRLESEG DEGESDKGFAEDRGSRNDDMAA DIAGQLSHAADLGTASHDDVT YAIKPTCWPGLDIIPSCL
7736	38104	A	7790	I	1069	MAEKEAGMSYMVAEVLGVF VIIAEASLKRIRFFENFTVAEERS TDETFSLAEETCSSNPAMVRK KIAISIIFSLCEKEEAQRNFQDF FSHFLPFESHHMNRLKSAIEKAMI SCRKIAESSLRVQFYVSRLMEA LGFRGTIWNLYSVPRIAEPVV LTMMMSGTLEKNQLCQRFKEF TLLIEQINKNQFFAALLTAVLY HLAWVPTVMPVDHPPIKAFSEK RTSQSVNMLAKTHPYNPNLWAQ LGDLYGAIGSPVRLTRTVVVGK QKDLVQRILYVLTYFLRCSELQ E/IPADLEWQS^R*PAMVRK KIAISIIFSLCEKEEAQRNFQDF FSHFLPFESHHMNRLKSAIEKAMI SCRKIAESSLRVQFYVSRLMEA LGFRGTIWNLYSVPRIAEPVV LTMMMSGTLEKNQLCQRFKEF TLLIEQINKNQFFAALLTAVLY HLAWVPTVMPVDHPPIKAFSEK RTSQSVNMLAKTHPYNPNLWAQ LGDLYGAIGSPVRLTRTVVVGK QKDLVQRILYVLTYFLRCSELQ ENQLTWSGNHGEGDQVLNGSK IITALEKGEVEESEYVVITVRNE PALVPPHPTTNSSRETQPLADR
7737	38105	A	7791	118	273	FSLSNLVQFFRVCNDHLYTKLH FCFLQAEVKASNFCIYDSLGH LGSIHHTVECIATDEHTLHLTSP MG*SQGKQFLHLRFWSACPGIP PHS

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7738	38106	A	7792	1	551	MQPELPIMNWVLSEPPSSHKG HGQQHISIIKWRWYICDWAvg RESTTINGLAIGWS,GTWKKHD WK\NDNEIWGK\SMWIDLSEW SKTVKIFVSHESAHHIT*KSSAE EDFNNNQWDGMMTCSDVTTPLS LTTSVIAKWAHEQSDHGRYRG GYAGAQHQHGLPLTKADLAMTT AECPICQQQRPSLSP
7739	38107	A	7793	1	782	MTKIQEPSTSVKFLGVQWWSGA YQDIPSKVKDKLHLAPPITTK EAYLGL/FGFWRQHIPH/LGTEQ EKTLQHVQAAVQVALFLEPYD PADPMVILEVSVADRDAIWSLW QAPISESQWRPQGFWSKALPSS AANYSFPERQLLAYYVALVET EHLTMGHQVTKQPELPIMNWV LSDPSSHKVGCAQQHSIIKW YICDRARAGPEGTTTPVITQWA HEQSGHGRDGYYTWQQQG LPLTKADLATAECPICQQQR PTLSP
7740	38108	A	7794	65	230	
7741	38109	B	7795	1	2115	
7742	38110	A	7796	1	246	
7743	38111	A	7797	1	1293	MAAAACLDASGEARPGLRPPW SQQRKQAGALPPTKLLAGLLA QLQPAEAPDLGPVLSATREDPL SPQARKCLLPLGLSPCSQHLL WCRAASCRAWGPSRSPSRVCTG LDATAVTPAPCRLSLPWTSGADK RGREASRGEGGSSKWACRHPSA QTAWAVEGDRHRFLSRKGQIT GKTPSSQGQPPEAWGLSCSCPH TLHTSFFLDTGPLNGGTEKAVT QTGPKHACPSPCGQQGGKGC GPSGTPDLGALRARAATVGLCS SWHLQASGHHCIPQYLLQKLL VVHLVQPQPCTKPVVPVPSFRLQ MTIENMNHLLKFIPHKDYTANRL VSGLLQLPSNTSLVIDETLLIEQ GQLDTPGVHNVTALSNLITWQ KVDYDFSYHQMEFCNIIKFIT SEGRSLLPADVPDSLTA KHGGST*TAFSQRCCLCP

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7744	38112	A	7798	1	2555	MPSHLNQHQIIHTKEKSYKCEE CGKSFKRSSNCCTTHKRINTGEK PYRCEECCKAFRWPSNLTRHK RIHTGEKPYTCEECQAFRRSS TLTNHKRINTGERPYKCEECGK AFSVSSTLNDHKRINTGEKPYT CEECGRAFNCSSTLK1THKRINT GEKPYKCEECDAFKRKHSSLA KHKIIHTGEKPYKTGSICLLQR YCWSSTT*TIHFKK*S/EN/PSC DLNTLRLKKDYQRVGNCKGK SSYNGIHQCLSATRSKTQCQYNK CGKAGFLCSIFTEHKKIFSREKC YKCEECGKDRCRLSDFTIQKRH TADRSYKCEECGACKKFNSL TEHNRVHTGKKPYKCEECGKT FTCSSALTKHKRNHTGDPRPYKC EECHKAFRWCSDLTKHKRINT GEKPYKCKECHKAFRCCSDLT KHKRINTGEKPYKCNECGKAF MWISALSQHNRINTGEKPYICE ECGKAFTYSSLISHKRJHMELR PYKCEECGKTFKWFSDLTNHK RIHTGEKPYKCEECGKSFCCSS NLIKHKRJHMEVRPYKCEECGK TFKWPFDLTNHKRINTGEKPYK CEECGKTFTCSSLIKHKRSHTG DR/PYKCKECGKAFRWFSALL NISKHKRINTGEKPYICEECGKA FIRSSLTSHKRJHMEERPVYKCE ECGKTCIIHIGEKPYKCNECGK GFMWISALRKHKRINTGETPYI
7745	38113	A	7799	212	461	TEEHLYSPHWKCGCRKVRLF QVRGRGRWIQTRQPGSMVKEP PLSEAGAESHVSC/RQGDCSRPP SFPLSPERVTPWLPDSIWT

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7746	38114	A	7800	1	1398	AAAERELELLRASLEHQRGVSE LLRGRLRELEEAREAAEAAAG ARAQLREAVTQTTPWPSCAEKAA QTESPAEIGPP^LRRARPDPWT TRAVAPAGVILKSIMKRDGTP GAQPSSGPKSLSQFVGVLNGEYE SSSSEDTNDSDDGSENGAEPP GSSSGSGDDSGGGSDSGTPGPP SGGDIRDPEPEAEAPQQVAQG RCELSPRLREACVALQRQLSRP RGVASDGGAVRLVAQEWFVRVS SQRRSQAEPVARMLEGVRRLG PELLAHVVLNLADGNNTALHY SVSHGNLIAISLLLDTGACEVN RQNRAGYSLALMAALTSLVRQE EEDMAVVQRFLCMGDVNAKA SQTGQTALMLAISHGRQDMVIA TLLACGADVNAQDADGATAL MCASEYGRLDTVRLLLTQPGIC DPSILDNEGTSLALAIALAEATG MKVAALLIHAHLSSGHPDTSQG VTPLAPQTANTW
7747	38115	A	7801	3	408	
7748	38116	C	7802	141	251	
7749	38117	A	7803	1	1173	
7750	38118	A	7804	451	853	LQMHRLLCGGHSLSGCGWHTAR GQELVGQCFL^GGGQLLGLQH PL/AENPTFQEYSLITSEAGLLEG RKKKNKTSRGPSGPATCPLCLGP RTSPGATRPGPVHS/AAIAASORD SSRTFRFSSSLDAAIARPYTTPSA
7751	38119	A	7805	1	2950	MAASRLELNLVRLLSRCEAMA AEKRDPDEWRLEKVGVTYSVA SGRVLFQDFTEQFQVLLPKDAQ PCREVISTLLEKMIDKRNQYQIG KTKVEPGV/EAWPLRRVRRQPD QRQGLGAHRAGEAPGTRGDAR PVHRGQLPVQVGCCQPHSGAPAG AADRPRSSQAGELPHPRHHRGA EAVAAGAACRAPHDLRTVRRLP PSRRAAGEAGAAGCH/RMPSW STFKPPTTPWDRDSSTLSSNHP LTASGAGWPCSRMST
7752	38120	C	7806	398	415	
7753	38121	C	7807	13	81	
7754	38122	B	7808	1	972	
7755	38123	B	7809	1	1803	

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7756	38124	A	7810	1	929	IAAPELLERSGSPGGGGAAE EAGGGPGGSPPDGARPGRSEL AVVARPRAAFTPGRPSAAAMAR PLVPSHKALLLELKGLQEEPV EGFRVTLVDEGDLYNWEVAIF GPNNTYYEGGYFKARLKFPIDY PYSPPAFRFLITKMWHPNIYETG YVCISILHPPV/DTD PQS GEL PSE RW\NPTQNV RDHSS*V*SSL E RRPNTFLR PANV GRP WL M QG SWEREQGGRIRELHRTSFRKQV LGTKVDAERDGVKVPITLPEY CVKDQGRRAPDEGSDFYDDY YE DARVE\EA DSCFG DDE DD S
7757	38125	A	7811	2	296	LSLSFFFVKAHFYVKSMLHSKD ASGISGMDFYYVQ*FWQTAY AGEVGRWLSPALTERGSQTL* TWCWRVFCVCLEGHMWVTEA YVTVKH*NYSKV
7758	38126	A	7812	397	410	SPGEI*G*VPPLLG*GVLLYQPP LFKIWEAPLLPDLLQQ*KLYSL WLNKALGK
7759	38127	A	7813	2	739	ELCALVFGVN TFFATIVKTIITFI VSDVRGLGPVRKQDSVVVFL DCPSIW*LYIDLLLRLVHLQIH LWGLRGRRAEFKHI/RSAEEKK LTRIPS VNGE*TGKSPAPANS\PP RGARDM WRTGRPAPR RPLVGG PSPSDRGPASTTSPELA VGVAVN GGPSSANISRGFWQQSFHGNC WFCAEPGVAGV PFTANIA GTEP GGLGQGRQCSLATQCHKPELK LQAKPAFPFSFSLSLFFFLLKHIL

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7760	38128	A	7814	594	2868	CWTSRNRPIP GSCHPMELPRPF RGKAKVQNHQLVHNKALIN RGSLTFWLDDGA QAWHCPVK TYYQYTPVSSKAMY/DAFWNG/ KFRDC/AFHSLWNEDPFVCEYQ GQSSDLPOPPVNAGGGSGGGGS GGGSEGGGSEGGGSEGGSEG GGSEGGGSGGGSGSGDFDYEK MANANKGAMTENADENALQS DAKGKLDSVATDYGAAIDFGIG DVSGLANGNGATGDFAGNSQ MAQVGQGDGNPLMNFRQYLP SLPOSVCERPYVLSAGSEIGAA CASRSGYDNKGVRDIGHYTICK RSELDLPLRHQILGGKKAIQFTL QGFPTLPEGAPAGNSGLAVHK TAQSSYRHALLIILT PMSGTRF PPIPGPVVNIRVFPFAPSSECRC YSWSWVPGSPVHCOSDGSPVPIP SYAPLASQYSSSFLFFRNRPQYA PYDYLSVMTSRTLREQIRIYRA PSAPRLPPPVEVYCSNSTIVYVRN NPSPGPTGFA GTLLEGRSGGP FRFYAKRAKGDVLKPKFSLNPL QTLMRFMVDIACGMEYLSRRNF HRDLAARKCMYEFWRTRGW TAAAYYGGTTFFRKESQKLQ QSAKKRDAELANGALGIELNN DYTLKKVVMKPLITSNTVTDIE RANVFKMNGKWYLFTDSRGSK MTIDGINSNDIYMLGYVSNSLT GPYKPLNKNTGLVLQMLGDPND
7761	38129	A	7815	2	474	RRFVSADNCRSSLRWKSLSYTPLD ADASVLISTGIDATQTNHGRQH LDETQVRVFGQHLMQGSYTTQ DGRSDVAISCSCKLEMCAQSQY DQLLAASTENWRQWWQKRRIT VNGG/GSSPASDADQTPAPGFR RDVGDRDWFAWRQCILLKSA RRRPVAYIVISSAMSGSCLPKQS D
7762	38130	A	7816	302	409 .	
7763	38131	A	7817	199	359	ARRQQVSVKSYRWEEDQHCG ELQGSE*VSDGLFKPP*S*HG VEEERQKEQN
7764	38132	A	7818	1853	2032	VKQSTALLPHAVAC*PKVISSG ARGLKSILVLIRIVVMMVSLMP QLALSGWGFRVLPG

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7765	38133	A	7819	118	445	AAGGEPGDAPWVPGVWEPPES VCRGPPPSSTFPHPVLSTFGASG PENSRCDSWLSPQH* AA*VASG NNGPQAAGQLSGIPDAATLSG I*RASILHVSVVEIISSPGFR
7766	38134	A	7820	I	770	MRVIGIETSCDETGIAKYDDEK GLLANQLYSQVKLHADYGGVV PELASRDHVRKTVPLIQAALK SGLTAKDIDAVAYTAGPGLVG ALLVGATVGRSLAFALGRFGDP CTPYWRASVSARCWKIPAPNFR CALLGSAAYAVNHGTGLSKKP TTLGSDHSKTPAQLAKRAGEA RRNGWQGALFPWESARSGEEE TP/ICRH*HSHRAAAKSGLGA GGTSSSGGRYRLGGYSILADHGG *KFHCA*RHGATSGDGKVLD
7767	38135	A	7821	3	834	VGRVEIADQYQDLAILWNCLG SDHASSRQRPFRGAKVQNH QLVHLQQSSHQPWLPHFLAG* WGDSGLGGGSLEGGSEGGGSE GGGSEGGGSGGGSGSGDFDYE KMANANKGMATENADENALQ SDAKGKLDSVATDYGAAIDGFI GDVSGLANGNGATGDFAGSNS QMAQVGDGDNPLMNNFRQY LPSLPQSVCRPYVFGAVRHDV RRIRVTGTRVTPEEVDTSVH SRGAHRIRSGFAPKRSVRVITD TCIKRNSTCGVKSLSLWDGGGF
7768	38136	A	7822	I	1044	

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7769	38137	A	7823	3	1472	GVVGERAGMARPGRPREGGSG/G/GYSRPVPPAGGP/GP/RGRTRI/SGLANGAPVVTFQFLTELTRLF/QKCRTSGSVYITLKKCKQREGS/RAMLPGFPYTPVSSKAMYDAY/WNGKFRDCAFHSGFNFEDPFC/EYQQGQSSDLPQP/PVNAGGGSG/GGSGGGSEGGGSEGGGSEGGG/SEGDGSEGDSGGGSGSGDFD/YEKMANANKTENADENA/LQSDAKGKLDSVATDYGAID/FIGDVGLANGNGATGDFAG/SNSQMAQVGDDGNPLMNFRN/QYLPSLPLQSVECRPVVFAGKP/YEFSIDCDKIKILRGVFAFLLYV/ATFMLPVIANIAIPQKRPFMQQT/RCEVOCREDIEVQKLKSYDKLL/ASINKPGVNGWQKRITVNA/GEAHDDQALDYALYHLRIMPT/AHDERSSIAAKGLTGEGYKGH/VFWDTEVFLLPFHLFSDPTVAR/SLLRYRWHNLPGRARRKRDGN/GWAGGAPISVGKARAACK
7770	38138	A	7824	601	853	
7771	38139	A	7825	2	644	MAQQG/RKFQAHKPAKS/TA/A/ASEKNRGPRKGGRVIAPKKA/RV/VQQQLKKVSLCCSGWS*T/PGLKASSRLCLPKCWDYRRDTL/WLFLSATFICRWNLRKSES/GKK/IEHDVVMKA/SSLPLRK/LALLK/APSPRNRGAAAATSSKTPSLRT/AGPQLQQHPTPLPSIWGPLQV/NSHRLSLFRMRTLSPSDWASPR/HSSGGPKGAENPGNDQGRYSH
7772	38140	A	7826	1	2616	
7773	38141	A	7827	1	504	

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7774	38142	A	7828	1	1068	MAEIQHKTIRPLLEGRDLLAATKTGSGKTLAVLIPAIELVVKLKFMPRNGTGVLLSPTRQLAMQTFGVLKELMTHHVHTYGLIIGGSNRSAEAQKLANGINIIVTPGRLLDHTQNTPGFMYKNLQVEDDLARISPKKEPLYGVGVDEDKANATVDGLEQGHFVCPSEKRYLLFTFLKKNQQKKLMVFFSACMSVKYPYGLLKYIDL/PVLAIHGKQKQNKHTTTF*YCNADSGTLLFQLEKLIEKNYFLHKSAQETYKSYIAYDSYSLKQIFNINNNLNPHIALSFGFKLPPFDLNMMNSNEGKQKKGQGFQYQTKKVEKSIIFKHISKKSSAAGSSLTQEPMVFILNNF
7775	38143	A	7829	3	1851	
7776	38144	A	7830	1	905	MVFDAYLTGWRFEDTVVQSNMKHQPFIVVNKHNVQEVYKGETKSFPPEVFFMVLIKMKEIAETYLGKTVNAVTVPAYFNDSDHQATKDAGTIVSLNVLRUIISKPTAAATAZRQKIDFNTSFIHALFEELNAYLFHGTLDSVEKALGNAKLDKSQIHDIVL/GPFEQGRH*MYPGPS*EIQS*R*EAEGQDVIQEFS*KLCIRYESSC*R*ETSRQD*R*GQTEDS**GY*NYQLAG*ESDSEEGRISTSKSGESLOPHNYQPVPEYRRHTRRNAWGIP*WWSSLCWSFPRAPIEAD
7777	38145	A	7831	2	886	ARGACSSWVFCGFLRYWSQAYTPATMSKGPAVGIDLGTTYSCVGVFQHGKVEIANDDQGNRTTPSYVAFTDTERLIGDAAKNQVAMNPNTVFDAKRLIGRRFDDAVVQSDMKHWPMPMVNDAGRPKVQVEYKGETKSFPDEVISSMLTKMKEIVAEAYLGKTVTNAIVTVPSYFNDSQRQATKDAGTIAGLNVLRIINEPTAAAIAYGLDKKVGAEARNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNHFIAEFKRKHKKDISENKRAVRRLRTK
7778	38146	A	7832	2	375	ASIEIDSLYEGIDFYTSITRARFEELNADLFRGTLDPVEKALRDAKLDKSQIHDIVLVGGSTRIPKIQLLQDFYEAVAYGAAVQAAILSGDKS ENVQDLSLSDVT PFP GIETAGGIVMTVPH

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7779	38147	A	7833	1	218	
7780	38148	A	7834	508	883	YYHHSYQADT/IILGGEDFDNRM VNHFIAEYKRKHKKDISENKRA VRRLLTACERAKSTVSSSTHAS TEIDSLSEGIDIYTSSTCASFEEL NADLFLSTLDPVEKALRDAKLD KSQIHDIALSINPDEAVAYGAA VQAALSGDKSENVQDLLLL DV TPLSLGIETAGR VITDLIKHNTT PTKQTQTTTYSDNQPGVLQL YEGEHTMTKDDNLLDKFELTG PPAPRGVPQIEVTFTDNTNSNGILN VS AVDKSTRKKNKITITNDKGH LSKEDIEYMVQEAKYKAEDQ KQR/D/KVSSKNSL
7781	38149	A	7835	1	194	
7782	38150	A	7836	1	1482	MVFDAKRLIAHRFDDAVVQSE MKHWPFMVNVNDAGRPKVQVE YKGESKSFYPEKVSSMVLTNM KEIAEA YLGKTVTHAVVAVPA YFNDSQRQATKDAGTIVGLNV LRINNEPTAAAYGLDKRHRSSL ILTASLIGAGSLG*STQ/A/SIEIDC LYEGINFTCTSITHARFEELNADL FRGLTLDPVEKALRDAFKDSQI HDIVLAGGSTRIPKIQKLLQDF NGKELNKGGINADEAVAYGIAV QAAILSGDKSENVQDLLLFDVT PLSLGIETAGGTQILTTYSDSQP GVLIQAYEGKHAMTKDNNLLG KFELMGIPPAPRGVPQTEVTFD SDANGILNVSAVDKSTGKENKI TITNDKGCLSKEDIERMVQAE KYKAEDEKQRDKVSSKNSLES YAFNMKATVEDEKLQGKINDE DKEKILDKCNEIIWLNENETAK KEEFEHQQKELEKVCNPPIITKLY QSAGGMPGRMPGGPGGGAPP SGGASSGPTIEEV D

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7783	38151	A	7837	2	2221	PRVRPRVRSAPAALGFFFASFVGIGRPTQQPWSKGPAGVIGDILGTTYSCGVVFQHGKVEIIANIDQGNRTTPSYVAFTDTERLIGDAAKN QVAMNPNTTVFDCQTV*LDGRFDDAVVQSNDMKHWPFMVVNDAGRPKVQVEYKGETKSL YPEEVVSSAMVLTKMKVEICRSLTLGKTVTNAVVTVPS YFNDISQRQATKDAGTIAGLNVLR INIEPAAAIALQKFRQKRFGAERNVLIFDLGGGTFDVSILTIEDGJFEVKSTAGDTHLGGEDFDNRMVNHFIAEFKRKHKKDISE NRAVVRLLRTACERAKRTLSSSTQG SIKIDSLS*EGIDFYTSITRARFEELNADLFRG TLDPEGEKAL DAKLDKKSQIS*YLSWVGGSTSYPRLQKSCCQDFFOWEKELELRISINPGWKAV AFIGAAVPGQPFLSGRQVLENV QDLLL DVTPPLSPWVLKTAGGVHDCPPSKRNTTIPTKQTQTFIT YFWTTQPGCGLFRFYEGRALPWTKDNQPALASFELTGIPPIAPRGVPQNEVTFDIDANGYTPWSLAVDKKYGKKRTKITITN*QGPFB*AREDITYGSREAEETVKLEGGGRQEGLTRVSSNDFT*GPMPFNMKSTLLKDEKL QGWRINDEGQNRRFLDQV*LKLSNWLI**ESRLLEKEEEFHQQ KELE*VCNP ITQAGTQSARRHCQGGNPWGAF
7784	38152	A	7838	3	757	PFPGGRVVRLHPVILASTVDSYERRNGAARVIGTLLGTVNKH SVEVTCSFSVSHNESDEVADM EFAKNMYEL/H*KVSPNELI G WHDITEHSVLIHEYYSEAPNP IHLTVDTLSLQNGHMSIKAYVST LMGVPGRIVGVFTPLTVKYAFY DTECIRVDLIMKTCFSPNR VVG LSSDLQQVGGASARIQD TLSIVL QYAEDILSGKVSAADNTIRKVGH FLMSLVNQVPKIVPDDFETMLH SNINDLLMVT
7785	38153	A	7839	1	1821	
7786	38154	B	7840	16	1305	
7787	38155	A	7841	1	359	

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7788	38156	A	7842	2	1085	GVAPWGRGRAAPRCASATVGG SGIGRLR/GITSSGLAKMDNKKR LAYAIQFLHDQLRHGGLSSDIA QESLAEVAIQCLETAFGVTVEDS DLALPQTLPFEEAAATGK\EMP QDLRSPARTPPSEEWDSAAEERL KTEGPKQMKWENFVEAAVHF LTEKFELNPSQRPSYFCNRRAA AYSKLGNYAGAVQDCERAICID PAYSKEYGRMGLALSSLQQHL EAVAVYYKKALELDPDNEYTKS NLKIAELK\REAPSPTGGVGFSF DIAGLLNNPGIFMSMASNLMMNN PQIQQLUMSGIMISCGNNPLETP GTSPS\QNDLASLIQAGQQFAQQ QMGSVQIPRVV**SAQESSIRS TPSASNDQQE
7789	38157	A	7843	225	398	FIIDYTNSCIFHQNCLICSNRNF RQSNVVMICHY*TLCIEKTC* MNSSLWSIIIF
7790	38158	C	7844	162	269	
7791	38159	A	7845	273	501	HKDQPIQTENDHPSTNFSFVLK LHDPLLNEMDLIVWVFS*Q*SC FYLVHVNCCSPLV*HP*SENPKF SNEYFLRVS
7792	38160	A	7846	1	867	
7793	38161	A	7847	185	1325	EEQQTNLASKKKSCIMLEKTEN KIRLVIVSEEEKKKKVLRMP*K MTVRHHGISRTPHSWVESNY YWDIDCQWMS/EPVGYMPQCQH CQVAKNTVIVAPKQHILLQGGKI PWSLVTVDLMGAFSYKPQKS/N VYAIIMTDLFTKWIVILPLCDVS ASEVSKAIINIFLYGPQKIJMD QRDEFIQQNIELYRFLFGIKQIVI SHTSGTVNPTESTPNTIKAFLSK HCADHPNNWDDHLSAVSFAFN VTHLEPTKNTPYFQMFKVEKNP LYYLPESTDLSLHEVDGDNTSMF AKILDIAKEADKIMENKTTSLG QMENNLLDELNKSJIVKKKKPK QLNPFHLKVGHGSFKTKEKLV GRMVVFQSWSNGVGPLCHRKY YRKWMCCP
7794	38162	A	7848	2	455	MADRLTQL\QDAVNSLAQDFC NAIG\VLQQCVPPASFNNIQTAI NKDQPanPTEEYAQLFAA\lia\ RTAKDIDVLIIDLSPSEIDSTAALQ AASLYKL\EEENH\EAATCLGG MLFIEGDMILLGGRYKGALA\di AQSOLEGQGSGYP*ASLFPS

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7795	38163	A	7849	229	560	
7796	38164	A	7850	1	1077	
7797	38165	A	7851	25	690	WPSDEAEGYSEHFVEFKDVR KRPQHTIMAGNVVTGEMVEE LILSGADIIKVIGIPGSVCTTRK KTGVGVPQLSAVMECANAAH GLKGHIISDGCGCSCPGRDVAKAF GAGADFVMLGGMLAGHSESG GELIERDGKKYKLFYG\MSSEM AMEEVLGGVAEYRTSSEGKT VEVPF*REMLEHTIPRH*GGIR SITCTYVGA/AKLKRR*ARTNYL HPEVHPAR
7798	38166	A	7852	768	1857	EGGHFFGGQQGADSAAPFGSASI LPIKLDVPHPDGRRAEKSPKG GNPQRQLYCOPPAGCLPGAVY RPRRSRGARMYSRSPAERRNP DQRAGYCQAPDRLRFSRADDC RSRWHRHVFHGTSRHCAGDRAV RPPPHSAEALPVLPVFO*PTA DQVLFLPSLIAACYNNHHQNKKIIL EQEMSCVLLATFIQTRAQQRKY KRRRNRRGIPRESTAREQARHINA NKAQQPRKHARNGASPAQQRK NRAAARDKDEKPAQQKDKAR QSAPEKKNRAIRGNTNSREQAAK AERNRRQRGGQKGAAQGGQHR EEAGEPTYVDEKAQAATSSPPQ TPHPAPDHDDAEDHRTDNTN NAHQPKVYTHKDPTTNESR
7799	38167	A	7853	1403	2028	RRIOTNGRTFHAHGGPSRLPE ELGKDHREREKETSSRTL*QFQPN AKSPGQNLRESMNPVC/MTQQ ARRLQLRAKDLLQVQVQVQDSG SWANNKVSALDRTLGEITRILE KERSRRGKGP SKEDLEGAA/N/G VRRTM/WMSGNLVKESQPHPT HRPNILT*YPSIFP*RSTLTLWL KVQLQQKL*KMEKSGKKKK PKR*KPG*TSGTLNLT
7800	38168	A	7854	1	675	

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7801	38169	A	7855	2	1110	AQEEEAKVNEIAFINTLEAQNK RHDVLSKLKEYEQLNLQER QRRQEKKQARDEAVQERKRAL EAERQRARVEELLMKRKEQEARJ EQQRQEKEKAREGAARERARD REERLAAALTAAQPRSYGRVTTEK NSAQA**KYSKAH/RNRLNKEK KKLLS*/VGDMQILIMPPN*PL YERKKQCSLCNVLISSEVYLFS HVKGRRKHQQAVRENTSIQGRE LSDEEVHLSLKKYIIDIVVEST APAEALKDGEERQKNKKAKK IKARMINFRAKEYESLMETKNS GSDSPYKAKLQLRLAKDLLKQV QVQDSGSWANNKVSALDRRTLG EITRILEKENVADQIAFQAAGGL TALEHILQAVVPATNVTVLRN
7802	38170	C	7856	65	425	
7803	38171	A	7857	1	1131	
7804	38172	A	7858	953	1311	FLFFIFFNYFFFGRKCPLLVP RLEVQMAVILGSLQPSPPGFK* FSLQPSPSSWDYRHAPTHAQPN NFVFLVETGFIIHQAGLELQT SGDPPTSASQTAGITGVSHRAW PGTILFLK
7805	38173	A	7859	2	857	FVDIFQRWKECRGKSPAQAELS YLNKAKWLEMGYGVDMHVR GRDGCEYSLGLPTGTGILIFEGAN KIGLFFWPKITKMDFKKSKLTL VVVEDDDQGRQEHTFVFRLD SARTCKHLWKCAVEHHAFFRL RTPGNSKSNRSDFIRLGSRFKFS GRTEYQATHGSRLRRRTSTFERK P**TLSIPETFNVQSKQPSDSSPA LLLKQIQKS>NNYQPPISILISIPS PAPGGILTPQMSGHFPQDDRSW WKASASGDDSHFELCPTTQNPE GTLGGMPKYDVSEINVMTAL

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7806	38174	A	7860	1	936	MELTHLQPHEPQEDVHVAGLL LGRLREQHHMVSEGPRQQSWQE ERTELAAVSRLLFNMYPLLIHK NHASPGIPNLLLHPRGLRAITIA VFGKQNTYIRLEPKINVLQEQT KHIEKLQCQEHNFPQEIQEGK SHQNQHEAHFVVELCKYFLCQ EYLPSQTILTTYTGQLFCRLKL MPAKTFAVGVRVHVVDKYQGE ENDIILLSISNRICVALSRAKKG MYCIGNMQMLAKVSLWSKIIH TLRENNQIGPMLRLCCQNHPET HTLVSKASDFQKVTEIEC/MLP CEFRLGCGHVCTRAPHYDSS
7807	38175	A	7861	218	580	
7808	38176	A	7862	3	1636	
7809	38177	A	7864	24	386	
7810	38178	A	7865	2	999	GRVGGFFAGNPQSDSFGGLLLG LTPVLRWVADGGTIPKRHELV KGPKKVEKVDK\ETELVAQWN YCTLSQE\KLRPIVAL/CNFAD FYNKIEPVIEFLLDKSAEKGS/SG RQASHIKTH\RIVDRAESFPDPN CPGKGKGN/D\KVDKHDILQA GASSSPVGGPGRWNGRHRFL PSGGCGLCFS\AEPWKEIKAG V\CHTCAGGLSRMMIIVLNGT KEDVDL\KTMEERRL\SEAG KENKENPRQSQLFQNQDVSERS PRAIKS\DRGSLKKPAFDSEK KTNLAPKSTAMNESSSGKAGK PPCGATKRSIADSEESEAYKSLF ITHSSAKR
7811	38179	A	7866	1	559	MGCDGGTIPKRHELVKGPKV EKVDKDAELVAQWNYCTLSQE ILRRPIVACELGRLYNKDAVIEF LLDKSAEKALGKAASHIKSIKN VTELKLSERALKEIKAEVCHTC GAAFQEDDVIMLNGTKEDVDV LKTR\WRREG\ERRGKKKTKKP KAAEVCFQNPDVSGRKPQGPS KVKTREALKKPSP
7812	38180	A	7867	188	368	YVACMPAWPNVTANQLFN YFPARDMTVPSSPG/CPVVQDQL STQQQARRDALEVVGYEDS
7813	38181	A	7868	179	554	LRPADPRSLVPGWALGLGP LGPGRVTFPGGRPPPHTPPSLF PPGGRQPLWVPALPAEEGRE/R LGREREEGRKGAGAGMA\AGL VL\CLQLQVQGQPLGGWSWL RLRSRCPHPWLRRHLP

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7814	38182	A	7869	2	131	YKSELEEQLTSVAEEMRARLSK ELQA*KDRLGENMEKVRGRLV KYGEGVQAMLGESIEELRVLA LYLRLKLCGTFLRADHL RPA GREYGESKRTL
7815	38183	B	7870	1	3639	
7816	38184	A	7871	279	1077	IQHPLRSADDFRVNCETEPAM/* HAVENDIHGLCELQLETEIQAF KEELL/FMKKNHHEEEVKGLQAQ IASSGLTVVVDAPISQDFAKIMA DIWAQYDEVAQKNRELDNNR SQQIEESTTVTTQESTVGAAK AMLTEL/RTVQ LEINLDSMRN LKASLENSLREVAYVALQME QLNGILIHILESELQWTWAEQGC QAQEYQALLNLIKVKLEAAIATY RRILLEDGKDFFNLGDTLDCSNS MQTIQKTTTRQRMDGKVLSSET NDTKLRH
7817	38185	A	7872	712	855	
7818	38186	B	7873	50	788	
7819	38187	A	7874	201	372	ICQMILKRRVLS*TQKHQATHG WNSAYSLSLTAPFPVSCQDHLC*P L*AEAQISIKEEP
7820	38188	A	7875	3	323	FFFETEFHSVAQTGVQWHDPSS PQPPPPRFK*LSRSPSLPSSWDYR HVPSHPGNFLHQ*KRGSTNQA GLELPSTSGLAAFASPARITG VSHCARPNYQCFLEFKY
7821	38189	A	7876	1	911	MLLTLAGGALFFPGLFALCTW ALRRSQPGWSRTDCVMISTRLV SSVHAVLATGSGIVIIRSCDDVI TGRHWLAREYVWFILPYMIYD SYAMYLCEWCTRDRQNAPSL TLRNFLSRNRLMITHHAVILFVL VPVAGRLRGDLGDFFVGCFITA ELSTPFVSLGRVLIQACMNEMT ESLKQQHHTLLYKVNGILTGNF FPCRILLFFPMVAWSYGRKKGL SLVPSTLQHPILTATWANAFAFP* APQIYWFCLLLQKAVERLFDTP QAKKD*MLLGVRSRSLTPAAS STQHSMMDQIVPWVASDFGY
7822	38190	A	7877	2	283	SCHCTPAWILALSPLRECGAIL AHCNLHLWG*SDSPASARVA GTAGAHCRAWLIFCVLVEMGF HRVAF/GLVLN\$AQTIRLPRPP KVLGLQA

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7823	38191	A	7878	1	1042	PKVRSPRIKRLAPAPAFVRKQE LKKIVDPLL*KKS*EFGHLDRDI QPQKRPPPL*KWPRIYIRVQG RRAILYKIRLKGPFCDYPGFTQG PGTPQTS*SSLLKL\AHKYRPRD KAQRSKQRVILLA\RAEKAAAK GAVPQERAHPVLRAGVNPVPSP PLVGEQEKLSLVIA\HDRGSPS ELVVFLPALG/RVKMGVPYCIIK GKGKTGDGLVHQKALHPLSAF TQVNNSEDKGAF/ALKLVGSYQ GPNYNMDRYDEVRGSTQNTVIH KSFSQTGWNLN*EVLSDDQLG TAKQN*RN*P*KSQKTVSQAN CLFLSFQIRRHWGGNVLGPKSV ARIAKLEKAKAKELATKLG
7824	38192	A	7879	3	472	GRGVAYRGPSPRGTGPGRGDE RLQHGGGSREGPPAAPAAAAP GYGQSCCLIEDGERCVRPAGNA SFSKRVQKSISQKKLKDIDKS DLFQLQVNTRLRRYKRHYKLQT RPGFNKAQLAETVSRHFRNIPV NEKETLAYFIYMVKSNSKSRDQ
7825	38193	A	7880	3	638	GRGVAYRGPSPRGTGPGRV*T ASARRRTAAKGPPPQLPQQRA TAKSCCLNEDGERCVRPAGNA SFSKRVRKSISQKKLKDIDKS VRHLYICDFHKUNFIQSVRNKR KKEDQVYDGRENS/SPSTDIDP EVDLFPACQVNTLRLRVRYKRH* QVARPRPGFNKAPVSRQL*VDT FRNIPVD*KETLALLSSMVKS KSRLDQKSGGWQAA
7826	38194	A	7881	1926	2448	DFAIIVITRKQLKTKYNAHHSK QAIIKHKHSPKISDLILCLKKIM NRHFSKEDIYAAKKHMKKCSP SLAIREMGIKTTMRYYHLPVPRM AIKKSGNNRRCRRGCIEGTLIH CWWDCCKLVQPLCKSMSWRFLR DLIDPAIPLLGIYPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP
7827	38195	B	7882	446	625	
7828	38196	A	7883	1	1875	

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7829	38197	A	7884	31	809	KPRLENVVKNAEASGADA\NW KKGY/LVMEDEMNMREGKF REKRIKRNEQSLQEIW\DYVKRP TLHLDIVPETLNAHHRKQERSK TDTLTSQI.KELEKQEQTHSKAS RRQEITKIRAE\KEIETEKTLQKJ NESRSWFFERINKIDRPLARLIK KKREKNQIDA\KNDKGDITSDP TEIQT\IREYYKHLYANKLENL EEMDKFLDTYTLRNQEEVES LNRPITGSEIVAHINSPLTKKSPG PDGSTAEIFYQRYKEEL
7830	38198	A	7885	1	2142	MIILIDAEEKAFDKIQQQFMKLTKL NKLIGIDGTYLKITRAIYDKPTA NIILNGOKLEAPLKTGTRQGCP LSPLLNFIVLEVLAQAIRQEKEI KGIGLGKEEVKLLSFLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNRNQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKP\LLNKIEDTNK WKNIACSWIGRJNIMKMAFP WELNNENTWTQEGEHHTLGPV VGWGKRG\IALVDIPVNNDKL MVLEV\ALARAIQKKEIKGIGLQ KEEVKLLSFLFADDMIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNRNQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPL\KEIREDTNKWKNP CSRIGRINIMKMAILPKVIYRFN DIPIKLPM\TTFTELEKTTLKFIW NQKRA\CIAKTILSKKNIAAGGITL PDFKLYYKATVTKTAWY\WYQ NRDIDQWRNTEASEVTSHIYNH LIFYKPDKNKKWGNDSL\FNKW CWENWLAICRKLLDPL\TPYT KIHSRWIKDLNVRPKTIKTLEEN LGNTIQQDIGMGKDFMTKTPKA MATKAKVDKWDV\IKLKSFC\TA KETTIVRSRQPTEWKIFAJYPS DKGLISRIYKELKQIYRK\KTTN PIKKWA\KNMNRHFSKEDIYAA NRQMKKCSSLVIREM\QIKTTM

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7831	38199	A	7886	209	3816	QGRPTFRRKYREHHKDTREEQLQDT*SSDSPKLK*KKC*GQPERKVVKLPTKGSPSD*KRISRQ/KTLOQARRQSWSFFEKINKKIDRPQARLIKKKREKNQIDIHKNDKGDITTDPTEIQITIREYYYKHLYANKLENLEMDKFLLDTYTLPRLNQEEVESVNRPITGSEIEAITNSLPTKKSPGPDGFTAIFYQRYKEELVPFLKLFLQPIEKEGILPNPSFYEAIIILIPKPGRDTTKKGNNFRPLSMNIDAKIL
7832	38200	B	7887	I	3570	
7833	38201	A	7888	2	1624	
7834	38202	B	7889	67	3156	
7835	38203	A	7890	I	1416	MIILIDAEEKAFDKIQQPFMLKTSKLGTDGTLYLKIIIRAIYDKPTANIIINGQKLEAFPLKTGTRQGCPLSPLLNFNIGLEDLARAIRQEKEIKG1QLGKEEVVKLSLFADDMIVYLENPIVSAQNLLKLISNFSKVGYSYKINVQKSQAFLYTNNRQTESQIMSELPTIASKRKLYQLIQLTRDVKDLFLKENYKPLLKEIKEDETNWKKNIPCSWGRINIVKMAILP RIDIQW/NRTEPSEIMPHTYNYLI FDKPEKNKQWQGKDSDLFHWC WENWLA VCRKLKLLDPFLPTYT KINSRWIKDLNIRPKTICKTLEEN LGITIQDYGVGKDFMSKAPKAMATKAKIDKWDLIKLKSFCATA ETTIRVNQPTTWEKIFATYSSDKGLISGIYNELKQIYKKKTNNPICKWA KDMNRHSKEDIHAACKHMKKCCSSLAI REMDIKTTMRYHLTPVRMAIIKKSGNNRCWRGCGEIGTL
7836	38204	A	7891	I	1932	

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7837	38205	A	7892	1	2347	MELKTKARELHDECTSLSRRFD QEERVSVMEDEMNEMNLPTK KSPGPDGTAEFPYQRYKEELVP FLLKKLFSQSIEKEGILPNPSFYEPSII IAKPGRDTTKKENFRPISLMNI NAKILNKMLANQIQQHIIKKLIIH HDQVGFIQPGMQGWFNIRKSINV IQHINRTKDKNHMIISIDAEKAF DKIQQQHFMPLKTLNKLVLLEVLA RAIRQEKEIKGIGQLGKEEVKVSL FADDMMIVYLENPNTVSAQNLLKL IGNFSKVSGYKINVQKSQAFLY TNNRQTERQJMSELPTIASKRI KYLGIGLQTRDVKDLFKENNPL LKEVKEDTNEWKNCIPCSWVGRI NIVKMAILPKVIIYRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVTKTAWWWYQNRDIAQ WNRTEPSEIMLHIYNYLIFDKPE KNKQWGKDLSFNKCWCENWL AICRKVKLDPLTPYTKMNSR WIKDLNVRPKTIKTLEENLGITI QDIVGVGKDFMSKTPKAMATKA KIDKWDLIKLKSFCATAKETTIRV NRQPTTWEKIFATYSSDKGLISR IYNELKQIYKKKTNPPIKKWAK DVNRHFSKEDIYAAKKHMKCC SSSLAIREMQIKTTMRYHLTPV RMAIIKKSGNNRKIQ/GGIWCD RIL*R*TTCRVAKEIQSQL*RRJ/W KRLQRTLSIPVLDAV*PPMF*AS
7838	38206	B	7893	1	1710	
7839	38207	B	7894	1	2265	
7840	38208	B	7895	1	2142	
7841	38209	A	7896	1	1791	
7842	38210	A	7897	1	1878	
7843	38211	A	7898	1	2091	

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7844	38212	A	7899	1	1751	MIISIDAEKAFDKIQQQPFLKTL NKLGIDGTYFKIRANYDKPTA NIILNGQKLEALPLKNGTRQGC PLSPLLFNTVIEVLARAIRQEKE IKGIQLGNVEVKLSLFAADDMIV YLENPIVSAQNLLKLISKFSKVS GYKINVQKSQAFLYTNRRQTES QIMSELFPFTIASKRKYLGQLTR DVKDLFKENYKPLLKEIKEDETN KWKNIPCSWVGGRINIMKMAILP KVIYRFNAIPIKLPMPFFTELEK TTLKFIWNQKRARIAKSILSQK NKAGGITPPDFKLYYKATVTKT AWCWYQNRDIDQWNKTEPSEI TPHIYNYLFDKPEKDQWGKD SLFNKRCWENWLAICRKLKLD PFLTPYTKINSRWIKDVKVRPKT IKTLQENLGFTIQDIGHMGKDFM SKPTAMGTKDIDKWDLILK KSFCTAKETTIRVNQRQPTKWEK IFTTYSSDNLISRIYNELKQIYK KKTNNPIKQWAKDMNRHFSIE DIYAAKKHMKKCSSSLAIREM QIKTTMRHYHLTPVRMAIIKKSG NNRNHLDFKHIRILGICYL/D*KI YQP*LHLVSRNRKPEKLSPKQA

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7845	38213	A	7900	I	2540	MGDFNTPPLSLDRSTRQVKNK DTQELNSALHQPDLDIYGTLLHP KSTEYTFFSAPHHHTYSKIDHLG SKALLSKCRTEIIITSYLSDHSAI KLELRIQNLTNQNHSTTWKLNNL LLNDYWHLHNEMAKAEIKMFET NENKDITTYQLNLWDAFKAVCR GKFIALNAHKRQERSKTNTLT SINKIDRPLARLIKKKREKRTQID AIKNDKGDITTDPTEMQTTEIRE YYKHLYANKLENLEMMDKFLN TYTLPRLNQEEVESLNRPIITGAE IAVAIINSPLTKKSPGPDGFTADEFY /HELIKENKIPRNPY/RGCEGP LQGELQTTAQ*NKRGYKQMEES HSMLMDRKKNQYRENGHTAQG NLQIQCHPHKATNDFLHRSGKN YFKVHMEPKKSPHRQVNPKPK EQSWRHHA!*LQTILQGYSQNQN SMVLVPKQRYRSMEKNRALRN NAAYLQLSNL*QT*EKQAMGK GFLI**MVLGKFLASHM*KAEYG SLPYTLYKNQFKMD*RLKH*T* NHKNPDRKPRHYHSGHHRHGQQ LHV*NTKSNGNKSQN*QMGSN *TKEPLLHSKRNHYHQSEQATYKL GENFCNLPI*PRANNQNQLQ*TQ TNLQEKNKQPHQKVVGKGHEQT LLKRRHLCSQKTHEKMLSITGH QRNANQNHNEIPSHTS*NGNH* KVRK*QVLNGLDDVQLFR*NK QPCCSHKA CLVVSSYRA*SLV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met codon	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * =Stop codon, - =possible nucleotide deletion, + =possible nucleotide insertion)
7846	38214	A	7901	1	1593	MGKKQRKTGNSSKKQSTSPPP KERSSPAMEQSWMENDFVEL REEGFRRSNYSSELQEDIQTKGK EVENFEKNLEECMTRITINTEKC LKELMELTKARELHEECRSLR SRCDQLEERVSAMEDEMNEMK REGKFREKRKIKRNEQSLQEIWD YVKRPNLHLMGVPESDGENGS KLENLQDIQENFPNLARINKI DRPLARLKKKREKNAQIDTICKN DKGDITTNPTEIQTTIREYYKHL YANKLENLEEMDTFLDTYTLPR LNQEEVESLNRPITGAEVIAINS LPTKKSPGPDGSIAEFYQRYKE E/PADKQLQQSLSIQNQCTKITSI LIHQQTNTREPNE*TPIHNCFK ENKIPRNPTYKGCEGLLPGELOQ TTAOGNKRGYKQTEEHSMLM GRKNQYRENGHTAQGNF*QC HPHQATNAFLHRRIGKNYFKVH MEPKKSPPHRQVNPKPKEQSWR HHTT*LQTILQGYSNQNSMVLV PKQGYRSMEONRALRNNAAYL QLSDL*QT*EKHAMGK/EFPI**
7847	38215	B	7902	1	2337	
7848	38216	B	7903	1	1677	

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7849	38217	A	7904	1	1722	MAGYPSEMKLPEELSGSNCCS AVFTVLQLPLLI PRQTGSGV р RQTPTDQLRLVTVRKRNKNQ KRTSTPKPHLYVTHKDQRSKKL TQNHS TTWKLNNLLNDYWW NNEMEKAIEKMFETSENKGTYI QNLWDITFKAVCRGKFIALNAH KRKQERSKIDTЛTSQLEKEQ EQTHSKASRRQEITKIRAEQKEI ETQKTLQKINESRSCFFEKINKI DRLLARRIKKKREKNQIDAQN DKGDITADPTEQSTIREYYKHL YTNKLENLEEMDKFLDTYTLR LNQEEDESLNRPITGSEIAIJNS LPAKKSPGPDRFTAЕFYQRYKE ELHINRTKDKNHNMTISVDAENA FDKIQQPFMLKTLNKLVLVEVLA RAIRQEKEIKGIGLQKGEVQLSL FADDVIVYLENPIVSAQNLKKL SNFSKVSGYKINVQKSQAFLYS NNRQTESQIMNNELSFTIASKRICK YLGIQLTRDVKDLFKENYKPL NEIKDDTNKWKNI PCSWVGRIN IVKMGILPKVVYRFNAPIKLP TFFTELEKTTLKFIIWNQKRARI AMTILS* KNKAGGITLP
7850	38218	A	7905	1	2310	
7851	38219	A	7906	195	791	GILSFAKDMNRHFSKEDIYAAK KHMKCKSSSLAIREM0IQTMR YHLTPVRAIIKKSGNNRCWR GCGEIGTLLHCVLDCKLVQPL WKSIVWRFRLDLEIPFDPAIP LGIYPN ЕYKSCCYKDTCRMFI AALFTIAKTWEPPKCSNMIDWI K/KMWH/IYTRDTMRPKNDEVO SLVG/TWVNWETTFSVTIAVQK PTRLSH
7852	38220	A	7907	1	984	
7853	38221	A	7908	1	2076	
7854	38222	A	7909	1	1872	
7855	38223	B	7910	1	3309	
7856	38224	B	7911	133	3213	
7857	38225	A	7912	1	1364	
7858	38226	A	7913	1	3249	
7859	38227	A	7914	1	2757	

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7860	38228	A	7915	1	2268	MAGYPSETKPPEERSDNICSSA IFTVLHPPLLIPRQTAFGMDLQQ MPTDQLRLVLTVKRKTNKQKG HPHQNPIRTSPSSKTEDFQPTKI KRDKEGHYIMVKGSIQQEELTI UNIYAPNTGAPRFIKEVRLDLQ RDLDSDHTIMGEFNTRLSTLDRS MRQKVNKD^QELNSALHQADL IDISRNLLHPKSTEYTFFSAPHRT YSKIDIHIVGSKALLSKCRTEII TKCLSDHSAIKLELRKNLTQNC STTWKLNNLLNDYWWHNEM KAEIKMFFETSENKDITTYQNL WDTFKAVCRGKFIAHNAHKR QERSKTDLTSQQLKELEKQEQQT HSKASRRQEITKIRAEQIEETQ RTLQKISERSRSWFKEKINIKIDRS LARLIKKKREKNQIEAIKNDKG DITTPNPIETQTTIKEYYKHLYK NKLENLEEMDKFLNTYTLPRLN QEEVESLNRPITGSEIVAINNSLP TKKSPGPDGFTAEFYQRCKEEL VTFLLKLFQSIEKEGILPNSFYE ASINLIPKPGRDTTKEENFRPISL MNIDAKILNKILANRI/WGN*AE ERNKEYSIRKRGSQIVPVCR*H DCVSRKPHHLSPQSP*ADKQLQ QSLRIQNQCTKITSILIHQ*QTNR EPNHE*TPIHNCFKENKIPRNPT YKGCEGPLQGELOTTAO*NKR GHKQMEEHSMLMDRKNQHRE NRHTAQGNL*IQCCHSHQATNDF
7861	38229	A	7916	1	4729	

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7862	38230	A	7917	1	2685	MGDFNTPPLSLDRSTRQVNK DTQELNSAPHQADLIDIVYRTHL PKSTETYFFSAPHTYQSKTDHIL GSKALLSECKRTEIIITNYLSDDS AIKLELRIKNLTQRNSTTWKLN NLLDDYWVHNEMKAEIKMF ETNEKDFTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQLKELEKQEQTSHSKASRRQ EITKIRAEELKEIETQTKTVQKINES RSWFPERINKIDRQLARLIKKKR EKNLIDAIAKNDKGDIITDPTEIQ TTIREYYKHLHYANKLENLEM DKFLDTYTLPRLNQEVEVESLNR PITGESEVAIIINSLLTCKSPGPDG FTAEFYQRAIRQEKEIKGIQLGK EEVKLISLFADDMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPTIA SKRIKYLGQLTRDVKDLFKEN YKPLLKEIKEDETNWKNICPSW VGRINIVKMAILPKVIYRFNAIP KLPMTFFTELKTTLNFIWNQK RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQNR RTDQWNRTPESEIMPRIYNL IFDKPEKNKQWGKDSLNFNKC WKNWLAICRKLKLDPLFTPYT KINSRWIKDLNIRPKTIKTLNEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLKSFCTAKE TTNRVNRQPTKWEKIFATYSSD
7863	38231	A	7918	1	1205	
7864	38232	A	7919	1	2274	
7865	38233	A	7920	1	2307	

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7866	38234	A	7921	569	3030	RKH*TWKR ^T SSTSHHKMPN* LEKQEQ ^T TH/SKP ^S RR ^T EITKIRA ELKEIETPKTAQK ^T INESRSWSE RINKIDRPLARL ^T RKKKREKNQI DTIKNDEGDTT ^T HPT ^T EIHTIIREY YKHLVANKLEN ^T EEMDKFLDT YTLPRPNQEEVESLN ^T GPIAGSEI QAIINSPLTKKSPGP ^T DGFYQRYK EELVPFRLKL ^T FQSIEKEGLPNSF YEASII ^T LIPKPG ^T RD ^T TTK ^T KENRP ^T I SLLNINAKILNK ^T ILANR ^T IQWHIK KLMHDHQVG ^T FIPGMQGWFNIR KSINVQHINR ^T TKDKN ^T HMIISID AEKAFDKIQQPFMLKT ^T LNKLGI DGT ^T YHKIJR ^T ANYD ^T KPT ^T AN ^T ILNG QKLEAFPLKTG ^T TRQGCPLSP ^T LL FNI ^T LEV ^T LAR ^T AI ^T QE ^T KET ^T EGIQL GKEEV ^T KL ^T SLFADD ^T MIVYLENPI VSAQNL ^T LLK ^T LSNF ^T SKV ^T SGYKIN VQKSQVF ^T LYTDNRQTESQI ^T SEL PFTIASKR ^T IKYLGIQLTRYV ^T KDL FKER/VNEIKE ^T DTNKWKN ^T IPCS WVGRINIV ^T KMAILPKV ^T VIYRFN ^T AI SIQLPM ^T FFTELEK ^T TLKF ^T FIWNQ KRAHI ^T AKSILSK ^T KNKAGGIMLP DFKLYYK ^T ATVT ^T KTAW ^T WHWYQN RDIDQRN ^T RTEP ^T SEIMPHVYNH ^T I FGKPD ^T KNQ ^T WGND ^T SLFN ^T WC WENWLAICK ^T KLKD ^T PFLTPYT KINSRW ^T IKD ^T LNVR ^T PKT ^T IKTLEEN LGNNI ^T QD ^T IGMG ^T KDFT ^T SKTPKA MATKD ^T KID ^T KWDL ^T MKL ^T KSFCTA
7867	38235	B	7922	1	3171	
7868	38236	A	7923	1	2646	

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7869	38237	A	7924	321	2211	CCQFSMARRGHLPRLSVPVQSVIPG QSPVPRAAAYQDGSRYKEPTAD C/VGPRQT*CMAPHCILGGWH MLALSLGKAGAGGKESTWEP SPGIRMTKTYSSTRREQSHPRTI/ KGQIKQMNLRETCWSFTHKKF LKTVAFQISHPHKNTCLAMAVS ANRSMRQKFNKDTQELNSALH QVDLIDIYRTLHPKSTEYTFPSA PHHTYSKIDHILGSKALLSKCK RTEHTNYLSDHSAIKLELRKLN TQNRSRTWKLNKLNNLYWV HNEMKAIEIKMFFETNENKDTIY QNLWDIAFKAVCRGKFIANAH KRKQERSKIDTLTSQALKELKQ EQTHSKASRRQEITKIRAELEK ETQKTRQKINESSSSWFFEGINKI DRPLARLIKKKREKNQIDTIKN YKGDIITDPTEIQTTIREYYKHL YANKLENLEEMDKFLDTYTPL RLNQEEVECLNRPITGAEVIAII NTLPTKSPGPDGFTADEFYQRC SRWIKDLNVRPKTIKTLEENLGI TIQDIGTGKDIMS KTPKAMATK DKIDKWDLIKLKSFCTAKETTIR VNRQPTKWEKI FATTYSSDKGLI SRIYNELKQIYKKKSNNPIKKW AKDMNRHFSKEDIYA AAKKHM KKRSSLAIREMQIKTTMR
7870	38238	A	7925	1	3057	
7871	38239	A	7926	1	1830	
7872	38240	B	7927	1	3192	
7873	38241	A	7928	1	3484	MGTSEVQNGEERAGTSGQGSV EQLSGSSVQLPGLKLCFPYFS SCASDCILHASPLSLMAASGSQ NPNLWASWLCKWVQCPERQ LGCHLTSSVIYGLRYYPQAKRS ELELRDCEGLCNQTSPLSSLDG MGWKA AAEESNSGIRNIWIPIP AFATHKQYNVRQVISPPSYWS HRGNGNNSLCVTRLSSGLKQP VAGTG RGLLEGGS GTRDLM PFL SAAPKEQPPILAPARRSWFFEKI NKIDRLLARLIK KKRE

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7874	38242	A	7929	I	1946	NLTQNRSTTWKLNNLLNDYW VHNKMKKAЕIKMFFETNEKNKT TYQLWLWDTFKAVCRGKFIALN AHKRKQERSKIDTTLTSRKLE KQEQTSHSKASRRQEITKIRAE KEIETQKTFQKVNESSSSWFFERI NKIDRPLARLKKKREKNQIDAI KNDKGYIITDPTEIHTTIREYYK HLYANKLENLEEMDKFVGTYT LPRLNQEEVESLNRPITGEIVAI INSLPTTKSPGPDGFTAECFYQR KEELAGRDTTKKENFRPISLMN IDAKILNKILANRIQQHHKKLIIH HDQVGFIPGMQGWPNICKSINV IQHINRFTKDKNHMIISIDAEKAF DKIQQPFLMLKTLNKLVLVEVLAR AISQEKEIKGIQLGKEEVKLLSF ADDMIVYLENPIVSAQNLLKLIS NFSKVSGYKINVQKSQAFLYTN NRQTESQIMSELPLFTIASKRKY LGQLTRDVVKDOLFKENYKLLSK EIKEDTNWKWNIPCSWVGRINI VKMAILPKVIYRFNAIPIKLPMT FFTELEKATLKFIFWNQKRARIA KSILSQKNKAGGIPLPDFELYV KTTVTKTAWSYQNRDIDQW NRTEPEITPHIYNYLIFDKPEK NKQWGKDSLNFNKWCWENWLA ICRKLKLDPFLTPTKINSRWIK
7875	38243	A	7930	I	4801	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFSFAPHHHTYSKIDHIL GSKALLSKCKRAEIITNYLSDHS AIKLELRKNLTQSRSSTTWKLN NLLNDYWVNNEMKAEIKMF ETKENK\DTTYQNLWDASFKA CRGKFIALNAHKRKQERSKIDT LTSQKLEKEQEQTHSKASRRQ EITKIRAELEKEIETQKTLQKINES RSWFFERINKIDRPLARLIKRR EKNQIDTIK

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7876	38244	A	7931	1	3146	MGDFNTPLSTLDRSSRQKVNK DTQELNSTLHHADLIDIYRTLHP KSTEYTFPSAPHHTYSKIDHV GSKALLSKCCRTEIITNCLSDHS AIKPELRIKKLTQNRTTWKLN NLLLNDYWVHNKMKAEIKMFF ETNEKDTTYQNLWDTFKAVS RGKFIALNAHKRKQRCKIDL ASQLKEVEKQEQTSHSKASRRQ EITKIRAELEKEIETQTLQKINES RSWFLERINKIDRPLARLIKKKR EKNQIDVIKNDK
7877	38245	A	7932	1	2669	MHINTDGNRFLSHWGVYRQALSI SKPASASLHPSSKTKPLGTQSKT VVAKRNREHGKKERSSPAME QSWMENDFDELREEGFRRSNY SELREDIQTKGKEVENFEKNL ECITRINTEKCLKELMELKTK ARELREECRSLRSRCDDQLEERR KQERSKIDTSQLKELEKQE THSKAGRROEQITKIRAELEKEIET QKTLQKINESRWFFERINKIDR PLARLIKKKREKNQIDTIKNDK GNITTDPTEIQTITIREHYKHLYA NKLENLEGMDKFLDTYTLPR NQKEVESLNRPITGSEIVAINSL PTKKSPGPDGFTADEFYQRYKEE LHINRAKDKNHMIISDAEKA DKIQQPFPMLKTLNKLVLLEV AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLKLL SNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSELPTIASKR YLGQLTRDVHKLKFKENYKPLL KEIKEDETNWKWNIPCSWVERIN IVKMAILPKVIIYRFNAIPIKLPM TFFTELEKITLKFIWNQKRARIA KSILSQKNKAGGIPLPDFKLYY KATVTKTAWSYYQNRRIDQW NRTEPSEILPRIYNYLIFDKPEKN KQWGKDSLNFKWCWENWLAI CRKLKLDPLKPYTKIKSGWIK DLNVRPKTIKTLEENLGIHQDI GMGKDFMSKTPKAMATKAKID

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7878	38246	A	7933	I	2962	MNNSIKEVKVLSLTWKEMMQTK PNNNTVVLKDAQEVNLSTTDY RKQHVMLPTEINSDSLLKIGV1 RLANWIKSQDPVSVCNQETHLT CRDTHRLKIKGWRKIYQANGK QKKAGVAILVSDKTDFPKPTKIK RDKEGHYIMVKGSIQQEELTIL NTYAPNTGAPRFIKQVLSLDRQ DLDSTVTLIMGDFNTPLSTLDRS TRQKVNKDTQELNSALHQVQL IDIYRTLHPKSTEYTFFSAPHH YSKIDHILGSKALLS
7879	38247	A	7934	I	4220	MGDFNTLLSALDRSTQKVNK DIQELNSALHQADLIDYRTLHP KSTEYTFFSAPRHTYSKIDHLV GSKALLRKCRTEIITNCLSDHS AIKLELRRIKLLTQNHSSTTWQLN NLLLNDYWVHNEMKAEIKMFF ETENKDTTYQNLWVVKDTRI SGMLWVYKAVCRGKFIHALNAH KRKQERSKIDTLLTSQKLEKEQ EQTHSKTSRRQEITKIRAELEK ETQKTLQKINECRSWFFEKINKI DRPLARLIKKKRE
7880	38248	A	7935	I	3229	MGKKQNRTGTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTKGKE VENFEKNLEECITRITNEKCLK ELMELEKTKARELREECRSLRSR CDQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLLRIGVPESDVENGTKLE NTLRDIIQENFPNLARQANVQIQ EIQRTPORYSSRRATPRHIIVRFT KVEMKEKMLRAAREKDRSTRQ KVNKDTQELNSA
7881	38249	A	7936	I	3227	MGDFNTPLSTLDRSTQKANK DTQELNSALHQVLDIDYRTLH PKSTEYTFFSAPHHHTYSTDDHIL GSKALLSKCRRTIEITNYLSDHS AIKLELRRIKNLTQNRSSTWKLN NLLLNDYGVHNEMKAEIKMFF ETENKDTTYQNLWDAFKAV CRGKFIHALNAHKRKQERSKIDT LTSQKLEKEQEQTHSKASRRQ EITKIRAELEKIEQTKSLQKINE SRSWFFERINKIDRPLARLIK REKNQIDTIKN
7882	38250	B	7937	I	2089	

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7883	38251	A	7938	I	3527	MELKTKARELREECRSLRSPCN QLEERVSAMEDEMNEKMREG KFRDKRKIRNEQSLIQLIWDFVK RPNLRLIGVPESDGENGTKLEN TLQDIIQENFPNLARQANIQQEI QRTPQRYSRRATPRHIIIVRFTK VEMKEKMLRAAREKAPHHTYS KIDHILGSKVLLSKCKRTEIIJTN YLSDHISAIKLELRKKNLTQNHST TWKLNSLLLNDVWVNHEMKA EIKMFETNEKDITTYQNLWD TFKAVCRGKFIALN
7884	38252	B	7939	I	5238	
7885	38253	A	7940	I	3587	MENDEDELREEGFRRSNYSEL WEDIQTGKGEVENFEKMLEECI TRITNTEKCLKELMELKTKARE LHEECRSLRSRCDDQLEERVSAM EDEMNEMKGEGKFREKRIKRN EQSLQEIJWDDYVKRPNLHLIGVP ESDGENGTKLNTLQDIIQENFP NLARQANVQIQLIQRMPQRYSS RRATPRHIIIVRFTK VEMKEKILK AAREKDRSTRQVKVNKTQELN SALHQADLIDLIDLIYRTLHPKS TNEYTFFSAPHHT
7886	38254	A	7941	I	6202	MVKGSIQQEELTILNIYAPNTG APRFIKQVQLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQVKVNK DTQEELNSALHQADLIDIYRTLH LKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIIYNLSDHS AIKLERLIRKNLTQNRSTTWKLN NLLNDYWVHNKMKAEIKMFF ETNENKDITTYQNLWDFAKAV CRGKFIAYAHWRKQERSKM DTLTSQLEELKLEQTHSKASR RHEIAKIRAEKIE
7887	38255	A	7942	2	3134	WRKIYQANGKQKKAGVAILVS DKTDKFPTKIKRDKEGHYIMVK GSIQQEELTII.NIYAPNTGAPTFI QQVLSDLQRDLDSHTLIQDFN TPLSTSDRSTRQVKVNKTQELN SALHQADLIDIYRTLHPKSTEY FFSAPHHTYSKIDHILGSKALL KCKRTEIIYNLSDHSIAKLEM IKNLTQNHSTIWK1.NNLL.LNDY WVHKEMKAEIKMFFETNEKND TTYQNLWDTFKA VCRGKFIAK NAHKRKQERS

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7888	38256	A	7943	1	4455	MELKTKARELREECRSRLSRNN QLEERVSAMEDEMNMENKREG KFREKRKRNEQSLSQEIDWYVK RPNLRLIGVPESDAEFGNTKLEN TLQDIIQEDFPNLARQANVQIQE IQRTPQRYSSRATPRHIVRFT KVEMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQEEEL TILNIYAPNTGAPRFIKQVLSLDL QRDLDSHTLIMGDFTPLSTLDR RSTRQKVNKDTQELNSALHQAD DLMDIYRTLHPJKS
7889	38257	A	7944	1	6108	MTGSNSHITLTLNINGLNSAIK RHRLASWIKSQDPSSVVICQETH LTCRDTHRLEIKGWRNQYQANG KQKKAGVAILVSDKTDKFPTKI KRDKEGHYIMAKGSIQEEELTI LNIYAPNTGAPRFIKQVLSLDQ RDLDSHTLIMGDFTPLSTLDR STRQKVNKDTQELNSALHQAD LIDIYRTLHPKSTEYTFSSAPHH TYSKIDHIVGSKALLSKCRTEIJ TNYLSDHSAIKLELRKKLTQN RSTTWKLN
7890	38258	A	7945	2	788	CGLAIYNCTIVDLHFPLALYKK LLKKKPSLDDLKELMPDVGRS MQQLLDYPEDDIETFCLNFTIT VENFGATEVKELVLNQGADTA NKQNRQEFVDAYVDYIFNTSV ASLFRCFSISGFHKVCGGGKGLR LFQPNEILQAMVIGNTH*WKG TGKDYRNTKGNIWAEHPTIKIF WEVFHIELPLEKKKIRFLLFLTG SIDRIPILGMKSLKLVIQSTGGG E>EYLPVSHTCFNLLIDLPKYTK KETLRS*T'SQAIDHNEGFSLI
7891	38259	A	7946	1	1647	
7892	38260	B	7947	363	550	
7893	38261	B	7948	1	1123	
7894	38262	A	7949	1	3136	MVTHQQPAARKPNMTSKPKP MGPKAHGIFSCTRKNNLEIYMD QTRTGIAKTKLSKNNKSGGMT LPDFKLYYKAIVAKIAACGGSMY NSDTDEDEETEPSSSGQQHIENSI TMNKMKLLKAKMKNMNLSSKK HITQVSDEEEDDGCDLFADSE KEEKDIEDIEENTRPKRSRPTSF ADELAARIKGDAVGRVDEEPTT VSYEDDRRGKQNQDAYTEEGGLS TIKTVCNCSSSLTRRSKTSEDTQ EKKERRTPSDDEED

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7895	38263	B	7950	303	1010	
7896	38264	A	7951	3	280	
7897	38265	A	7952	3	514	FYLKELDPAEHSYVLIRKIDPAL VWGLTGDQGTPKTRLLMITLD SIFMQASCVPPEEVVWEVLRVLE AHSSKKKHVFVFGESMKLITKAS VQQEYLVHK*VSHSNPTLYVFL WGLSKETRQMEVPEFVAKVN THPSSFSVGSK*GI*EKEGGRYP VPEMGSCRIVTVTSASV
7898	38266	A	7953	2	351	
7899	38267	A	7954	2	529	EKGERPHWSNKPSNLKRTHEL DIDENPASDFDDSGSLLGFKYG SGQKYGGIPYFSHRQVR**EKN VKLAKAYLNMRGQIKMKNKHI FFTKETEKPFFKSKILSKVEKF LTWVNPKMDDEAQSSESSHND GHDASTSCDSEEQDMSSVKKG DLLETTNNPEPEKCGQSVSAGEL
7900	38268	A	7955	1	1370	MPVGTNSFLLLGLLENPNPLPT RSPFPSPSQREASWGIQKATTGP GEGETRLGFSLLLVDVFCALHG PREKCEVILRSGHLLAISPGVVR EALISDETYNIVVWGHHRGFAQV AIDAKVVEKFLTWTNVNPKPMDDE ASQESSSHDNVHDASTSSDSEE QDMSSVKGDDLLETNNPEPEK CQSVSAGELETENEYERDSL TVPDEQDCVTQEVPDSRQAETE AEVKKKNNKKKKVVNGLPP IAAVPELAKYWAQRYRLFSRFD DGIKLDREGWFSTPEKIAEHIA GRVSQSFKCDVVDAFCGVGG NTIQFALTGMVRIAIDIPVKIA LARNNAEVYGIADKIEFIGDFL LLASFY^KADVFLSPWGPDY ATAETFDIIRTMMSPDGFIEFRLS KKITKNNIVYFLPRNADIDQVAS LAGPGGGQVEIEQNFLNKKLKT TAYFGDLIRRPASET
7901	38269	A	7956	3	560	RIHTGEKPYDCKDCGKAFGRTS ELILHQRLHTGVKPYECKECGK TFROHSQSQLILHQRTHTGEKPYV CKDCGKAFIRGLQLTVHRRHI GARPYGVLCKGESLDDSTS* LLHQRIHTGEEPYECKECGKG FIHSSEVTRHQRJHSGEKPYECK ECGKAFRQHAQLTRHQVRVHTG DRPYESAED

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7902	38270	A	7957	155	1288	HTTASQTTMSQAV/RRRSDYL SSARR/RDPPARSKPTQGGPPPN PPTRQRPTALTNPSPQRPRH AHPHQHATPKPRTNEEQEGR HTKQPNNPRTTEPRPPNRRGRPN PQTRRTKQONTTPQAHTSTRKN ARTPGLCP^CVKGKTEGGYDA RASARGPYMAGVSWPGEHEDP GAPEARRGRRALPGIGSAPEM STHTESTPKTTAHTSNDRRNRE QRVKKKTYKTRSRGANRNST ERHEDGYFYGSLLTGPLPWHS IHSVSAQGPWSLKFTVTGLQQAS EGYFSQSQERSLPRNKSSVPRLR LLFLQQASRLSELPLGTGPGSL LLRPREEELACTGKRRKTGGAIM GEVSVCCELSLPAPAFQSPVQLC GCQPEKA
7903	38271	A	7958	1	2045	REAAAATPSFPSSSSVRPSVRAS VRSARSGPKHGRRLQLQRPPP /RWRLTRR*SERRARPGLCLTH MKMAPMTSSLQHQEKGACRSF RDTLRTRRCTASA VSRTPKIRS AKIRAHQLGGRRCA*CPVQRLC QPRG*GGRVLPGCRRDRERQ RGRHRRGCHRAAL*RAGATL QPCAAPTAAARG*ER/SSPAPP TRRRMQLWK*SGLTTESSSGSRP RRKKSCGRRRSRGPWMRGSG SSRGWSRSRSRSKRSASGATGS GSSRSRSTGGNSRL*KRKPRG G*RSSSLVТИGMRKRPT*RSQ SRRWRRQQLLLPSGLTTQGSSS SSRKESHRPLRAAVMYPRPSTI DQAATWTATGGWRPLPSRGA RLTPAPPPLSLSR*SGPWMRSPR P/PQPPPLPPPPPPKPRPRSPAPS* TVRRPEQQPLRPGPAPWRSPLR HRRLPGGQAQLQT*CSWLSQS RLSWLLPWSLPQLTPRSTMQL TPLKLTLPLLTPLLPTTYPFFFF SLTYGLATGKGPBHSRVSPP RHPRVLRSPWQRCPWCWRWL RSHCCQQAKAVPPFSTLMSCS RQPSPSVQRKWKGSPWLPPRQ LCPQPLRSWSKSRSRSPTC*PM ARPRRRGPRPSEGYSQSQEEE FAQSEELCAKAPPVFYNKASE NVIIHMLGCRPSSRRGGGLRGW
7904	38272	A	7959	3	174	

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7905	38273	A	7960	3	862	GVMASRTL LLLL GALALTET WAGTHISIRYFSTAVSRPGRGEP RYIAVG YVDDTQFD AATPRM* PQSPWLE QEQGPEY WDSTRNIR PAHRLTRVNLPMPM PRRYYHQS* AGTGIFHGIRY/ YIPDTCVQTHM IHHSVSDYKATLRCW ALGFYP VEITLAWQ\ QDEEDQ\ TRDHE\ \ VETRPAGDGT FQK WAAVVVPS GQEQR YTCHVQH EGP KPKPLTL RWEPSQPTIPIV GIIAGL VLFGA VITGAVVA VAM/ WQEEELRTFS SHR^ SELT SERASS DH AQGS DV SL TACKV
7906	38274	A	7961	1	591	MVTDV AIELFLQ ASL ILLS STLP YNEREM GLS IF ALL TLTV FLLL ADKV PET SLP VPII KYLM FT MV LVTFSVIL SVVVL TLH HRS PHTH QMPLL VPS DLSL HS QTS AVP ASKK AQT RER PDAGA PSL FFS RKWL G YIARQL QEQE HD/VA EGG LAV CGH GSG PPL PVDF HHL HQR WD PSHL PG R HVPL A PSRPL S
7907	38275	A	7962	1519	1888	ILKHPTLD KEI LITYLF IYLF IFL RRNF TLVA* ARVQWC DLAPPQ PLSPGFKPF SCLR FPSSWD YRYA PPY LANF VFL VGTGF SML VRL VSNSRPQ/CDPP PAS ASQAG ITG VNHH A\ RIT FN F
7908	38276	B	7963	280	1977	
7909	38277	A	7964	994	1651	CRGSQP APP LTPH PPNAP LGPSD LH SQTS A VP ASK KA QTR /GD LM PEPPHCSSPGSGW GRGT DEY FIR KPPS DFLFP KPNRF QPEL SAPDL RRFID/VSKPGCGPASG ATGGIV SSIS YIARQL QEQE HD/VA EGG LAV CGH GSG PPL PVDF HHL HQ RW D PRSSW SHVLA PSRPL S KT GGL R PGP LPV E VREF GDT VK PYPSLPLNS FTRNL GLL FRSG

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7910	38278	A	7965	10	533	DEVSLCCQAGVQLHDVGSLQT ASQVQAILLPOPPEVAEISGACH HACLFVFLVEMGFHHIQAGL KLPPTSGDL PASASQSAGITGVGS HRARPASSYLF**DEVSLCCQ AGVQLHDVGSLQLPPLPRFKRFS C\PASRSS*DFRRLPPLPNFCIF/ M*RWGTILARLVNSRPO/CD LPASASQSAGITGVSHRARPASS Y\CIFFLRWRLTIAQAV**CNL SSLQPPTPGFKWVSCLSLPSSW DYRSLPLLPANFCIFS RDGVSLC SLSWSRTPDFK
7911	38279	C	7966	312	467	
7912	38280	A	7967	31	678	TGLYFLFLFCLRRSLA/SVAQPG VQWRDGLSQLPAPPGLRRFSFL SLQSSWEYRCPLPRPADFLYF*S RRGFSTLVRI.VSNSRPQ/CDPPA SASOSAGITGVSHCARLFFSFE MEFRSVAQAGVQWRDLDLSQL PLPPGVLT*FSCSLSPRLGAA/WD YRRVPVCPAIFC/IFFFFSRDRVS PCWWSQTPDPQVIRPPRPSQ SAGITGVSHARPSHIS
7913	38281	A	7968	23	99	YIMI1GPGWRPL*TGHPHPT WPGGSSSHHQIPHRPCVFG
7914	38282	A	7969	144	1239	ERTEPDH/TITLTH*P/ELPADTTA TVEDMLPSVTSVTNTSDTITETF ATAQYILTSETTLTSSIAAPPAT ATPDNSVPAGQATPSKGPSAS APSPAPASAPKVAPLVLDSDTP TSTPAASNLSSSVLANQQGAVLS PSAPAGVGEASKAPPASKPTPA PVPTPTGAASPLAAAAPATEA PQAKQEAPSTKGPDPPEPTQPGA AKSFAEAATALASPKSEAASVS TTNPSQQGEDFKMDEGNFKTPDI DLAKDVF AALGSPAPAAGASG QAPELAPSTADSSVSPAPAKTE YGLLSA VIGLCPVVSGWEDSG LPSIKWLGLKVQEKG LNLNSGK NTASGINLGLEEERTRSSDSVLL NYGC TLESGLCF
7915	38283	A	7970	3	375	ARQAMKSCLHQCFLLP RQAL EASSCNSTG WGGEGTGKSGLQ RG P*NQCWEPS PAQQAAFTSS* AVATAAGQGEELPLLPPSTTP GKNTASGINLWLEEERTSSDS VLLNYGCTLKSLACF

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7916	38284	A	7971	1	2230	MFEASVGWFMRLLEERTRLHD QAQDEAVTADLEAAAGYPDLA KIIDEGGYTKQQIFSVDDTAFS WKKMTRLTFIAKEGTNTDGS SATSSLVSLCLELCFLRAHHDV GFYCDLDVYQSAVYAPTCPTG YSLPQAKEESDFIPLEYEKGKRIT STAGQQGDVEPEMEQLEKGSIK GVTETRTGPLGCSNYNDLDSVS SVLVQSPENKVQLLGQLVILP YLRRERFVAALSYTCSSEGE VCKENDCWCKCSCPFPCECNCPD ADIQAMEDSLLQIQDSWATHN RQFESEEFQALLRKLPDDRFL NSTAISQFWAMDTSLQHRYQQ LGSWL^KVLFKKTHRILRRLFN LCKRCHRQPRFLPKERSSLYW WNRIQSLLYCGETFPGTFLEQS HSCTCPYDQSSCQGPICPA GPACAHCAPDNSTRCGSCNP YVLAQGLCRPEVAESENFLGL ETDLQDLELKYLQKQDSIREV HSIFISNDMRLGSWFDPWSWRKR MLLTLSNKYKPGLVHVMLAL SLOICLTKNSTLVEPVMAIYVNP FGGSHSESWFMPPVINEGQFSL TW\ERTNVDAAA\QCQNW HLGGIRWKTFETVHVYLSR IKSLDDSSNET\YYEPLEDDWIP LRNLGYVMKINTL\QVFGYSLPF DPDIAIRDLILQLDYPYTTQGSQD SALLQIELRDRVNQLSPGKV
7917	38285	B	7972	62	232	
7918	38286	A	7973	3	258	KLSPPPPPLPPSPLPRPGPA\GPP SRLPSP/PASASPQGV*LGPA AELPGIRSR*PQVAAPEAETHP WCCC\RSSPQQQRISH

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7919	38287	A	7974	1	1048	MAHSQNSLELPINATQTITAY GHRALPKLKEELQSDELQTRQK ALMALCDLMLHDPECIYKAMNI GCMENLKALLKDNSNMVRIKT TEVLHITASHVGRYAFLEHDI VLALSFLLNDPSPVCRGNLYKA YMQLVQVPRGAQEIIKGGLSSL VVKLQVEVEEEEFQEFLDTLV LCLQEDATEALGSNVVVLVLKQ KLLSANQNIRSKAARALLNVS SREGKKQVCHFDVIPILVHLLK DPVEHVKSNAAGALMFATVT EGKYAALEAQAIQLLLELLHSP MTIARLNATKVALTMLAEAP RKALQTHVPTFRAMEVETYEK PQVAEALQRAARIAISVIEFKP
7920	38288	A	7975	1	782	MAVTAACWSLRPLARRDVCV GVALASPFPVKPTHWFCKTLLEP CRPTGMGAQEIIKGGLSSLVW KLQVEVEEEEFQEFLDTLVLC QEDATEALGSNVVVLVLQKLL SANQNIRSKAARALLNVS GKKQVCHFDVIPNPWSHLLKD PVEHVKV*RCRLPLMFAITV EGKYAALEAQAIQLLLELLHSP MTIARLNATKALTMLAEAP RKALQTHVPTFRAMEVETYEK PQVAEALQRAARIAISVIEFKP
7921	38289	A	7976	1	300	VEQTGRGE/RAYDIYSRLLRNA FLCVMGPIDDSVASLVIQQLFL QSESNNKPIHMYINSPGGVTA GLAIYDTMQYILNPICLPRRTVR MSPRWCRRSL
7922	38290	A	7977	2	470	RPPORTLQNLGLAQRLCHATAT RALPLIPIVVEQTGRGEASYDIY SRLLRERIVCVMGPIDDSVASL VIAQLLFLQSESNNKPIHMYI/N QPSGGARGQATDIAIQAEEIMK LKKQLYNIYAKHTKQLSQLVIES AMERDRYMSPEMEAQEGIILDK

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7923	38291	A	7978	3	864	SCRYPALGPRLAAHFFPAQRPPQ RRPPTACSLQRCLHATATRAL PLIPIVVEQTGGRGERAYIDIVSRL LRERIVCVMGPIDDIVSAISLVI AQLLFQLQSRSNPKHMYINIS PGWVWVTAGLGHLTDTIAVTF LQPDFCTW/CSLGPAGAASMSGSL AFFAAAGTPGMRHFAPQLPVFMQ QPALQEAGGGQSPPD^IAIQAEENP*KLIKQQLYNNI* RQRTTQTRS LQGDRVPPMAEGTA*HEAPME GPQEFGVILKTRFLVPPSPQDGEV DEAPRLVQKEP^VEAAPAAEVP
7924	38292	B	7979	1	2088	
7925	38293	A	7980	412	812	FQSFLTCVLFHFKFSLTIHHMNS QPF*RIRSTFFFKLQSL/DSVTQA GVQWRDLGSQPPPQPGFKQFSC LSLPSSWDYRRRAPPHPANFYF F**QTG^I/THVGRMVP*PRDPP ALASQSPGITGMSHCTRPRIR
7926	38294	A	7981	2	178	
7927	38295	C	7982	279	322	
7928	38296	A	7983	2	760	GVRRSGGGR GRPGGGPRKARR GKAEDKE*MPVTKLGHLVKDM KIKYLEDV/YFSLPLIKESETIDFF LGSSLKEEGLKIMPVQKQTRAG QRTRFKAFVATGDYNGHVGLC VKCSKEVATAIRGSVILTKHSIV PVRRGY/WGNKMDK/PHTVPCK VTGRCGSVLVHLIVSAPVPKKL LMMAGIDDCTSARGCTAT/LG NFAKATFDISKTSYLTLDLW KETIFTKSPYQEFTDHLVKHT RVSVQRTTRAPAVATT
7929	38297	B	7984	318	406	
7930	38298	C	7985	333	439	
7931	38299	A	7986	2	171	
7932	38300	A	7987	1	668	MGGLFWRSALRGL RCPGPRAPG PSLLVRHGSGTIMGVFAVGTVI PVPSRVPCIEADTLKPGGPWSWT RERTLVAVKPDGVORRLVGDV IQRFERRGFTL VGMKMLQAPE SVLAEHYQDLRRKPFPCCPSRR YMSSGPVVAMWEGYNVVRASR AMIGHTDSAEAAPGTIKGV DFSVHISRNVIHASDSV^EGAQR RIQLWFQEQQ*SWVSWA\DIQGQ HSSIHPA
7933	38301	A	7988	1	897	

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7934	38302	A	7989	1	142	MEYYAATKNDEVMMSFV/GT/W MKLETIILSKLTQEQQTKHHMF SLISGS
7935	38303	A	7990	287	1086	EPWREMFIISVYTLQKLGALFTI AKTWNQPKCPSMIDWIKKMW H/IYTMEYYAAIKKDEFMSFER TWMKLETHILSNLTQEQQTKHR MFSLISGSRTMRJHGREGNITC QGLLGGEVCVHTVATRGSPATE DESCRMNVNDYGGNSPSTLQV KTSPQGRAEKGNVNVRTWLYSN LVCWPSLGLSGLMGKLDRVIKR VIYTHTAGDVSMSHEEGFQFPLK QVSSLLLCAIAFQPSLVAAALV HITMEAAYTLEVTLLQIHSPFLC FLPKCHF
7936	38304	A	7991	1550	1835	DTISHQLEWQSLKSQETTALLTI AKTWNQPKCPSMIGWIKK/MW HIHTEYYAAIKRNEFMSAGT WMKLETHILSKLTQEQQTKHH MFSLIRGS
7937	38305	A	7992	164	647	DLPVEPHIGKMLFEALVL/HCL DPVLTIAASLSFKDPFVIPLGKE KIADARRKELAKDTRSDHDTV VNAFFEGWEAARRGRFRYEKDY CWEYFLSSNTLQIM/MKIIKAVI CAGLYPKVAKIRNLNGKKKKK VKVVTKTGTVAVVHPKSVNVE QTDFHYNWLI
7938	38306	A	7993	66	345	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hol	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
7939	38307	A	7994	1	2367	HRVTVISGETGCGKTTQVTFQFI LDNYIERTGKGSACRIVCTOPRRI SAHSSCGKSSCRKGQNLVASGN STGY^QIQLPESVAQGNRVLVSYT VPTRNHPSSGSQSDPYLSSVSHI VLDEIIHERNLSQSDVLMTVVKD LLNFRSDLKVILMSATLNAEKF SEYFGNCPMIHIPGFTFPVVVEYL LEDVIEKIRYVPEQKEHRCQFK RGFMQGHVNSQEKEEKAQYK ERWPDYVRELRRLRYSASTVDVI EMMEDDKVDLNLIVALIRYIVL EEEDGAILVFLPGWDNISTLHD LLMSQVMFKSDKFLIIPHLHSLM PTVNQTQVFKRTPPGVRKIVIA TNIAETSIITDDVVYVIDGGKIK ETHFDTQNNISTMSAEWVSKA NAKQRKGRAG^RVQPGSLLFICI NGS^EASLLGWTIQLPFEEEPF WEGLTLFTK^RFLRLGEIAYFLSR *MDPPSNEPVLLSIRHL^RSLNA LDKQEELTPLGS^HLARLPVEPH IGKMLFGALFCCLDPVLTIAAS LKFQ^SPFVPLGKEKIADARRK ELAKDTRSDHL^TVVNAFEGWE EARRRGFRYEKD^FCWEYFLSS NTLQMLHNMKQFAEHLLGA GFVSSRNPKDPESNINSNEKII KAVICAGLYPKVAKIRLNLGKK RKMVKVYT^TDGLVAVHPKS VNVEQTDFHYNWLIYHLKMR^ TSSIYL^DCTEVSP^YCLLFGVG
7940	38308	A	7995	25	312	WLIYVITDARMYRQRGRYYFL VSSSLDKVLMISFLLGWRSSR RLRAFLVLHLRASPWAPRSFVR PVSAFSVGMCHMKTRVFENTF PFTLGHHTVRYVGREIF^CRRVFT RYRESIKISLPTYLTCVPVRKG VFSNTRVFMWHIPTLKADTGR KLLGAQGEARRCKTKKARKRR EERLQPNKKEIKTLSKEEETKK
7941	38309	A	7996	2	417	QQIRKLKVGLIHKPVIVHSQV GCQKSTFS^RTRKGRHMGTG^R KSTANFQMPEKV^TWMMRMRL HWLFGRYHESKKTDHMHYHSL YLKVQGNMFTNKQILMEHNHK LKADKAHKKFLADQEARSSK TNKASKLREER
7942	38310	A	7997	3	124	KKRPELRDNLNQARKETL/ARK EDRSASSGAEGDVSSERE

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met ho	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
7943	38311	A	7998	911	1497	SQRKARDQRRKRKNKRASSIAK HKEPKRPILPSGKNSQEGVATH TKPLAQGKVWLDP/NETNEIPN ANFRQQIRKLKIKDGLILRHRKPV TVHSRAQGWKSTLARRKGRHL GIESKKIDRHMYHSLYLLKKG VFKHKRILTEHSHKLKADKAR KKPLADQAEARGSKTKEARKL REEHLQTKKEEIJKTLSQEEAK
7944	38312	A	7999	34	279	EVIIHAJIGEKGSY/NA**PWVE EQLTRQPLIHHQPAHLHSVY/RC RYHSLYLLVKVGNVFKNKRILM EHIHKLKADKARKKLAA
7945	38313	C	8000	351	530	
7946	38314	A	8001	356	921	WRATACTYPSWAPPRLVATGP AAVSAGLPSLHGTRAGPQAPCT AAVPAPLPPHRPAS*G/MPAGP VQKGAPT/AAAAG*RLLKHGQS RRQGRGGAERTEGCQHAVTFQ DCFLRCFFG*C*CLSG/ERAIALE QGASHAAEQLPRLQAFKRPGPL /QVNPDAPQKSAASSSLKVLSG LPKHQPRRFCQNTGS*SGP**T TGRRSAAGAA/GKPENPGSPA PHNFISGTNPV/TTHHPVGSKP RPEPHGNSEA
7947	38315	A	8002	495	653	MTLTSDPVLTFFFNLNECPL/VFT ATASSGLGEVE*AIALN
7948	38316	A	8003	1	1433	MPESNCSTLWRHSVGRAVAAQ GGEHSSQGASLVLGEPRGSS WLLGLEGDTGLWGGLKEGRL TDGKGKTIDCKDAIFIMTSNV SDEIAQHALQLRQEALEMSRN IAENLGDVQISDKITISKNFKEN VIRPLKVRGLSWHFLLEPKAHF RRDEFELGRIGEIVYFLPFCHSEL IQLVNKELENFWA/KRAKQRHNW TLLWDIREVADVLVDGIVYNVH YGARSWKHEVERVRVNNQLAA AL*SRTELPGGCTLRITVEDSD KQLLKSPELPSPQAERKRLPKLR LEIIDKDSKTRRLDIRAPLHPEK GRLTDGKGKTIDCKDAIFIMTS NVASDEIAQHALQLRQEALEM SRNRIAENLGDVQISDKITISK FKENVIRPLKVRGLSWHFLLEP KVLTTFFNLSVLYLHGNQIQL GEVNKLAVLPRRLRSLTLHGNP MEEEGYRARRGHSLHQGIEK YICESDDIFRKYCCNNQFL
7949	38317	A	8004	1	789	

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7950	38318	A	8005	1	409	LRLELSFCSSCLLEPPWS/TTVV CLYCRPATD/HPSGSGRVSAIL LIQ^*G/RPLPLLIRLKACHCSHTA KCPGSSPSSMSPTAEEEQKSGTA EERREGASEHGEFGW/GRLERS AVEWPNSRGSSSSHSIIPPAEPR
7951	38319	A	8006	1	1787	MSKGESRKCNNEENVSSSKVV KVFIVLTPQFLSRDKDQLTKEL QKHVKSVTVSCKSPRKLLSHIT RLHPPSKGQQGENLHLVDSLKA TIWCQPWETVEGQRRLRVNGC (DFTNGCDLVGSSSLHNMLVCS SYDINRQDTFQKDRTSEKHLLD SVFTALQDSAGQQWPARLHPQ RGEEVADPRGAPSRIIVEPEPNS PCQGNQEAGKAGARALCGQ ARRSPATMPPPLTTRSLCEFAVF LLHWLFPELFHYRKLGQEFDSCY GDGGKQELDPQRLQIICNFTEV YFPHMQEEEAWRQAGPGPAEA AD/TSATSRSTSPTCRRRRPGC SGAPSASTTSFRAWGWTOAAK ASPPRDNCYNSSLPDIDSLFTH DNLHKQHQSCSDSLGKKQLDPS CIKLIRH^VHLLYLCTKNNRVRW TLEFMGNLHWNRNRGAPTSSS ARSTCWPRV^RHEELCNQS*EV QRGV^GSPAAPERSSKDFCKIPL DEVVVPH*/DFPVRSVPYLLSDKE VCKIVQQQLSVGNFAAGLL/LPP RTSSCSTTIFGL/DNKKQLDPTQ LRЛИCH^*VEAVYPVEKVEEVWH CECIPSND EQCHCPNKKCNIL

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Net mol	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
7952	38320	A	8007	1	1475	MAVDFSLAVLMIVSSYDINRQD TFQKDRTEKHLLDSVFTALQD SAGQQWPARLHPQRGEEVADP RGAPSRRHVEPEENSPCCQGNGEQ AGKAGARALCGQARRSPA TMP PPLTRSLCEFAVFLHLWLPEL FHYRKLGEGDSCYGDGGKQEL DPQLRLQIICNFTEVYFPHMQEEE AWRQAGPGPAEAAD/TSATSR STSPTCRRRRPGLRCAQCIND KLQGLGLDAGSEGEPPTRQLLQ LLQPAR*HLSNQGGG*LQGRAL FTHDNLHKQHSCSDSLGKKQL DPSCKLIRH*VHLLYLCTKNNR VWTLEFMGNLJHWNRNGAPT SSSARSTCWPRV*RHEELCNQS *EVQRGV*GSPAAPERSSKDFC KIPLDDEVVPH*/DFPVRSPTYLL SDKEVCKIVQQQLSGVNGNAAGL L/LPPRTSSCSTTIFGL/DNKKQL DPTQLRLICH*VEAVYPPVEKVE EVWHCECIPSND EQCHCPNRKK CNILKAKKVEK
7953	38321	A	8008	1	3524	MCNNLJHSLANNKITTINGLN KLPIKILCLSNQNQIEMITGLEDL KALQNLDLSHNQISSLQQGLENH DLLEVINLEDNKIAELREIEYIK NLPILRVLNLLNPQEKEQSEYWF FVIFMILRLTELDQKKIKIVEEK VSAVNKYDPPEVVAADQHLT HVNVNSVMQPQRIFDRYLLEIQR PEFRLVLLKLVGNESLPIASADSL ALTSDMVNRNGLGDLFYDFRAC HTTPPYFGEGRDVYHFISQD VFDEVMNMKGK
7954	38322	A	8009	258	719	MTPPSVLP*PSLY*HDYSLPF PFSPPVLCFPHPVQQLYSLVLFN TAAEPREKSAMAILPLSGHACS HVCLGSHQSLFQRACCRCPRPL SGSLRSHCHWLILIGVKKCSPP EAGKAII LTTDRTE TMNISWKP RNPSHTVPHPHICCHWR
7955	38323	B	8010	1	1953	
7956	38324	A	8011	32	533	GRERPLLSPYMETLYRPVFLVL ECPNLKLKPPWLHMPSAMTV YALVVVSYFLITGGIYDVIVEP PSVGSMITDEHGHRQPVAFGL QSKMDNNNINGKGLCIQAS*FTM GGFRFS*LDPIECTKYPKTSIDS FFCSIGISSVVLLEFFPWARSNS MRNGNCGPLI

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
7957	38325	A	8012	670	1052	TRRDSRCKGTWLLSVKTLAISAVKSQSKASECRFTNRSSSTAVIRVLLPGILSSKLRCMSMVLATERDDSDVGVTISSINPQDSHFSCLLLRISSNSC*IC/CNFFAIRVHLAEVCI*QTSLLL
7958	38326	C	8013	40	186	
7959	38327	A	8014	1	1216	
7960	38328	B	8015	1	1032	
7961	38329	B	8016	1	1761	
7962	38330	A	8017	108	708	LTNQKKSRTTRJHSRILPEVQGGAAADRHCPIDRLGSQDHRRSRLLSQWSP*KSTHD*HGFSLYQS AEDIRKKLQQQAEGAFGMNTSEL LQIANQAFVNRAVSRKENHR DNERQAQRNTDLLAAIRGVPP KRQKGKGGPKETQPQGQSLQR NQCAYCCKEIGHWKNCQPLKR KPGDSEQEAPDKDEGALLNLA EGLLD
7963	38331	A	8018	1	512	LSRSSPLPLVWHQAMVGSMDVPEAAWVLMTFCWDTPRQSGVPRERMPHTGTWRTVGRCPKK KLRSANSSMMRGKVQPFPRP/DI QAYGAAPFEDLQVDFREMPKC GGNKYVVLVLRRTYSGWVEAYPTRTEKTREVTVPVLLRDLIRRFRP PLWIGSDNGPAFLAALVQKTA
7964	38332	A	8019	3	764	KQVLVNGDAVSREEKKENER QARRNADLLVSCSNQSGPKEAREELWTKDYRPQGDQLLRLSQATLTFHPTVPSPSPLLGLLPAEDSWFTCLDLKDRAFTPIRSAPESQKLFAFQWEDPEASALAKTVRQRC VSCRQHHAIGKVQPFPR/DI QAYGAAAFEDLQVDFTEMPECGGNKYLPVLRRTYSGWVETVPTRAEKAREVTRVLLRDLIPRLELPFRIGSDNGPAFVADLLQKTATVGLITRKLHAASRPQSSKG

SEQ ID NO: NO:	SEQ ID NO: of peptidic sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
7965	38333	A	8020	19	1548	CIYGAQLCTGPSAPVWYCPLGT MAPTGLPGHPAVATATEPHRE RGSP/LIDSTVLVPPQDKHILRPP TVDRKRGGEASGETPPI/AARLRH KTGIQMPLREQQTGIDEYGHV VERRVFYGQPFSAHLLNWKS NTPSYTEKPQALIDLQLQIIQTH NPTRADCHQQLMFLFNTDERR RVLQAATKWLEEHAPTDYKNP QEDVRTQLLGTYQPWDNPNERQ DMQRNLRYREALLEGLKRGQAQ KATNINKVSEVIQRKEESPAQF YERLCEAYRMYTTFDPNSPENQ CMINMALVIQSTEDIRRKLQKQ AGFARMNTSQLLEIANQVFVN RDAVRSKENQKENGWPPCLR ALAATALLVQEANKLTGQNL NIKASRAVVTLMLNTKGHHWL DARLTQYQTLLCENPRITTEVC NTLHPATLLPVSESPVEPDCVE VLDSDVDSRPDLRDQAWASVD WEYLVDGSSFNPQGERGAGY AVVTLDTVVEARSLPQATSAQ KAEVAFIRALESE
7966	38334	A	8021	1	895	MDGAGICYLHQTNAGTEIQTIPH VLTYKRELNNENMWAHRGDN THWGPEGSTNSPASASGVADV SRVGSLQWVVLGLADFKNEAKE LRLYKQEKEAKRWKETEKG FNGDYGVMTPTGKWRTYFEID WSKLEVGPSEGTLERSLVS VWHKVVTGKSGHSDDQFPYIATW LQLVLDPPQWLRGQAAVLVA KGQINPKDPTPPGRGKSTPEVL FDPTSEDPLQEME/PSDPPSGALP LPGKDAPHS*AHSPCASTRQTY P*ATRSRQERK*SLERNPYIGSS FKTNQNWDTNAPERAVVYWD R

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
7967	38335	A	8022	1	1959	MLKNFKKGFGNDYGVMTPG KLRTLCEIDWPITLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTWLPQWVRGQAAAVL VAKGQIVKEGSRSTHRGKSTPE VLFDPTSDDPLQEMAKVIPVVP SPYQGERLPTFESTVLVPPQDK HIPRPRPVDKRGGEASGETPPL AARLRPKTGQIQLMPLREQRYTGI DEDGHMAERRVVFVCPFTSAD LLNWKNNTPSCTEKPQALIDL QTIIQTHNPTWADCHQLLMFLF NTDERRRVLQAATKWLGHEAP ADYQNPQEQYKEESPAQFYER LCEAYHMYTPFDPSHENQRM NMALVSQSQAEDIRRKLQKQAG FAGMNTSQLLEIANQVFVNRD AVSHTGAEHHSVTVTGPVAPLSK KTIDIIGAMGVSAKQAFCLPRT CTPGTKDYRLVQDLRLVNQAT VTLHPTVPNPVYILLGLPAEDS WFTCLDLKDAAFFSIRLAPERQK LFQAFQWEDPESGVTTQTYTWTW LPQGFKNSPТИFGEALARDLQK FPTRDLCGVLLQYVDDLLLGH TAVGCAKRTDALLRHLEDCGY KVSKKKIAQICQQQVRYLGTI RQAERTLGSGRKQVICNLPEPK TRRQVREFLGAAGFCRLWIPNF AVLAKPLYEVTK*GDREPFEW
7968	38336	A	8023	2	367	
7969	38337	A	8024	3	687	GGRRQRRSKVTSWWQARESS CRGTLLYKTIRSCDTYSLSSEQ HGPNLHLIGVPESDGQNGTKL ENTLQDIIQENFPNLARQANIQI QEIQRMPQRYSSRRAZTPRHIIVR FTKVEMKEKMLRAAREKGRT HKGKPIRLPADLLVETLQARRE WGPINFLKEKNFQPRISYPAKL SFISEGEIKYFTDKQMLRDFVIT RPALQELLKEALNMRERNNWYQ PLQNHAKL
7970	38338	A	8025	1	993	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Net id	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7971	38339	A	8026	I	842	MAEQEQLQSAVPSPLLVIPRQK GSGVDFQQSPTDLQLRDLTDRR KTNKQKGIASTLTKRTSTPKPH LYVTNIKDQRPNPRLIGVPESD GEKGTKLENLTDQIIQENFPNL ARQANIQIREIQRTPQRYSSRA TPARHLIVRFTKVEMKEKILRA AIREKGGRVTHKGKPIRLTTADL SAETSTSQKTEWGPIFNILKEK NFVQPRISVYPAKVLSSFISEGEIK\Y YFTDKQMLRDFCHHQTCLP*KS TRPALKEELLERKHLNM/EKGN WYQPLQ\NHAQICKDH
7972	38340	C	8027	320	433	
7973	38341	A	8028	9	189	
7974	38342	A	8029	26	738	VAASSFDTCADHLCALHLLQV LHYLAIQKPADLARHLPPCVIH AAVLKVKEEESLENISSVKIIK QIISHSKVLHFPNPEDDKLLEEII HQITNVEALIARARSLKAKFGT EKCEQEEEKEDLERFVSCCLSEQ PEVLVTGAGRGHAGRIIHKLFV NAQNVAAAMTPPEEELKRMGS PEER\RQNSIVSDFP\PPAGREFIL RTTVPRPAPYSKALPQRMYSVL TKEDFLAVKIIDGDV
7975	38343	A	8030	3	2961	MAADESEPESEVFETDFTTASE WERFISKVEEVLNNDWKLIGNSL GKPLEKGIFTSGTWEKSDEISF ADFKFSVTTHYLVQESTDKEG KDELLEDVVPQSMQDLLGMNN DFPPRAHCLVRWYGLREFVVIA PAAHSDAVLSESKCNLLSSVSI ALGNTGCQVPLFVQIHHKWR MYVGECQGPGVRTDFEMVHLR KVPNQYTHLSGLLDIFKSKIGCP LTPLPPVSIAIRFTYVVLQDWQQ YFWPQQPPDIDALV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
7976	38344	A	8031	1	1688	MREKPCQSNECGKAFNYSSLLR RHIIHTHSREREYKCDVCGKIFN QKQYIVYHHRCHTGEKTYKCN ECGKTTQCMSSLVCHRRLHTGE KPYKCNECGKTFSEKSSLRCHR RLHTGEGKPYKCNECGKTFGRN SALVIHKAIHTGEKPYKCNECG KTFSQKSSLQCHHILHTGEKPY KCEECDNVYIRRSLERHRKIH TGEGSYKCKVCDKVRSDSYL AEHQRVHTGEKPYKCNKCGRS FSRKSSLQYHHHTLHTGEKPYTC NECGKVFSRRENLRHHRLHA GEKPYKCEECDKVFSRRSHLER HRRHTGEKPYKCKVCDKAFRS DSCLANHTESSILGEKPYKCYIK CCGGFLIQKGSLPQHQVRVHTGE KPYECNECGKVFVNQKASLAHK QRVHTAKKPYKCNDCGKPLPD QSTLFHHQSNSPIGVGKRYQICN DCHKVFSNATTIANHYRIHIEE/ KIYCNKCGKFRRHS*LVHQ *THTGEKPYKYHDCKVFSQA SSYAKHRIHTGEKPHKCDDCG KAFTCSHSLIRHQRHTGQMPY KCKGGKVFTLWSFAHEHQKIH
7977	38345	A	8032	25	1091	IHIYSDSCSLSLQDSGDEKEFNL DDNVFSRASLWDLAAGPGOGG GGGREKWRAVISRTMNRKMG KMMVKALSEEMVRPADIGDGV SRGPGRSGRM*AEKMALAFS EQEEHELPVLSRQASTGE*GMR GTPAESGGKDWTAVLVAGPF CGRARVHTDFTPSYDHDSLKL QVRASAGLLWSLAGCAQKGSW TEPVGSFKFIYVDLPEEAUGH ARPSSRQSKGKRPKPTLHELL ERIGLEV*AWSSLVSIRESAQLP QGWGPGLHNELNIMDPQHRAK LLTAEEELLNDYDSEWL*ERPGE GAESSSQEPGIGEACPKVDIRPDS GCFFEGSESGRDDAELAGTEEQL QGLSLAGAP
7978	38346	A	8033	35	437	
7979	38347	A	8034	1	1845	
7980	38348	A	8035	1	212	
7981	38349	A	8036	371	915	
7982	38350	A	8037	1	2460	
7983	38351	B	8038	10	1510	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
7984	38352	A	8039	1	188	SASTTLWGGLLFLIHLRLGTLARA VSSWGTIIILTAKEVQWGH/DCG THWSYHHLHQPRAGHKEC
7985	38353	A	8040	3	2332	FFFMWDWPQHF/TFI/VLPQYYNN SPGLYSTVLRDLENLDL*NIKF LYFIDINIMLTGMDE*EEDGTLE ALVKHLLSRGVKINKPYRDSEV ATAVK/FLQV*WLGSRGVPNS NVKDKLLHLC NPCKGREAHCL G*ALF*VS*HN PTCKVVSFGDP HF*VT*EECPAWEWSL/QQERTL QQIPGHGAVTILQDPLVLKVPV GGVRFGVELNQAPVGESQWKG LGIWSKAMSSTAQKYAP/QSRE EICWKQLLACY/W*ALI/EIECLT MGHKTTM*FQ MPLRN*HLCNS *SHTLDMPOQHPIMRWKSFL*/ D*A*IPMLTSPRKHPNLKWP*TT KQKH/WKL/GQPSWPVSPGRVG WVHKWSKHSGRD/GGYLWVQ QY*LPPTKVDPDTATSKCPTHQ HLNPMIFP/R*GSISLGDDQDPK* GVDYIALFPS*KGQRFMFTGIGT YSIVGFSRVEVIPSVSTTFWGLL IFVIHRLGTASPCSSSGWGTHT AKEVQWGH/DCGTHW/SYHHHL HQPRAPGP*RMLKRASIGTAQR QLAGST/LCGWEGAIFQDMVHF KNQRHLYSSVISVGRTRGSRYQ GVEVDVAPYPIPSTHLSWDFAL LSQNHSAG*KVLDKSGGYP*K ETNECPLNYTLQLP/PGE/FGQY VSRDQRVRRGVPSPPGTVIDPD PQEAWLLSHN/GG*EEFWNP /GDPLGGLLV/LPCIVSVRRIVQ
7986	38354	A	8041	1	1296	

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7987	38355	A	8042	498	2219	KSVKTST*DTLRTKAKTGQGHI TGLOPWLGLRIRQEP/SAKTEK KAAIQAKAGAEREATGVVRPV AKTRAKAKAKTGSKTDAVAE MKAVSKNKVVAETKEGALSEP KTLGKAMGDFTPKAGNESTSST CKNEAGTDAWFWAGEEATINS WFWNGEEAGNSFSTKNDKPEI GAQVCAEELEPAAGADCKPRS GAEEEEEEENVIGNNWFGEDDT SFDPNPKPVSRIVKPQPVYEINE KNRPKDWDSEVTIWPNAAPAVTP AVLGRFSQAPSEASP/LFIYCSG LR*RKCLFFACGNSLPPF*EPRS CSQPIPECRFDSDPICQTIDEIRR QIRIREVNGIKPFACPCKMECTY MDSEEFELVLSSLKSTTDPLIHK IARIAMGVHNVHPFAQEFINEV GVVTLIESLLSFPSEMRRKKTVI TLNPPSGDERQRKIELHVKHMC KETMSFPLNSPGQQSGKLIGQ LTTFVHHIVIVANYFSELFHLL SSGNCKTRNLVLLNLMSENPT TAARDMINMKALAALKLFNQ KEAKANLVSGVIAFINIKEHIRK GSIVVVDHLSYNTLMAIFREVK
7988	38356	A	8043	1	453	MEKLDELKIKIDNINGALICARH FSKCSSNAQSHLCPYLQAFPGG PG/VRGPGWPGRTGSRELGHG WRGC/GGLVSGCQTMGLSGA/P AGSPQPTGGTRAHAVRGRP*V PARSQGSRPLARPQQED*GAAP DFDPAAGVPGVPALEQAQI
7989	38357	A	8044	3	690	SLSLPSSWDYRRAPPRANFVF LVETGFTMLTTIVLIS*PHHPPA SASQNAGIV/GVSHSPRPGIACLI TRLDF/IQGTQSRVPALGSS*PIP HARPRGHTLKALPYRLYTQTA RGFGQPRVRIPILLSLLSLKPSE LRGQVGHAFASAIFASAISLCVF TLLVEGKLKPPGASVRRCQLQSNN RDLGFRATFPPTSHRGHGALGLN YISQRATGTPNLWLPLFRFRVV LQAACG
7990	38358	A	8045	106	299	
7991	38359	A	8046	306	445	
7992	38360	C	8047	570	926	

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7993	38361	A	8048	47	988	ASRPGRSRVSLMFGAAGRQPDRS SSSPGTSWPPFPVEPMELVHDL VSALERELQSKPRGGFAEPGDP FSEVY/PCLPLKPKRKRRKR RFV*CASPVGGLVTVA*SEGSDS SFRRTKSKKRLKLIIQGPKIQD EGVVLESEETNQTNKDKMECE EQKVSDELMSEDSSLSSTDA GLFTNDEGRQGDDEQSDFWYE KESGGACGIGITGVVPWWKEPD TELDKNVPDPVFEISLTGSPLM SHPSRKGFTKTQSAFMCQLRJ LKNLEGQLQLQWYPLAQWVTR EWFFIPRILITMTIGLALGLGQS MTSISF
7994	38362	A	8049	3	476	LTRPVD*RPGTIHLGRGVRA ANRRQRARRGAIAISPAGPCSV AGFLRGRLG/PEPGDNQHQLGE PWLGCGSLFA*RA*CSRSTRCT* RRRAPGDRELPRAPATWAPPK LVRPVFSSKVVGQGVSGLV CLGQDSILNQSNKHNSVASSNT ITVIG
7995	38363	A	8050	2	143	
7996	38364	A	8051	1	161	
7997	38365	A	8052	3	1189	ESPLGHHSSSDAARRRSVSSFP VPQDNVDAHPGSGKEVRVPAT ALCVFDADHGEVNAVQFSPGS RLLATGGMDRRLVKLWEVFGEK CEFKGSLSGNAGITSIEFDASG SYLLAASNDFASRIWTVDYYRL RHHTLTGHSGKVLSAKFLDNA RIVSGSHDRTLKLWDLRSKVCI KTVFAGSSCNDIVCTEQQCVMSG HFDDKKIRFWDIRSESIVREMELL GKITALDLNPERTELLCSRDDL LKVIDLRTNAIKQTFSAPGFKC GSDWTRVVFPSPDGSYVAAGSC *RALLYIWDVLTGKVEKVLSK A\HSSSHQCGWPSPSWART\W VSVDKGCKAVLWGTVLTGLSG LGGPQCPHEEAHGLLQPWSW QVNVLGYSMDLPEKLKANVGH

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, ^=Stop codon, /=possible nucleotide deletion, *=possible nucleotide insertion)
7998	38366	A	8053	116	92I	LSKSNCW*GCEEKGTLLHCW WEC/KFNPLLKAI*RFKLKEV LPLDPAIPSLGLSKIGTGGKVW QRLPNCPITISLSFFFHKNRHTGT YRRRFLSDLAVRCPCNPATFGS KSDVCNFVWMPSTGKKCALPS HPLFPNGLNADVVCLSDSENL QKILLILEVSDSLGVGKLSHKNII QHDCIEEPLTLRNNTQQRFLCI ACHGCTSQYSTFLVKASWTRS QGLIQRQPSAGSGYPEKPLFSEG AGDEGVDLLPLAKPASPDEQL
7999	38367	A	8054	35	422	SCSEVTEASWGSVPELRDAQLG VGLHSPTYRHPHRETLTCCPAG TLQAWPFCGRIRVRVVPWSLGE PGRGLIPGSGSAASSECLPGLHG RAPLGLTSCRPGRPLP/WNQPPP LAQPGHRDPDADAATERPGLQ RPSRTACERFPGMGSVSRRRVEA HSQLGVPPELRD
8000	38368	A	8055	3	277	GPPRPPA*RGHGGRPENTVAPP RWPPPWPSPAPLPPRACADV THPPVPTGKRTTPPIGGAPAAR AAPRPPAPSCFSAPTPGCSLTG
8001	38369	A	8056	3	179	PPPHPGQGPPPGRPPGC*RP/1/QG RQVFSMKPGRTPERTAWS/PPY PGCLGSRPRPSAPA*SGAHCV VAPYPGCLGSRPRPSAPA
8002	38370	A	8057	3246	4682	ENTLSFASFFFFFEMLSLCRPGW SAAAPCQLTAASTYWVKRFSC LRLPSSWDYRRAFPQHANSFCI FSRDRAL/TMLVRLVSNS*PQVI RLQPKPVGLG*ACCGFCGS GMAPGCRVVSHAGAPGGTR PP
8003	38371	A	8058	3	718	UTRLVLSPDAPD/RATHLIAA/R AGTEKVLQ/AQE/CGHFHVNP DWLWSCLERWDKIEEQLFPLR DDHTKAQRENSTPLPDREGIPP TALSHPMILPKAQPSPEVRIYD SNTGKLIRTGARGPPAPSSLP RQEPESSF/RVDDILGEGSDDSD EKRRPEEQQEEEPQPRKGPTRR RTLGA PASSERSAAG/SRG/PRG HKRKLNEEDAASESSRESQNEY EGSSSEADEMAKALEALNDL
8004	38372	A	8059	273	468	NVKGTAANGD*G*RGEAAPA/G RSRARVPEADAASESSRESSNED EGSSSEADEMAKALEALNDL M

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8005	38373	A	8060	1	2886	MEVPAAGRVAEAGAPTAVAE VRCPGPAPLRLLEWRVRAAGAA VRIGSVLAVFEEAASAQSAGAS QSRVASGGCVRPARPERRLRSE RAGVVRELCAQPQGVVAPGAV LVRLEGCSHPVVMKGCLAECCG QDLTQLQSKNGKQQVPLSTAT VSMVHSVPPELMVSSQEAEQLG REDQQRLHNRNRKLVLMVLDQ TLIHTTEQHQCQMGKGFHFQ LGRGEPMILHTRLRPHCKDFLEK IAKLYELHVFTFGSRLYAH
8006	38374	A	8061	2	680	
8007	38375	A	8062	658	1657	PGILSLRNALLTGVDCKVVVPV PPGHHTHPQLRLFHFKPTCSGW GEWGDHGVVWAGPAPA\YHL HRDVQALWTNDHALAW*AM TSERTLWPGHELSARPGRSWRI SCPTGLPQCGGDDRTRGHWVTA TCCSADGLRLCRYGDGVRGGL PTVAWP\LTGCSCLRYSQGQOC CYTADGTQLLTADSGGSTPDR GHDWGAPPRTTPRVPSMSHW LYDVLSPFYCCCLWAAPDPGKD RAGLGCPTP\PSLTLASAFAFGD HFVTFDGTNTFTNGREYVG G*NQGGRLEPSGSRSAPTTAGT ETRGTGLTAVAVQEGNSDVVE VRLANRTGPER
8008	38376	A	8063	873	1791	RCAGCPHSSFFERGQ*AAVGP CCHGHTYRKASSV*RVSV*HPP HDRGRSRK/QSLSGR*STGLS*MP SGVASSASV*FVNVFSLSSSN*L AQSTARFPFGSVRGLQGRAG GG*APGHGADHPTGRQHS*GSP APVTWLWWPPPRHQAAALAPAP STTPYDNSPPLHCRPGSPQSSSH HSALPGT/SVPGSSPLEIVPGSSL YVS*SLIRALAAPISSSSVGKNC RCTERLAIKPAAESCRTSSSAG QSVEFSRFTSL*AFTG*AR*PSAS AADLLVKASILLAQLLIESLAS STRMYSFRDCTSSFSA

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8009	38377	A	8064	2	935	YSPARGSGRGLSRRPGAGRRRA GQGPQVGAKPGGAEEYVWRAGG AGGMKGAGGSSGSGGSRE AG*PGVPRGRGWRTPAEPPG WGPGRQQACGA*G/EGRAAAQ VGGAPAAAGGGVAREEAPS*P GDAAGGSGTPTGAASVQVSAPP AQPOQINLSAGARAGVAARRCVC RGAES*GPGDPGPGSRR*PPAA QSPPPCPSALFLHPSPGLCRP QPSRAQQGEVSGALRAVPLRG GAGNLAALPCQLPGSGGLTPGC /QASQQLGVGLVRAQPAWSPL DGPLDQKVFSPQTSLWNQRCS LAAAGPVIIIR
8010	38378	A	8065	3	367	
8011	38379	A	8066	2	1246	TPAWSREILAEELCTPPDPGAAF VVVECPDESFIQPICENATFQRY QGKADAPVALVVHMAPASVL VDSRYQQWMERFGPDTQHLVL NENCASVHNLRSHKIQTQLNLI HPDFP/AAHQFPL*EGGPHQC AHGSC*MPHQVPAFPQE/WSAR GMPPLLAILRNS*LRCSCFTSS RALQEYRRSAQDCPAPAEKRS QYPEIIFLTGSAIPMKIRNVSA TLVKIQSPDTSLLLDCGEGTFGQ LCRHYGDQVDRVVLGTLAAVVF SHLHADHHTGLPSILLQQRERAL ASLGKPLHPLLVVAPNQLKAW LQQYHNQCQEVLHHISMPIAKL PSGRWLRSRSPVQLQWKD*FSLLR TWIWEEFQTCLVRHCKHAFGC ALVHTSGLKVVYSGDTMPCEA LVRMGKDTRKQADELISFQG
8012	38380	A	8067	121	880	GAAASQLPAPVPOPVPGGPAPH QYDSQQMPSGRG*DLSQCSGKI DQFA/AWTTCDEEFQTCVLVRH CKHAFGCALVHTSGWKVVYSG DTMPCEILLVRMKGKDATLLIHE ATLVEDGFRKREA/LEKTHSTTS QGHSAWGMRMNAEFHY/VLN HFQARRY/SKVPLFSPNFSEKVG VAFDHMVKVCFGDFTMPKLIIPP LKALFAGDIEEM EERREREKREL AGAGRPSCSRAGRRPLEGEDP QQKRAHTEEPQAKKVRQ

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8013	38381	A	8068	1	607	SPGSWETRLWVWSFYRSCKHS LCPCLVGEFLVFNPMQSGSAG EPPRLQF/GAPLPGA/APGNYRRT GRGRGPWPPP LAPSLFAFSDL GSSPGRTSWRPPAVSRRLGPTFP PPAPGRRGRPRRAA*TGPSAQ/PP RSLSTLSPAPAAPAVRTAPPVAS PRAAPAPLRAITLLATKSEELPV VSFFSSRLVLAKRPKRLAQMH WGH
8014	38382	A	8069	1	290	QFLDAESGSAGEPPR/LAVPAPF PGGAPGNYGRTGRGREERSWP PPLAPSLFALSDFGSSPGRTSRR PLAVSRRLGPTFP PPPPLPPAAGR GRPRRAAP
8015	38383	A	8070	1	565	SPGSWETRLWVWSFYRSCKHS LCPCLVGEFLVFNPMQSGSAG EPPRLQF/GAPLPGA/APGNYRRT GRGRGPWPPP LAPSLFAFSDL GSSPGRTSWRPPAVSRRLGPTFP PPAPGRRGRPRRAA*TGPSAQ/PP RSLSTLSPAPAAPAVRTAPPVAS PRAAPAPLRAITLLATKSEELPV VSFFSSRLVLA
8016	38384	B	8071	475	913	
8017	38385	A	8072	145	275	
8018	38386	A	8073	1	310	VEELTARTGGGAPPGCQADAK RMPQQPPQRTPWGHGFAGAAPFP ISKPHGPPAGQL*PG/PSCEQT/E PPSPVNVTVTHLRANSATVSV DVPEGNIVIGYSISQQV
8019	38387	A	8074	1	483	GSHRVGRWAALCDRAAPRGLT NRETGGGAPPGCQADAKRMPQ FPSQRTPRGHGFAGAAPFPISKPH GPPAGQL*PG/PSCEQT/EPPSPV NVTVTHLRANSATVSVWDVPEG NIVIGYSISQQRNQPGQVRIRE VNITTRACALWGLAEDSDYTV QVRSIGLRL

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8020	38388	A	8075	2	854	RPPAARARRWLPKSPARRSRRPAHRCRRTCTPQATRPGRMR*APAAACGPTGRRS/RLPALKIALEYIVPCMNKHGICVVDDFLGKETGQQIGDEVRALHDTGKFTDGQLVSQKSDDSKDIRGDKITWIEGKEPGCETIGLLMSSMDDLIRHCNGKLGSYKINGRTKAMVACYPGNGTGYVRHVNDNPGDGRCTVCIYYLNKDWDAKVSGGILRIFPEGKAQFADIEPKFDRLFFWSDRRNPHEVQPAYATRYAITVWYFDADERARAKVKY/RNR*KRCEG
8021	38389	B	8076	1	205	
8022	38390	B	8077	1	806	
8023	38391	A	8078	1	2279	MKVGLDQIIEVVPSHSVTSGAA AGECGGVHCDSVCAFGRWGPN CSLCYCKNGASCSPDGICEC APGFRGTTQRICSPGFYGHRC SQTCPQCVHSSGPCHITGLCD CLPGFTGALCNEAYSQ/SCPSGR FGKNCAIGICTCTNNTCPNIPDR SCQCYPGWIGSDCSQPHCADKC VHGRCIAPNTQCQCEPGWGGTN CSSVKKKSTVCES*KCEPWEER PCGGLHWDIAG*/P/GKHGGYL NELGAFGLDRSYMGKSLKDLG KNSEYNSSNCSSLSSENPYATIK /GPTCTYPEKLRVWLCGDEIAG TKRFPICRDQ*LNFSQEQCL*S* TYSECPRSIQQ*WASFPGSI*PP KNSHIPICHYDLI.PVRDSSSSLK QEDSGGSSSSSSSSSE*APKDR LGLLV**RS*SM*TNRLAHKPK QPGRKGPKI**HGTWKSSQEKF/ HAEEOSGKLAATLCGKDWLIQ REGWPYIISRMFL/CFISTDGRE SESLWRKSNGNSKFKF*WGRPG KGGL*EGQREEVWGLGNNSLYC LAGQL*CLDCECHH/GFQECCP VLGHSGWYKS/CLRNPLKGLS SRCAGLAVRDSLAPNSQGWKA TFDFPSLECPSCGYGGRQICD CLNNSTCDHTGTCYCSPGWKG ARCDQA/GCYHSWKSEQLKPN QYCSPC*FLPDRGHCRHHHSCP SCSLPTGIVHYL*TQAEKGKIH
8024	38392	B	8079	1	2909	

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8025	38393	A	8080	332	602	NSLNSRWLKGLPGAPG QEIKE MWRCMSSICQKEGWRMTAGS LGHHRSLLHVQ/GAGNDVDR GSLPASVR/QHAYYTASSVEGR VSYKLTY
8026	38394	A	8081	2	422	FNISLGFACPRLRIDFFGWFFFVFF LSWSFTLFAQAGVLWCDLGS QPPPLGFKKFSCLSLPSSSLDYRC LPPRLTNF*FLVEMGFHHVGQ AGLELLTSGDPPASASQSAGITG MSHRAQSAALSFK*SGISKNRY FIFWA
8027	38395	A	8082	1	951	
8028	38396	A	8083	1	924	
8029	38397	C	8084	271	738	
8030	38398	A	8085	1	575	
8031	38399	A	8086	2	332	
8032	38400	A	8087	1	897	
8033	38401	C	8088	181	804	
8034	38402	A	8089	1	1923	
8035	38403	A	8090	294	2340	EKCRHNCSRSRVWQSLVLSQSVW ATEQQYGRTKNARPVQVKIDS ASFYQRRYYPLRLEAQQGLQKI VKDLKAQGLVKPENSPCNPNTIL GVQKPNQGWKLVQDRLIINEA VPLVPAVPNPYPTLSSQIPEEAE WFTVLDLKAFFCIPVHRESQF LFafeDPSNPTSQTWTVLPQG FRNSPHLFQGQALAQDLSQFSYL NTLVRLYDDLLAAILETLCH QATQKKTGIALGVLTQVQGTSF QPVAHLSKEIDVVAKGWPWHCL WVVAAVAVLVSEAVKIIQGRE LTWWTSHDVSGLTAKGDLWL SDNLLLNQALLFKRPVRLRHTC ATLNPATFLPNKKEKIEHNHQO VIVQTYTIQGDLLEVPLTDPDL NLYNGSSFVEKGLRKAGIHPS RQWTPLWPKGAGPEMLSQRQLV ESGILKAFLVPYILLVAVLGSIDF NGKPPVAVFSLSQAHRFLCAT WLLQYGEVWIHSHTAIKYQ RRRSQDGRIGTAPVYSSQRERR RRRVISAFPSEGIPTDLQLRVL VRRKTKQKGHPHQKPICTS SRPKVDKTTKGKKQNKRKTGN SKTQASPPPKERSSSPATEQS MENDFDLREEGFRRSNYSLELR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSQCDQLEERVSAMED

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8036	38404	A	8091	158	865	NPAARTPFFVIKKGGKRGEGCL AKAGAAIHLNIG/GTPVCCPLLE EGINLEDWATEQYGRAKNAR PVQVKLKDASFPHQQRQYPLRP EAQQGLQKIKDLKAQGLVKAC NSPYNNPTLGVQKPSQOWRLV QDLRIINEVTVPVLAVPNPYIL LSQIPEEAEWFTLDLKDRAFTCI PVHPDSQFLFAFEDPSNPMYSQL TWTVSPQGFRDSPHFGQALA QDLSRFSYLGTLVLWYVD
8037	38405	A	8092	1	748	MNQSQDEMTGAFVHMKSYTG LISGVAVKMERHIYQDRRIAEK EFNSCRTGCMGDWSFTITQIRL LENTGIRVFKDNLVEEEAEWFTV LDLMDAFFFICPVHPDSQFLFAFE DPSNPASQLTWTVLPQRFKNSP HLFGQALAQDLSQFSYLDLTVL RYMDDLLLAAYSETLCHQATE ALLNFLATCGYKVSKPKAQLCS QQVKYVLGLLSKGTRDLTTFLP VNEEKIE/P*LSTSNC SKLRCRS TSRGSLG
8038	38406	A	8093	194	1377	NPAAGTPFFVVKKGGKRGAGL LHRQYPLRLEAKQGLKKIVKVDL KAQGLVTPCSSPCNTPTLAVQK PNGQWRLVQDRLRIINEAVVPLY PAVPNPYIILLSQIPEEAETFTVL DLKDAFFCIPVHPDSQFLFAFED PSNPMSQLTWTVLPQGFRDSLH LFGQALAQDLSQFSYLDLTVLQ YMDDLLLVTHSETLCHQATQV LLNFLATCGYKVSKLKQAQICSQ QVKYLGKLSKGTRALSEERIQ PILAYPHPKTRKQLRGILLGITGF CQIWIPRYSEIARPLHTLIKKTQ KANTHLVRWTPEAAAFQVVK KALTQAPVLSLPTQGDFSLYVT EKTGIALGVLTQHYGEERNS*L PTEYLSNIRKPLGDYYWLYRNL KRWQSYTARVIRKERKGK
8039	38407	A	8094	3	521	

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8040	38408	A	8095	1	3203	DSPLSTKAMILGMLVKDHWS AQTPFPVIKEGGKRGAAGLLHQ LILDKDFITQSAADIKEKLQKST LGPERNLKTLNLATSVFYNRD QEEQAERDKRGKKATTLVMA LGQADFGGSGTRKA ANRMP NRAYFQCGLQGHFKKDCPSRK PVQLTIESQEVNCLLDAGAAF SVLLSCPGQLSSRSVTRGVLGQ PVTRYFFQPLSCDAGLPFSHA FLIMPESLTPLEREILVKGAAII HLNIGEGTPICRLL
8041	38409	A	8096	13	183	VHLHPQGHVPVKHPTGLGYS SCRHILLGRACY KGEVGAKA GMQVSDALPRLGGVS
8042	38410	A	8097	1	2427	MSKFSCASLTATESDGTPLMEQ YVPCPVCTAWAQHTDPSEKS EDVQYFDMEDCVLTAIERDFIS CPRHPLPVLQELVPLEFMTD FPARLFLENSKEHSEDEGSVL GQGGSGTVIYRARYQGQPVAV KRFHIKKFKNFANVPADTMLR HLRATDAMKNFSEFRQEAQML HALQHPCIVALIGISIHPHLCFALE LAPLSSLNTVLSENARDSSFIPL GHMLTQKIAQIAASGLAYLHK KNIIFCDLKSDNIVWSDLVKE HINIQLSDYGIQRQSFPHEAGLV EGTPGYQAPEIRPRIVYDEKVD MFSYGMVLYEILLSGQRPALGH HQLQIAKKLSKGIRPVLGQPEE VQFRRIQALMMECWDTKPEK RPLALSVVSQMK/APDFCHLV *TVLWEADSLLIIPGPVGHRGV LGWKRGVQELHGGINTEKGLM EVQRMCCPGMKVSCOLQVQRS LWTATEDDQKIYIYTLKGMCPLN TPQQALDTPAVVTCTFLAVPV KNSYLVLAGLADGLVAVFPPV RGTPKDSCSYLCSHTANRSKFSI ADEDARQNPPVVKAMEVVNSG SEVWYSNGPGLLVIDCASEIC RRLEPYMAPSMVTSVVCSSEGR GEEVVWCLDDKANSLVMYHS TTYQLCARYFCGVPSPLRDMPP VRPLDTEPPAASHTANPKVPEG DSIADVSIMYSEELGTQILHQE
8043	38411	A	8098	1	1641	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletions, ^=possible nucleotide insertion)
8044	38412	A	8099	1	1075	VLHKFPYRMVPALPPKRLMGA DREFIEARRRALKRFLVNLVARH PLFSEDVVLKLFLSFGSDVQN KLKESAAQCVGDEFLNCKLATR AKDFLPADIQAQFA^SRE^LIRNI YNNSFHKLNRRAERIAS/RAIDNA ADLLIFGKELSAIGSDTTPLPSW AALNS^TWGSLKQALKGLSV E^FALL^ADKAAQQGKQ^EENDV ^WEKLNLF^DLIQLSYVKLDCE/R GHEKGIVF/HTKHQRALAQSTA* LKRPD*LSATGAEPRSPEVRGS KLKSRRIGARENA^QTMEMLRN Y^FSLYCLH^QETQLIHVYLPLTS ^HILRAFVNSQ^IQGHKEMSKVW NDLRPKLSCLFAGPHRTLTTPC SPPEDGLCPH
8045	38413	A	8100	1	974	MPQVPAP/PLPSITSGHGPGEPA RPSCCSLFSPQPCNSITPPSSLRLR QLAVAAAAGGGGGHGA^PALSST GWQQVCKSPQVRSVPDNPTTA DSTASLAWKFGEVLRSHINCGY K^KQOPLLL^PVHAQRRAQVSAP/ APPAGLSCGQHS^LPOP^PPRCSDSL LGLHPGRPLPCDRGHCPPLPV PTPD^KAGPILDPAQSCPFC^SPIPA PPKQPSPPARFPEMKRKKTLM MPPSEGSLSLASGM^EASFV^F^ORL LSRCTCLDQATV^IWGF^CYMQV QASQGIPCRGKDELLR^LAPLPV KEARRTKPRSPGKHAKAPPSS ACSPHLCCSSPILQALD
8046	38414	A	8101	1	460	SLQAPRRNSRAEHTR^TLNSECP RRRC^CIKGC^TT^LDAV^P^PPP VLDWLVQPKPRWLGGNGWLL DGPEEV^LQAEC^STTDEGA^EPL LCPSGYECHILSPG^DVAEGIPN RGQC^VQRRQADGRILRH^KLY KEYPEGDSKNVAEPGKG^VQRH
8047	38415	A	8102	3	219	NNHRLDRTLPRDYCHAATAYT THELA^FGDFRLPTEGH^QELCHN SHLIY^FRRDK*THCTWRSVDSL TGVTHR
8048	38416	A	8103	230	555	NVRPS*ALQAPWGRH^HLCVT^P MQLRMTLVVSSLGKGTG^L^LSL AQ/CAPVQE^GTHGGSP^V^EWGL AA^TRTC^EGCRRENTMKNV^GSR KYAFN^S^LQLKA^FPKHY^R^P^EDL RKS

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8049	38417	A	8104	23	304	KGFYLFNKQQTIEQTNNGKSFA KRNTEGHDDLLLQGFQQSQTPS FLSSSGRCYSWGAIGP/QFGALS G/FSPFPHSAAANRQSSALDFWIT TSISF
8050	38418	A	8105	99	375	VLEFGALSGSLSISPLCTIPALVE PPCGQPQPSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSPQGVQ LPLGPR/RLKMNTPEPTRP
8051	38419	C	8106	5	376	
8052	38420	A	8107	545	990	GLCHVLQPCDPCPLPGTMQEAQ PPEVLIKTAGKAGGQEPG*^L*^RIP *GSLCPPCPVAFGAAAELPLPSS DPVSRTGAPPQOG*^WLGFYFS SNEGPSQAGG
8053	38421	B	8108	252	801	
8054	38422	A	8109	169	1226	PNGLRPPCPSPASETPGNAPVCD PGSSSQGAQGKL/KPGGLPGWL FPFFAQPSSEG/GLCPCPVAFG AAAELPLPSSDPVFRTGAPPQ GSW/P*^SPGRSQTADPVKG VAGRERCLPLIE*ASPGPPHG* AGQVPGAGPPTAG*GV*TGTA PCPKAOPRK*QR*R*RCSS*VG* ESA^IVCPQGDAEG*RKGP^G/ SHRRNVP/SYNSNHGPYDSNQ PHRKTKitFEEDKV DSTLIGSSS HVEWEDA VHI PENESES DDEEEE EKGPVSPRSR PRKRP/PSATRAAA SRLRG*^TLG LLLCIFAFFAPP SPTEGACAHPAQSLSGPRLSRFC HLRILCPARGLHQGRDDG
8055	38423	C	8110	58	504	
8056	38424	C	8111	203	1874	
8057	38425	A	8112	32	1026	KLLEQCLHSVSTWETI^QYRRPP SPS*^RGSREOPCSFSSPRDTPGE NHWLSPQRD*^AGPPVR/PSAG GFMTP/PPRGVPTVEVPPDPTC/S PNHTRPRPFPFSKNPCFRFPEPL RAPTLVPGPLPPTHPGRVPHLE RNLSALGLGKSEGLKRNPVCVEP /PAPTPIRFPKITGTPLR/PAADH ALLGMRDQSLSGQSPGPKSPDA DDQLQNDRHTETEQRISGRSS ALAPESQLQQGCAGIHFRGRFC KAPPLASGP/A/PPCLSI.LPPPWW APVRPKPPR*APPAP/PPVSPIN HPRAEECGRTARDWQAAPLAA LVRDPLDEASWAPESGGDVEN LYV

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8058	38426	A	8113	3	909	TEGGASHRAHPVGPAAPRG\KRH SGATEPANGTWARRRGPGRDS SNQSSGGERSQLRHGRWRL SRPLLPPGAASPLAGEDPERNA G\GWRRGGAAPMRPKRGPMMNG GCGPGAGSGAGGEALGRGRGA VSGCRPAPPVRPPPPPPPPGG WLRRTAGSGPEYV/GSRCARGS GQVSAGGGLCARAARGKLAP RLRALRGRSPWPAPLGRSPAR APARVPAGRCGPAGA*GRCAL GGQGEEGPAGSEGAGRPLPGRP GCPGTSPRLLPRRPVTKTDVGN RSSFFRAPGRAPHAQCPTQFLII
8059	38427	A	8114	I	454	
8060	38428	A	8115	2	172	MFIYTSIFI*QFTNSINIPI*TSFC *TASVHLSCIVAVFCFHCQCQCSS SFIQCTTN
8061	38429	A	8116	I	594	LAPVFKLIPMPVS/YGIFLYMG WAALSSIQFTNRVKLLLMPAK HQPDLLLRRHVPPLTRVHLFTAI QLACLGLLWIKSTPAAIIFPLM LLGLVGVRAKALERVFSPQELLG LDELMPEEERSIPEKGLEPEHSF SGSDSEDELMYQPKAPEINISV N*LE*ESGSGDPRKQHEVLTQE VRTFLAFGLTSRCSVGLKD
8062	38430	B	8117	I	3402	
8063	38431	B	8118	I	4614	
8064	38432	A	8119	3	435	DHAKLGTRTSGMRPHLSLCCFF SSSYDILMIRITKDRVKNLTCITY TILPTDLPQPGCGLPRSFYFPSSKP TSFWLWACKLFPPPLPISFNPSPA HSKTAHGHSKGKHTEAQM*WS* TGEGITGRCCFVSIKAPPLPSSG PVGGPVGG
8065	38433	A	8120	I	525	MALLPTVLCWLWAQAQFLVDLG QSNSKHQEHQLAPDVAFAKMK GACVCAAGFRGRWRCEELCAPG THGKGCQLPCQCRHGAASC DPR AGECLCAPGYTGVYCEELCPGG SHGAHCELRCPCQNGGTCHHIT GECACPPGW/IG/TV*GPPSPGS LGCLPRETSISLISSIQLCLYLLL

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8066	38434	A	8121	I	1050	MLIMTFHGLLPCMQMACKWQ LRVLVAGIRCSTCPCPGRWGPN CSVSCSENGGCSCKPDGSCCEC APGFRGPLCQRTVHILYPRGCGI RDVGESGNRKQKAVEQYREH WTVSPEVQCSASHFSSVRPKSA CPPGFWGpacFHACSCCHNGAS CSAEDGACHCTPGWTGLFCTQ RCAPGTFGYGCQQKCCECMNNS TCDHVGTGTCYCSPGFKGIRCDQ GIMLLL/CPHCGAAAGPICLASAA AEREGPRPGSPCLLHTCHEDDQ HRLLLPLSGANSIPTYR*SGRPS PLRTEALIILPQICQKFSGSQGEV CAVSCAAGTYGPNCSSICSCNN GGTCSPVDGSCTCKEGRIICLQ
8067	38435	A	8122	3	732	IRCDSTCPCPGRWGPNCSCSVSC ENGGSCSPEDGSCECAPGFRGP LCQRICPPGFYGHCCAQCPCPLC VHSSRPCHIIIGICECLPGFSGAF CNQGVQAPTGNPSPGWYRS*EM TDPRCSCR/CLSGESTRHTSPVL LGTDASETQVIGFVNLAQFLIIIC PRKLHYKAQNSKKSNNGDASS DWKDWGIWDRESCHEELCPGGS HGAHCELRPCCQNNGTCHHIT GECACPPGWTVGA/HC*ALCCP
8068	38436	A	8123	77	864	PAVPEL*VFQAKPERKSRYWQL HFPPHSSSPTSWRKSLPEPMYRC TCPPLTPYGCCTCPLSPYRRTCP PLTMYRRICPPLTPYRCTCPPLT PYRMFSSPLHKEITSQAQRSPEPS SRPHSSKAAALR*QPRIMEKQRI YGPSPTSVQPASPPPCLDDPRKK AERPDRATGKRHLPESTL/YA ELVRRAVENPEDSEAPAPAPAA LSPASEHRTDPIQETKARKSSD NDGSTPLAQTPTRRSSSQWRLG QFQQQEDDSSGLYSTG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Net hood	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, =possible nucleotide insertion)
8069	38437	A	8124	314	1188	KHFLNFCLPYMILNKYRNQYCT FNDDIQGNKIFTAYGSITCLKLV HNCIKKIWLVDSKGLIVKVRIC HF*PER*LCHSWGPSNLEAIVQ EIKPTALIGKHFLSLLPYPLF*P DCFFNERPIIFALSNTPSKAEC SAEQCYKITKVK*NYNRYFNNQI FIHYREATLYPGQGNNSYVPG VALGVVACGLRQITDINFLTTA EVL*NPLSLPRV*NTKCAOPRN TIRDVSLKIAEKVKPLFLKLHYF SFLFLNMQEAFVRSQLQMYSTD YDQIQLPDICYSWPEEVQKIQPO
8070	38438	A	8125	1	1115	SPAQMVFQCLWKSCGKVLS TA SAMQRHRLVHLGRQAEPEQSD GEEDFYYTTEL DVGVDTLTDGLS SLTPVSP TAS/IAACL*PPGAAR AAGAPSPA*SPAACAPAPAP CPEHRC*PPVLSQ*PCLPRAA*R PPAWSRMRP RRLPEAHPCCPPGS ESS*GSPAATRISAGM*VGMEA PGPPGAQPAAGRKP PAVPGLK SGSFKNIKLPPS P SPPP GPG AET ARRNPQGAGPS PAAGSAFNW VGVPDLTLEPFP PPPGPEGSPPT QS/SPLKKPSFLH*SPNPHPLSPF TPKPGGGSHPSRLSARRFIKG V MGPALGGQS RCTLRGVGE GTP PLALNSTALGPWGCYPCFLK LQVSHVWAATRRREKLKI
8071	38439	A	8126	116	333	KLRDRCLSH*K*NGASPPRPTN VSIMRPSLV/SLVHHSGL*FPQM LRALS*L RVFGVAVSSP*MVPL NPCI SH
8072	38440	A	8127	5	829	KPSPQQPCPRPGPPRARFLRRSP DVEKIPFA*RPCDVGRRPAGG ARRAASLG/PWVRRRLQARP G/LFRPRDFYLRSRSPRSYGT R* KSP QSSPRGSARPDPGPA/PPPEPV KRRARGVLESSRHAAPR VRVFL GREREQSQEGPAWPKRGRPAPS PQRTATW RPAAGGGK*GSAAT S*ARAGPARRGKRRGY*EPREN R RAGRPA TRGRPPGRCCPPA*S PRPSKRSSPLCSPRPSWPTRPS KSSYGA SLARTT LQWKFSVN L IRKQIRDAQ

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8073	38441	A	8128	5	844	KPSPQPPCPRPGPPIRARFLRRSPDVEKIPFA*RPCDVRRLQARPGRARRAASLG/PWVRRRLQARPGRFAPGTFTCGAPRSYGTGP*KSPQSSPRGSARPDP/GPAASARATREAQSQARGLGELAARGSQAGLP LGKGARTEPGGSS/CSQGPAPWKRGRPAPSPQRATWRPAAGG GK*GSAATS*ARAGPARRGKRG*EPRENRRAGRGRTRGPGRRCPPA*SPRPSKRSSPLCSPRPSWPPTRPSKSSYGAISLARTTTLQWKFSMLNLIRKQIRDQA
8074	38442	A	8129	795	914	RGIKLASEMYPLTCFWRS*LYRGSLARIALVNCRRNAL
8075	38443	A	8130	4073	5350	YSLKSGSVTPLALFFLKIDLA MQALFWFHVNFKVVVFVNPNSKK AIGSLMGMTLNL*ITLGSMAIFT ILILPTHEHGMFFHLFVSSFISLNS NGL*FSLKRSFTSLVSWIPRYFIL FEAIVNGSSLMIWVSVCLLVY KNACDFCTLILYPKTLKLILIS RRFWA/GQWGFLDIQSCHVQTG TI*LPFLIYEYPLFPPLLNCPCQN FQHYVE*QW*ERTSLSLPVFKG NTSSFCFPSMILA VGLS*IA LII RYVPSIPNLLRVFSMKGC*ILSK AFSASIE/YNHVVVFVFGSVYMQ FLLVPLVEFGCESIWWSWTFFGW *AIDYCHNFRSCYWSIQRFNFFLV*SIGRVYVLRNLSI SSSRFSSLFA *RCL*YSLMVVCISVGVLVVISPL SFFIASI*FLSLFFFTSLASSLSILL IFSKNQLLDSLIF

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8076	38444	A	8131	1	1715	MDGIGGGKRALRERHSKSKAL GRCPWPTNITPPALPGITNDTTI QQGISGLIDSLNARDISVKIFEDF AQSWYWLVALGVALVLSLLFI LLLRLVAGPLVLVILGVLGVL AYGIYYCWEEYRVLRDKGASIS QLGFTTNLSAYQSVQETWLAA LIVLVAYLEAILLLVLFRLQRIRI AIALLKEASKAVGQMMSMTMFY PLVTFVLLLICIAYWAMTALYL ATSGQPQYVLWASNSSPGCEK VPINISCNPTAHLVNSSCPGLM CVFQGYSSKGLIQRSVFNLQIY GVLGLFWTLNWVLAQGCVL AGAFASFYWFHKPQDQIPTPPLI SAFIRTRYHTGSLAFGALILTL VQIARVILEYIDHKLRGVQNPN ARCIMC*FKCLCWCLEKFIFKFL NRNAYIMIAIYGIKNFCVSAKN AFMALLMRNIVRVVVLDKVTDL LLFFGKLLVVGGVGVLSSFFFVS GRIPGLGKDFFKSPHLYYYWLPI MRNPITPTGHVFQTSILGAYVIA SGFFSVFGHVCGTRSFLCFLGK DLGSVNNGFPGDRPY/MVPRAF FLKILGIKKNEAPPDNKKRKK
8077	38445	A	8132	1	208	GTRASSPAPCPSSSSAPAHSFEAC CCRMSLWGSCGGSGDGSSACG SGWNLSMAGTSCSSPAMCSPSR APS*RSASRPTWRATTAASS WAPRRCWCWA*SAT*PSSTTT ISSSPHCWPCPASCASAAAWL SSTWATASVAGSCWGPIM*SSA PAHSFEACCCRMSLWGSCGGS GDGSSACGSGWNLSMAGTSCS SPAMCSPSRAPS

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8078	38446	A	8133	28	1956	SRAARERGRSDGGRSRDPGCPA VPACVPRSRPSMTAPAGPRGSE TERFLTPNPGYGTQAGQSPAPPT PPEE/VRSPSPSS/TNTFS*VPATSF EPRAASPAS*CCKWSRSWWSR CSSSCLGSVISWL^HSGKRTPSP SDTSSCWATRTERMTPSQPTRG SSCTRPPSSMLWTSAGGRAGAG GQAGAVPGVA/WTCHWAGLLS ASGTTTEATWTRPTHTLTLIRW WLLTASRWRIPPSGPLRPPATISP SWKAAPVTRTSRSNSTACSL EGGPVGVSTW/QGTLALGAGRDP KTPLTLTRASCLGWMSMPSTSG *RPLTSRASSIMRSRTAIPSAS*S RLTTKHTVGGSPSAWRPRPTSR SVSTPVSSSTGGQQLPGSCLTW WSYSPAPCTSSS/SPLTPSRLPAA EQSLWGSCCGSGDGSACCGSG WNLSMAGTSCFVTSDVLHHLG HHS*RSASRPTWRSRRAAS SWAPRRCWCWA*SAT*PSSTT TISAHPWPCLSACSRSMSGTTC L*RSPPCRRSRAAAAWCGSSPS STFTPSSSLFILHGAQPLHRAHH RAPTYTIKHSRRRRRKRRASCR PYIAQCPGQPHLRQVPPRERAR PIAILLLLRKGPLGGAFAAEGLI RPDCRWTVGPGLQRPPTPLIYL
8079	38447	A	8134	1	2994	MQRPCLCVEPMRLCFDSFLLLV NQGEEEEVGVPVPCLEENGRAAA DPGPQDQDCLLPTLTPSLSGDE APDRITQSSGDPRERCGYLSVTC EEGDNRFAFCLCGSWRLNHG HADWCQDRRSQISNRLPASLGII VGTRGSRHLLAALRGVKEDRQ TKGCVQTAPSLPWLPGSSET RAQKTCVLLIDYATFLKLAND DDDGCLDCCLQPGVRTAWASSQ HGIRAPRKSVQGSASSPSLRTW ALTCTQNWFCCVLLVK
8080	38448	A	8135	215	418	

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8081	38449	A	8136	767	1458	WREHLTGFNVWGKQHLESNS QQKNMRCPVRSQTRPTDVKP VSRSGRREDRRAAGEGGADR QGPGTARAPGSPQRGG*GR NLRIQAGPPGKGHRGIPPPQTRG RSRGAPPGTPEGPRHPPRASRA PGPATGAKRPQPQTQRQGHIA RDSRPPSDPVPLRETGAPPWD A SQGQAARPRATQTPSSAVPA TRQSGGRRADSRRRGVTRTER CAQPSLAWSRVPTR
8082	38450	A	8137	3	424	
8083	38451	A	8138	1	813	MVQKELEEEGRKSTPQSWSGRE NMEKALNSSLKASLGLSGGVMI CASVKALLTVIAKVVLGRLL ES LFLLLQTQTA*QLT/RHTNRNI SHQYQDEIIILGSIDLPRMSPRR KYEPVVFPGRKTYKISIRGKAN KKCEEARQEKEAMVMKYVRG EKESDLRKEKETLEKKLRDAN KELEKNTNKKIKQLSQEKGRHLHQ LYETKEGETTRLIREIDKLKEDI NSHVIKVKWAQNKLKAEMDS HKSFKNPLVRCNFAATFGYYK KLIPIEKTGSSH
8084	38452	A	8139	3	808	NVRVEPTDSSFMEAIEFAQKG FDAYAVVGGGSTMDTCKA\AN LYASSPHSDFLDYVSAPIGKGK PVSVPKPLIAVPTTSGTGSETT GVAIFDYEHLKVKGITSRAIKP TLGLIDPLHTLHMPARVVANG FDVLCHALESYTTLPYHLRSPC PSNPITRPAYGGRNPISDIWGYS TRWGFVG*VS*RRAVQEIPMDL *KARSHMHLASAFAGIGFGNA GVHLCHGMSPISGLVKMYKA KDYNVDHPLVPHGLSVVLTSP AVFTT

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8085	38453	A	8140	2	1154	IDPLHTLHMPARVVANSGFDVL CHALESYTTLPYHLRSPCPNSPI TRPAYQGSNPISDIWAHALRIV AKYLKRAVNSTDK*RRRMSLR APSWEWPSPSRGPARCLPFRFY IT*GS*QRYLLWPLLETVDKEVY VSLQFSFRRQQGVV*ITCLIFLPTE *HFFFFHHIP*GSSLFCRNCQC* CVIVRYLYHSQGWQKSR*S*RQ GLIWHILGKCFLLGIGFKCWVF ICGHGNV/SYPISGFRWKDVKG KGIVNVGHPTGWPPWAFSVPV HVPOQRCTFHGPRCFPERTPWR WQEILGADTRTAQ/RSQDAGLV LADTLRKFLFRSG/IVDDGLAA VGYSKADIPALVKGTLPP/QER VTSFAPRPRQSEEDLAALFEASN ETVLNVHLN
8086	38454	A	8141	2	990	WENWISIC*RMKL/DPYFSPYTK IKSKWIKDINVKPQTMKLLQEN IRETLQDILGLGEDFSQAAQATKA KVDKLDHVVKFKNFCTAKETIN KVKRKPKEWKEKILIFADYPSDK GLITRILFIDHSWVFLGEGNLAG SSDNSSGGKAWKHLLPLLASRCSCS GTHSNLRAKLRLSQGTVATWP VLKREGEKSCGPSESPDLGAPQ ARDVTPCLGICCSSWLLQASGHH HIPWCQLWKLFWVYLVQLQPH REVALVPAPGAAHPTTASVPVC AQWLDPMVIHSHTLCSEPDPS LAGMGRPVQAQAKHNPARPSG WNESSRPEQNLDKGATSHRGF WLAR
8087	38455	A	8142	1	196	GQYPWPLETNPRFLRE*TLPKS LQKSLL*DSPVPE*SLCGTCQQA RSLSEEVDESSISQQVCCPT
8088	38456	A	8143	3	413	ITLGKDICIIMHGMYML/KLGNPFL TQWQRRYFTLFPKNI*WRRRG SIRQNLLTMEQILSVEETQIKDK KCILFRIKGGKQFVLQCESDPF VQWKELNETFKEAQRLLRRA PKFLNKPRSGTVELPKPSLCHR NSNGL.

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8089	38457	A	8144	705	1983	EIKVDSSLKSFLDLMMNGKQNL ENLNALKDFAMMLNLISYATEII LGLEHMHNRFVYRDLKVRTI DRLILHSRYCVNGPLEDKVTEK DFPGNPEIKPSIGKWLGCP*KS PTLSQRGLMTLPQCTLGSG*LSF PE/VLDLP*WTNAHFADWFSLG CMLFKLLRG*VEMHPPSSAVLM AAGAWMKTTVVRGFKTVFLSV W*LSCFIPSKRDVSKRLGCHGG G*AIVPAFRYLQKSKIVLNFQ YPPPLIPRGEVNAADFIDGSF DEEDTKGIVHMIChLFLFYFYF WM/VMISVGKQEVTETVYEAV NADTDKIEARKRANKNQLGHE EGKIAHVSQNISNAVNQFNFLY LTQWQRRYFYLFPNRLEWRGE GESRVSLRQPCHRACFPVRTMAY GYWLRLRAPKFLNKPRSGTVE LPKPSLCHRNSNGL
8090	38458	B	8145	156	281	
8091	38459	A	8146	2	181	VWCCSRATLRTRNCCRRC RGSRTWKRSGRSSSRRAH/SQ YDLERLRAAQKQLEREQE
8092	38460	A	8147	3	670	ETGLKNEGRVLRHSAWCPLL WGREGSRSSLSSWPELQGSPLC ASQGVVLQQDSYIEDQKLVLSE RALTRSLSRPSSLIEQEKKQRSLE KQRQDLANLQKQQAQYLEEKR RREREWEDERELRIDGRPSWP SARRCSRGSRTWKRSGRSSSR RRAH/SQYDLERLRAAQKQLER EQIEQLRREAERLSQRQTERDL CQVMLGPAESNLMMILKTPCV LSKVRK
8093	38461	B	8148	47	699	
8094	38462	A	8149	1	242	MNRGGFAVKILALLDALSTVCS QRVQAKKQQHLQNKEHFKA LLKQKEKLKQQEDL/RKKLF*IQ GIRCPQATPHHGQCSL

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8095	38463	A	8150	3	929	ASSCVVRAVPPG/SGVWGFRCG LCGPDCESGLLISGSRNFAGPQ G/PGAGTAVTLLAAGEEGLS STAQHGSGLCSEPPPVPRRHA WQGKSYSRNWLPPARPRPALA MSSDTRGQAQLSPSWQLEKKG LSSSTAQRGCRALQGRAASARR QRGANPTAGTGWLRLAPGLP LLCPQTGGGRHSCHPPG/K/PGK EGLEQFYSSARLQGFAGKSRQV PDVTRGKANPTAGTGWL/R/H GPRGEACAMAVGRPRSHEQR CPWSAGADSV*^GHCIE/TDGR VASGACLQVDSRGSAGQNPL DPEHW/HIVFCFDPP
8096	38464	A	8151	2	1749	WVQGASLCVRASRAPLPLARP* VQGAELTHPWGPAAHP*TRNQ KPALGSSGPHSP/GNPQPTPTQA GQP*PHTARHGPVQEHRGRQR GPHLHKTETPQEATP*EVGSIAT EQAWLPHLCL*RPPPFHQGLFP RGPCMegaQQRVEGSSQAQGT QVCMGPKTAGDWDPWLVCW FH*GEAAARILRPLGLGGLSGHP LWPQGGQMTVGYGGASEAC GAGELLMRRAPPQSPGKARGL PA/HYWHQQTGPKAEI
8097	38465	A	8152	1	583	MAAVVAATALKGRGARNARV LRGKERDPGEGRTAEDPPFSFTS SPTIAGGILAGATA NKASHINR TRALQN/HTASPEGKEP*/DPLS PELENTPRKEGQRTPMESCGN LPWAIGFPLWFLPLSSFTQAG KWDK/VTVLKAD*RLRAEHCG FSNTGRV*RARRFRALFPEVAPF PLMFSGVGSGGADLRSVCDPP
8098	38466	A	8153	141	341	GTRGSPSKKGERVRRDAQQTA TW*TRSPASGCFQICEGNKQDE ACDVRLQHCEHSLAGPREY
8099	38467	A	8154	1	521	MKNRSRNKG/NVEWQAEIRSK RSVGKQRPSKAKIPSGDKNGVS LTHNEVINNDNPLESNDEKEGQ EATCSRQIVP/EFQQ**LFRPE* WRRASGNLQLIPKKRVS*A GTR GSPSKKGERVRRDAQQTAW* TRSPASGCFQICEGNKQDEACD VRGLQHCEHSLAGPREYMP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
8100	38468	A	8155	1	619	PEAELHNHGIQINSCSVRLVDIK KEKPFNSNKVECQAAQARTHNN QASDIVISSEDSEGSTDVDEPLE VFISAPRSEPVINRATPCELKC* KEG QEAIC/SRPRDVPRALGFR KFPSFEEFRKGLLQDQDPFPD SIEKKPPAEASSG\ALRSKIHGEK APMTSRSTSTWRIPSRKRVFSSS DFSDLNGKELQETCSSLRRG SGKE
8101	38469	A	8156	362	1043	PTTPPSAGSSWTTASPPS*GKA WLGTGRPPSPWRRMSAMRTS EEDGRLQPQLPL*AH PSESSQ DRGNQVSVGREADCGQD/SPVS TMTRSHPGRPCAEGC**PCCSR P*PCPCGSGLVTSPPLSLPAPSF WLPLRPS\SPPGLPPLQSSLFSPP PPPPVPQPPAPPALQWGLHLPR VPQGVVPAGRRVVRLSAKHLPR LPDHVS*GAPGRRLREHLPQH RPGDQ
8102	38470	B	8157	52	633	
8103	38471	A	8158	15	3054	AGPDGLAAPASCQGARGQTRV PGAFSWLAPGSHHASEGLAPG VPPAGGVSAQELTAPPQEGWG LGAPPAAPRPESDEKRAGSDAV RSFSRGARDLSLGQRRLGGTRGA GPAGKGAQRTMGPASGGFHSSFP RPHQEPPSRSSCWQHLLWHCP WPQPSRLPRLTPAQLLQQPGVLU AAPPGP\HVPGLAQSPWPLPS GPRSP*DPLHQGALVPLPQGGS PHTAPHCLPSVLSPA QQPLLPT AST/SSRSPASTMAP
8104	38472	B	8159	748	3111	
8105	38473	A	8160	1	463	GGGGGRGQRGRPSRPRYLCGP GPTG\PGACAAGGVTVGPSED NGRPLLPPQRHPVGFDSRRRC RFLRLPKHKERSPDARFKEGPGG AA/GPGARGQ*DSARTPDS\ALK LVRPPLPIPTGRPSCASGGR*PA GKRGHLSAPPGRGRSSPGSQ

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8106	38474	A	8161	1	2733	MALRRAGAGR TGC FIA IDTML DMAENEGVVDIFNCVRE/LRAQ /RVNLV/QTEEQYVFVHDAILEA CLC/GNTAIPV/CKLQNLFQNTK CTAMS NYTLTQGLLQHWLS*T T*FIWLAGTMRLCLSLCVDAAAS APWVLKTLNIVT/PRVRPEDCSI ARP NHDKNRSM DVLPLDRCLP FLISVGESSNYINAALMDSHK QPAAFVVTQHPLVTFVADFWR LVFDYNCCSVVMLNEMDTAQR GQS FVGPLEFGGAQL
8107	38475	A	8162	1	307	
8108	38476	A	8163	3	969	GLFC SKRTTPSK*KH NVIASDK AAEK SVVHEHEHS HDHTQLHA YIGVSLV LGF VFM LLDQIGNS HVH STDDPEA RSS NSK I T T L GLVV HAA VF YV SLP NIADGV ALGA AASTS QTS VQLI VFAIM LHKAP AA FGLV SFLM HAGLER NRIR KHL LV FALA APVMS MVT YL GLSKSS KE ALSE VNAT GVA MLF SAGT FLY VAT VH VL PEER L KL VTVL GA GLLC GTAL AVIV P E GVHAL Y EDI LEV VP SFY CHLY VY EYL MFSS HF CSDP PW DQQL LT LRVC SSTS ASLGE GLGVSSI RK GMEL SVQA QHH VEVAKA
8109	38477	A	8164	164	240	
8110	38478	A	8165	2	417	QQIR KLIK VGLI IHKP VIV HSQV GCQK STFS/RTR KGRH MG TG*R KSTANF QMPEK VT WMR MRIL HWL FGRY HESKK TDHH MYHSL YL KVQGNMFT NKQIL MEHN HK LKADKA HKK FLAD QEA RSSK TNK ASK LK REER
8111	38479	A	8166	1	86	RTR GCL SHHHHH *HL RHR HHL HHYP SY*HHH CL NYH/APYL F HWLYH/APHHLNQH A HYL HLY YHHH YH NHHHHHLHHH HIRSHCH HHHHHL T HLLC QHHHHHF HPT KHLLAHP QAL QTH HNNH DMD/ HHHYP SY

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8112	38480	A	8167	50	1156	LLLQFSRATFILFQPPANTFTSA FSQTRARRGGSGRGGGQESAEETSEFGDRHAPEAAAATRGSR APEPKHASSCGTRGQCACARRE VEAQVRAKGDVTAAERARRGGR WLTRSGMEHLERCEWLLRGTL VRAAVRRYLPWALVASMLAGS LLKEPLSPLESYLSNKRNVLN YFVKVVAWTCLLPPFIALTN YH/HDRQGWLGPAAD*/CTLLV GTAIWYICTSIFSNIEHYTGSCY QSPALEGVRKEHQSKQQCHQE GGFWHGFDISGHFLTCALH DCKKRCLCLQ*^rKTDRSHCLH TAITTLVVALGILTTFIWVLMFLC TAVYFHNLSQLKVFGTIFGLLS WYGTYGFWYPKAFAFSPTSSPEL
8113	38481	A	8168	2	926	
8114	38482	A	8169	2	1053	TRERFSVANRVGTGSETVPKAEA GPESAAGQEEEEEDEELSG TKVSAPYYSFWGTLLEYHNAMV AGTEEARDGSGAGVRVLYLYPT HKSLKPRPVSLLEGKCRFKENCR FSHGQVVSLDELRPFPQDPDLSS LQAGSACLAKHQGWPLERQHA SPMWWDNGYLHSQV*LAAAIRE AVVGGRHPAPTAHKRPQESD SDS\EVRVTPAMPPEWWQQLMWW TLGPAALPLLGEVHTRGIGSR LLTKMGYEFKGKGLGRHAEGRV EPIHAVVLPRGKSLDQCVCETLQ KQTRVGKAGTNKPPRCRGRGA RPGGRPAPRNVFDFLNEKLQQG APGALEAGAAPAGRRSKDMYH CQQECQAGP
8115	38483	C	8170	166	419	

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8116	38484	A	8171	55	1157	ALDEPHGAGASEERAGDVFGPP RRVPGPSLWPLEAWPTSSQKV MPQVRCLHLHQVWGRQGGPPR IKRWAWAARGHTGLCPTPHGP SIWTHSNFLKEKIF*KMFAIKV GPEAKQSPLPNGFPGVATAWSP VRSSVCPLFIKARPSC*QLQDSC WDPGGTTADPGHGTGLELRPF PPKPTLPLALSEAPVPQREEKTQ GRGHYPAPQCLPGDPCSPHHPA PQPHQPHPAR/HN*PPPPIPSSHP PTTVPPTRPQPWPQPGCCAQPPR PCLH*RGGN*VY*GMQLHQKS VSWPHSQWPQKREGNGSSHIEI HPSCPPSGFHGPSPERGMRPTQA GALHSWVPGLSLSHGSGPHPPP RWTATVQAARPRVPPLTNL
8117	38485	A	8172	1	362	LFDNTVYCPRTERLLKNDTKH QRHAQSACOQLSTTLVCSQHRK VSDFIFQHKHSAPLPQKSKRKQ NQQSFMKTLTKNLGIIDEMYRA IYDKPTANIILNGQKLEAFPLKT GTRQGFSLSPLL
8118	38486	A	8173	1	655	MIISTDAEKAFDKIQQPFMLKTL DKQGIDGTYLKIIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPF SQLLFNLMLEVLTAVREEKEI KGIGKYLGIQLTRDVKDLFKRN* KPLLNEIKEDETKKWKNIPCSWI GRTNTVKMAILPKFR*WTR*RQ FSTVHKD*KLSETVSHSYLKIKF WKLKRPFLLLHSEPLKERQQDSV SLMNWVCMSSKTGQY

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8119	38487	A	8174	2	1936	DKPTANIIILNGQKLQAFPLKTG TRQGCPPLSPLLFNVLEVLARAI RQEKEIKGIGQLGKEEVKQLSFA DDMIVYLENPIVSAQNLALKLIS NVSIVKV^GYKINVQKSQAFLYT TNRQTESQIMSELFPFTIASKRKJRK YLGIQLTRDVVKDLFKENYKPLL N^EIKEDTNKWKNIPCSWIGRIN IVKMAIL^PKVIYRFNAIPIKLP TFFTELEKITTLLKFIFWQNQRKARI AKSILRQKNKAGGITLPDFKLY YKATVTKTA^WYWYQNRDIDQ WRNTEPSEIMPHIYTIL^FVDKPE KNKHGGKASL^FIKWCVIENW LA^CRKLKDPLTPYTKINSR WIKDLMVRPKTIKTLEENLGITI EDIGVGKDFMSKTPKAMATKA KIDKWDLILKLSFCTAKETTIRKA NRQPTTWEKIFATYSSDKGLISR IYNELKQIYKKKTTNNPIKKWAK DMNMRHSKEDIYAAKKHMKCC SSSLAIREMQIKTTMRYHLPV RMAIIKKSGNNRCWRGCIEG LLHCWWWDCKLVQPLWKSVWR FLRDLEIIPFDPAIPLGIYPND YKSCCYKDCTCRMPIAALFTIA KTWNQPKCPTMIDWIKKMWHI YTMEYYAAIKNDEFMSFGVTW MKLETIILSKLSQEQQTKHRIFS LIGGN
8120	38488	A	8175	2	1105	LPTKKSPGPDGITAEEFYQRYKE ELVPVLLKLFQSIEKEGILPNF YEASILIPKPGRDTTKKENFRPI SLMNIDAKIP^*KY*QN^IPAAH QKSSLHHHD^KVGFHPPGMQDW FNIHKSIINLQHINRAKDKNHM IISDAEKAFDKIQQPFMLKTLN KLIGIGGTYFKIJRAJYDKPTANII LNGQKLEAPIFEMLKVMYRAF RQNKOIKGIIILEKEEVKLSLIFAD DMIVYLENPIVSAQNLALKLISNF SKVSGYKINVQKSQAFLYTNTNNT QTESQIMSELFPFTIASKRKYL GIQLTRDVVKDLFKNYKPLLKE IKQDTNKWKNIPCS^VGRINIVK MAILPK^DVLASPSPFTMTVT RKQVQL
8121	38489	B	8176	120	2036	
8122	38490	A	8177	3	316	

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8123	38491	A	8178	1	1447	MSIRVTQKSYKVSTSGPWFFS CSYLSGPAHSSLFSRAGSSSF QGGLGRGYGGASGMVEITAVM VNQSLLSPINLEVDLNQIQAMHT *EKEQIKTLNKFASFIDKQVFLE QQNKMLENKWSLLQQQKMAQ SNLDNMFEYINNNLRWQLETLG RKKLKLEAELGNMQLGVEDFK NKYEDEINKYTEMENEFVLIKK DVDEAYMNKVELEYRLEGPTD EINFLRKLYEQEIRELQSQILD SVVLSMDNSHSLDMDSIIAEVK VQYEEIANRSWAEAERMYQN* YEELQMLAGEIHGDDLLSTKTEI STINQNISWLQAEIEGLKGQRA/ SLESTITDVEQRGELVIKDANA KLSQLEAALQRAKQDMALQHL EYQELMNFKLAQDIVITTYRKL LESEGSWLESGMQSMISHMKMT TSGYAGSLSSAYGGLTSPSLSYS LGSSFGSGAGSSFSHTSSTRAA VVKKIEAQNGKLVSKSSDVLPK
8124	38492	A	8179	272	1813	KCGLRSRSSFSAPSRSIAWFPP ASTPASTMSIRVTQKSYKVSTS GPRAFSSRSYTSGPGSRISSSFS RVGSSNFRGGLGGGYGGASGM GGITAVTVNQSLLSPLVLEVDP NIQAVRTQEKEQIKTLNNKFAS FIDKVRFLEQQNKMLETKWSSL QQQKTARSNDNMFESEYINNL RRQLETLGQEKLKLEAELGNM QGLVEDFKNKYEDEINKRTEM ENEFVLIKKDVEDEAYMNKVEL ESRLEGTLDEINFLRQLYEEEIR ELQSQISDTSVVLSMDNSRSLD MDSIAEVKAQYEDIANSRAE AESMYQIKYEELQSLAGKHGD DLRRTKTEISEMNRNISRLQAEI EGLKQQRASLEAAIADAEGRGE LAIKDANAKLSELEAALQRAK QDMARQLREYQELMVNLKAL DIEIATYRKLLGEESRLESQMG NMSIITKTTGGYAGGLSSAYG GLTSPGLSIYSLGSSFGSGAGSS SFSRTSSRAVVVKIETRDGK LVSESSDVLPK

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8125	38493	A	8180	1	3519	MHKELPALAACGLVADFDPVG EEETADFGPLVLDSDDDSVDR DIEEAIQEYLKVGSSKDQGSASP VSMSRADSFEQSIRAEIEQFLNE KRQHETQKCDGSVEKKPDTHE NSAKSLSKSHQEPATKVVRHQ GLMGVQKEFAFCRPPRLAKTN VQPRLSRKVTTTQQEKGST KPATP/TRPSEAQNKGSIKRSA STARRGKRVTSVAQAAPEASDSS SDDGIEEAIQLYQVQVKTHKEAD GDPPQRVQLQEER
8126	38494	A	8181	208	445	AACVWRERHHRAEECGCPGVH LPLLH*KSKWPGRC/RLRGN AAHHPPWGQQQATPALCGGLQ QPESSQ*GLSSLGGSR
8127	38495	A	8182	1	1607	MDMFRSGIRRGGGLGDGVRA RRRRQGALAGSSQPIQAAAVPR GPGPAPRDRPSWPSCQGSSGEA *PYWKLEGAGLE/RKRGTETIRA VGEQLESWRSWRKDVGACQSSP TPIPEFGAAAPTKS/GPAGPSSTQ QPSSRIWAAPRKRLAG*DTAHK NHPSAAPPAPQDRARPK*PPR ADPQRSVTPPRSPKG*GSPFP KQ/PRIPKSGAASEASNPLLAITS QVVGGESETRVEGLMKEESV REGNAAFSFLRKSV/ACKPPAS EKDRGSRAAEGDEHAASNLQEP IPHLP*TALGERPEARQGPIFRP PGEPCSHPRSVNELGTGEPHTF QLGCLQRHPGAVDQAGPRGPG AGSRARETGKTGTNSEAAVRQ EPKQRILSKIHTSTSPTGHRL/EPT AFRTRSARSPELASGHQAGKVV AGPRVRARGA PPTGRPGLAAR PTEAERASRAPC PPQTDARLF TARPRGKSGCRLPAHSPPDPPSR LPGPRSRSR/LSPA VRVVAAGEK EASGAETA FPAWGTMALFWSL QPRALQAL

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8128	38496	A	8183	3	683	ERGITAGPPGVHPPTARSAGAA LPVWDSSACVEGVRPAPAMD *EHQLRISGLGCQDTLMLIESGP QVSLVLSKGCTEAKDQEPRVTE HRMGPGLSLSIYTTFVCRQEDFC NNILVNSLPLWAPOQPADPGSLR CPVCLSMEGCLEGTTIEICPKG TTHCYDGLLRLRGGGIFSNLRV QGCMPQPVCNLLNGTQEIPV GMTENCRNKDFLTCHRGTTIM THGNLAACI
8129	38497	B	8184	230	252	
8130	38498	A	8185	29	316	GRVSRCLPFKLVTPVLCFCLWH RSY*EYRNFMNQISKTQLKQR PTRFTG*QPWPRWW/PAPPRPS QGRLAGREWSTQAHPRDSQGP RLCGEGRGA
8131	38499	A	8186	1	57	SRPVQAGPKATGTQPQPPPS*PEP VERPLSMASSGTHAQGSPSPSW PQLTGAVAQDSPSPGLLPPRDT APAPSMPТАDGVQRCAROSGN TGPRVAT*PVAPTSFPAGPDSGE MG/ESCRRRPGT*PTPFQSRFLR RRPSASRIYGLLGPcvISL/HKK QKSLPPLAAPPGTITVDILFTWAS SLFSLNATEGHTVRHV*CSRRN YQKANA PRTPTASPNTRSHSLG NAKTPPQTVPHRDHPTQEHGT DTSSCAVLSANTRERA AVEC GVTVLNLD*LK*TARYSMSA STGVAGSVQGKR/LRTSALSSG G*GPKATGTPQPPPS
8132	38500	A	8187	1	3564	
8133	38501	A	8188	154	256	
8134	38502	B	8189	1	1206	
8135	38503	B	8190	1	1311	

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8136	38504	A	8191	2	2491	EAGEWEEGPGSQNGLVLVQGEKL PPDFMPKLVKNLLGEMPLWVC QSCRKSMEEDERQTGREHAVA SLSHTSCKSQSCGDDSHSSSSS SSSSSSSSSCPNGFDWDPSF LAEHKRLGLWNSPHSIGAMPGS SLGSPTTIPGEAFTPVEHHHQHSD LTAPPNSPTGHHPQPA/LSNP/AL TPAPLAP/APPHPLLPTPAAPFP AQASECPVAAAATAPHTPGPCQS SHLPSTSMPLLKMPPPPFGCShP CSGHCGGHCSGPPLPPSSQPLP STHRDPGCKGHKAHGSLACQ LPQPCCEANEGLGEEEDSSSERSS CTSSSTHQRDGKFCDCCYCEFF GHNAPPAAPTSRYNTIEIREKLR SRLTRKEELPMKGGTLLGGIPG EPAVDHRDVDELL.EFINSTEPK VPNSARAARKRARHLKKKEKE KAQLAAEALKQANRVSGSREP RPARERLLEWPDRDVRNSFL SSRLQEIKNTVKDSIRASFVCE LSMDNSNGFSKEGAAEPEPQSLA PSKLSGSSEQQPDINLDLSPTL GSPQNHTLQAQGEAPPWAEM RGPHPPWTEVRGPSPVFVPENG LVRR/HEHRAQPIPQGDLGQDTQ AGVHPSSSEEASSKEVPSCKQELP EPVSSGGKPQKGKRQGSQAKK SEASPA PRP/TSQPRGSQCQGPG RWP/TSSQAGS*SLPK*AAV LKL ERGAGGA GQDQVGLAVPKLRR
8137	38505	A	8192	277	434	
8138	38506	A	8193	4	168	
8139	38507	A	8194	26	219	PRLQCIGQPRLTLPFGFK*FLCP SLPSSWDHRQPT*LANF*KNY F**IWGFTMLGMGSCTCNP
8140	38508	A	8195	1	498	
8141	38509	C	8196	105	251	

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8142	38510	A	8197	1	1620	MWGVGKIDDPKDVTDLIPGTC GCVTLHGERHFVVDVIAGPTRS VQGNPKLGSKKMVE SIMKTQE SIKLTWKATTQRNRNNE NGPT TEFHQSTMNTNSDTWMVLD PMKPGGPFEVMAQQTLEKINFT LRVHDVLFGDVWLCSGQS NM QMTVLQTLSCGVVTVFIM TLA GAHGSTLSSGIFS YQSDSLKCK SGRKAPVGRV LRTGYTWSQE NSTGNPDLFVQDHTWQFC TKH SGSYVASMETVDETA FILSTHT SFRTDWELKCFTVRRQLGRQY ERTCYLSFRPVANTVE CIGFRF ASYINNDMLV LQKEPAGAVI WG FGTPGATVTVTLRQGQETIMKK VTSVKGLISLLVCLSQFEIVPED DPQNAIVSSADACHAEL RTIS TTMGKLM PNLPA GAD DFFGS HPAIHNLIQSCP GARKC INLPAS RPVGLSIGPLSP LD SYQWV KFD VCKPDGQLPEGLPENDAAMS FEAFQRQIFDEDQNDPL *SSL* PWLVIMVPL/WSSGIFS/TISK*L FEV*VGSEGSSGSPCAE DR LH VSRKFHRKSRPVCSGSYLA VLH *ALRILCCFHGN SG* NCFHSLHP H*/HSALTGNSSASSQ* DASL GG SMREHATCLLDPLLLT*STVL V FALLHTSIMIWCCRSSL LGQ*Y GASVHLEPQ*P*PCA KV RKP S*R K*PV/CKGLISLLVCLS QFEIVPE
8143	38511	A	8198	1	900	
8144	38512	A	8199	915	986	IITDRPGFHD ESAIYPV GYC STRI YASMKCPDQKCLYT CQIKDGG VQPQFEI VPEDDPVRNAIS FFW QMLVMQNIQSDYK ALLWGKL MPNLLPAGAD DFFGF SHPAI HNLI QSCP GARKCINYQWVKFDVCQ TLEMQQLPEGLPENDA A RALK PFQRQIL**R IDKRNL LLIKQL KVFGKTTITRTH DEIPLVSSL SELLPSFIYPKILV
8145	38513	A	8200	3	414	
8146	38514	A	8201	1	2445	
8147	38515	A	8202	1	248	ENGNL GPIQA EVKGAT GECNIS ERKSPGVEIKSL REL DSG LEV H KIAEGFSESKR SSEDEN KIE FR/KGGF*GGGFLRRK
8148	38516	C	8203	70	324	
8149	38517	A	8204	1	675	

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8150	38518	A	8205	692	808	
8151	38519	A	8206	1	1954	PGTGEETVRLGFPVDPRKVLIV AGHHNWIVAAYAHFAWYRI KESS*WQQVFTSPYLDWTVIERV ALNAKVGPGHDKDMVA ASESSILWSVQDGGSGSEIGVF SLGVPVDALFFIGNQLVATSH GKGVVWNAVTKHQWVQDVV PITSYDTAGSFLLGCNNGSIY IDMQKFPLRMKDNDLVTLY HDPSNDAITALSVYLTPKTSVS GNWIEIAYGTSSGPVRVIVQHP ETVGSGPQLFQTFTVHRSPTVKI MLSEKHLVSVCADNNHVRTWT VTRFRGMISTQPGISTPLASFKI LSLEETESHGSYSSGNIDGPFG RDDQQVFIQKVVPITNKLTVRL SSTGKRICEIQAVDCTTISSTFV ECEGSSRMGSRPRRYLFTGHTN GSIQMWGSGPLLWDMVNKE DKDVSGPTEEELLKLDQCDL STSRCATPNISPATSVVQHSHLR ESNSSLQLQHDDTTHESATYGS MRPYRESPLRARRTESPHSY RDFQTINLNRNVERAVENTPENG GPIQAEVKGATGECNISERKSP GVEIKSLRELDSGLEVKHIAEGF SESKKRSSEDENENKIEFRKG GFEGGGFLGRKKVPYLASSP SIDGGTDSPGTASPPSPITKTP RHKKSDSISGQEYSL
8152	38520	A	8207	2	383	
8153	38521	A	8208	13	332	SKGFIVLLKCLQILKTPSLPGPN QGLNAGKESRGGGLVSVA*RA RPDSWRPGPPLSISITLRRLK RRHHRALPLCCITLASSPNC AP/TSVP*IPRLHPFWL
8154	38522	A	8209	1	1839	
8155	38523	A	8210	1	364	
8156	38524	A	8211	3	3723	MIPAGGRAPGPPYSPVPAESESL VNGNHTPQTATRGPSACASHSS LVSSIEKDLQEIMDSLVEEPGA AGKKPAATSPLSPMANGRYL LSPPTSPGAMSVGSSYNTSPA SPLSPASSGSCASHPSGOEPG PSVPPVPARSSSYHLALQPPQS RPSGARSESPLSRKGGERPPS PGLRGLLTDSPCTTVLAEA ATETPRLGQLPVVAISLSEY ASGALSQPTSIPGSPKFQPPV PRNKI

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8157	38525	C	8212	398	415	
8158	38526	A	8213	3	45	
8159	38527	A	8214	1	929	IAAAPELLERSGSPGGGGAAE EAGGGPGGSPPDGARPGPSREL AVVVARPRAAPTPGSPSAAAMAR PLVPSSQKALLLELKGLQEEPV EGFRVTLVDEGDLYNWEVAIF GPPNTTYEGGYFKARLKFPIDY PYSPPAFRFLITKMWHPNIYETG YVCISILHPPV/DTDPQSGELPSE RWNPTQNVRDHS*V*SSLLE RRPNFTLRPANVGRLPWMLQG SWEREQGGRIRELHRTSFRKQV LGTKVDAERDGVKVPTTLP.EY CVKDQGRRAPDEGSDLFYDDY YEIDARVE EEADSCFGDDEDDS
8160	38528	A	8215	80	430	IAQGPYPPGWCSPGGGNNTSSP RPPPTGGKGK/PGGPQK/PLAPRI PAVFTRGDSG RSCPATTPLSA GSPSLPHRIPEPKPPHRIPEHKLH RACAHPDPGSGLRIFTAVH HGKL
8161	38529	A	8216	3	645	FSVSHLDLEEAGDMVAAQAD ENVGEAQRSLAESPGILTSGTAT PQQNDNDQLNSEEKKRKQRNN RTTFNSSLQLQALERVFERTH*T PSSLFLFSFLMPSCLLTILQVWF QNRRAKFRRNERAMLANKNAS LLKSYSQGDVTAVEQPTDLQLCE TNACYSPCSLLCPYSAMATSYSA TCAINNSPAQGINMANSIANLR LKAKEYSLQRNQVPTV
8162	38530	A	8217	3	907	RVDDFVAVQLGRPIGSCFGRA QLQEVQKPOAMA VGNINELP ENILLELFTHVPARQLLNCR VCSLWRDLIDLVTLWKRKCLR EGFITEDWDQPVANWKIFYFLR SLHRNLHHNPCAEEGFFEWSDL VNNGGDEWVKVEDLSRDQRKEFP NDQVKKYFVTSYYTCLKSQVV DLKAEGYWEELMDTTRPDIEV KDWFAARPDCGSKYQLCGHLS DAAQGPHTFQPDPATIQQKSD AKWREVSHTFSNYPPGVRYIW QHGGVDTHYWAGWYGPVRTN SSITIGPPLP*HPLSPHLLNPDW
8163	38531	B	8218	117	398	

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8164	38532	A	8219	1	3063	MSLEVDRSVE ^T MC ^S GDE ^I LLPD LPKADVA ^D PLWGPF ^P VQNCLS LARS ^D SREQGLVLVME ^S RNRE VVPPGVSY ^K DGAKSLKGDV ^P ASEVTSKDSTFSQFSP ^I SSAAE ^C GDDEKIKVVD ^D PLTRRTCNQASG SAPQQDYD ^K LKA ^F GGENSSKT GLPSGNME ^K NKVVKR ^E A ^N SINLSVYEPFKVRKAEDKLKEN SDNVLENRVL ^D GKLSS ^E KNDT CLPGTAPS ^K TKSSKL ^S SSAI M ^A LSAKKAASDSCKEV
8165	38533	A	8220	1	1188	MPLDEDPSKLCRHNLKC ^E CECN ^E IFQDKTSLATHFQQAADM ^S GQ KTCTICQMLLPNQ/CQR ^I HQIHK ^S P*T ^C PECRAICR ^I S ^H CEVFYKC ^P I CPMTFKSAP ^T HSHTY ^T QHPS ^I K IGESKIIYKCSMCNTVFTLQ ^T QL ^T LL YRHFDQHIE ^N QKR ^D VYISHVRK EHGKQMKKQPCCQRDKP ^F SSS HSLCW ^H NR ^I HKVIRK ^V YTCSH CSDSRGTFTKQLM ^L EKHVQLT HGIKD ^P DL ^K E/TDRRHQ*G ^N R NKRRPQGPQS ^V EVERTGSGV QASQGAITQPKLEINVF ^V KVH ^I KC AVCGFTTENLLOF ^H EHIPOHKS DGSFYQC ^E REHLFVA ^H KLKEP ^O H VSKQNGAGEDNQQENKPSHED ESPNGAMSDRKCKVCAKT ^F ET EAALKTHMQTHGM ^A FI ^K SKRM SSDEK

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8166	38534	A	8221	842	2687	KGECLPSALSLNGNGRESLES ESLSLEGFTRGRAGLRTCSPPCL SLPAPPWAVLPPEPRRGAPPAP RRPVPTTQQGLRSAGARRGTGR QLHLRPCR/ADPLGEASWAPES GSAPA LKVRIKTIKMSGGEIKR TVTRVLPEVDLDSGKKSSEQTA SVMASVTFLSSPASAIALS/SSP QGASPVHGHDCSFTC/SSSPLN RAPA/GAI KAANAIQQQTVVVP APSRANAKLVPKTVHLANINLL P/HGSATN/ISRQ*SMQQ/RSQPP KKVSRVQVVSSLQSSVVEAFN KVLSGVNPVPVYIPNLSPPTNAG ITLPTRGYKCLECGDSFAVEKS LTQHYDRQSMRJEAADTRGQK TCTICQMLLPNQCSYASHQRH QHKSLYTCPECGAICRSVHFQT HVTKNCLHYMRRVGFRCVHCN VVYSDVAALQSHIQGSCHCEVFY KCPICPMASNQNKEDKTSMNG KEKLEKKSPSPVKKSVETKKVA SPGWTCECDRLFIQRDVYISH VRKEQGKQMKHHPCRHLCQH NRIKHKGIRKYYACSHCPDSRR TFTKRLMLEKHVQLMHSLKD DLKE/TDRCHQ*GGNRNKRRH QVPQSQAPLHCTQVKGTSASV QAKWSWGR
8167	38535	C	8222	1	438	
8168	38536	B	8223	98	463	
8169	38537	A	8224	1	2679	
8170	38538	A	8225	1	1209	AADTRGQKTCTICQMLLPNQCS YASHQRIHQHKSLYTCPECGAI CRSVHVFQTHVTKNCLHYMRRV GFRCVHCHNVVYSDVAALQSHI QGSCHCEVFYKCPICPMASNQNKE EDTKSMNGKEKLEKKSPSPVKK KSVEETKKVASPGWTCECDRLF FIQRDVYISHVRKEQQGKQMKK QPCCCQRDKPFSSSHSLCWHNRI KHKVIRKVYTCSHCSDSRGTF KQLMLEKHVQLTHGIKPPDLK E/TDRRHQ*GGNRNKRRPQGPQ SQEVERTGSVQASQ/GAITQ PKLEINVFKVHKCAVCVGFTTEN LLQFHEHIPOHKSDFSYQCRE HLFVAHKLKEPQPVSQKNGAG EDNQQENKPSHEDESPNGAMS DRKCKVCAKTFETEAALKTHM QTHGMAFIKSKRMSSEDEK

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8171	38539	A	8226	58	391	FAKNDGFQLHPCPEPL/PWSQT RTQSAAWA*GCNYLQPTGAA LLAYTEFLGPEGKTGW*QGLDR DATGAPSPTARQ/RVGKALGT AASLIPSFIPL*SKKMARETAAW SEW
8172	38540	A	8227	993	2235	NGGPHLWRLPTAHRRAACGERH GQAVACCGAVAEALVGPAPT VGLRRGCPHSAPGGYACPVSSS TYSGLGQRCRVFPHYSPRAVPN LVPALGAPKP*MPGASGL*GD MLPAASVSKRAPTAAGPWMLYP YSPARLDSA/LQALSTKKVAS DSSKEQVANSKESSSLSEKVN SPRAADKSPESQNLDGTTKCTS LKQLDSPRNISSENSIKGTPASP AGSTPPIPKVRIKTTKTSSEIGKR TVTRVLPEVDLDSGKPKSEQTV SVMASVTSLLSSPASAATLSSPA RVPLQSAVVTKQFPLQSPPLN SQSSLWLLSSQCLL*RQQDPK SLI*SSLTTPR*KPRSYLLPLSRV PAAPSLKLANAIQQQTVMMPA SSLANAKLVPKIMHLANLNLLP QVAPATSELCPVSIKTQPOI
8173	38541	A	8228	1	3370	MIINTIIITTTTIIIFTIIMSSPPI ITNIITIIQHHHHHNIDQRPSLKG CRGLYIRVRKVPGERATANSRC PINAGQIESCWNGVMALWLGP NSTCSRLLPELTDSEDCQIYGDTE RKRRHSRKTCRWEYQVETKDT FLEELLFEPALRTGIQSKQGGPL LQLAANNYNLEPKQHFGSWFG TMKQLGETESIFSFAYEVCLTV YEIIFGLPGIAPSKTKFSNFLSCI TAIAALSTKKVASDSSKEQVAN SRESS
8174	38542	B	8229	1	438	
8175	38543	A	8230	38	597	VPCGPHCRLPSAWRTSPPRLWN DTTSRKWKSGVAKSSCYNL*PS AGMRKRKF*LRAPSTLGSALL *NRLMRSRRFCATSSCAS**CEQ RTSLSFEGSLWRSTTTSRPPPSA ARISSASA P T R R R C A S E A C R R S T G R A G P G P G G K Q Q M K A G R I R G T A Q P S S P H P L G I P T H H P D T R G A S R Q T G H L
8176	38544	C	8231	1	1062	

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8177	38545	A	8232	3	595	WSSAQPRASRRAASRSSLRLHSSRRLCLRCRAPRRPQLVASAAGRASSARSRRGSRSSRK*GRARSGGGMSPLAQRLK*ASSSSGRGAAWSRASRGAAARGSGPLTGRRSAPLHSSSTVPCSPRYARPGPPRATA/RGPTRATCLPSHRSTITSRP PPSILPVAVQPALPPGAAGAAPPSPRAGGALAAALGPGLTVGAGR
8178	38546	A	8233	2961	3005	SRLQQTIQADAFAEAKAGCWP GGM/DELEAETSSSLFLAMQVWMCGGRMEDIPCSRVGHIYRK YVPYKVPAGVSLAR/SKNLKRV AEVWMDEYAEEYIYQRPEYRH LSAGDVAVQKQLRSSLNCKSF KWFMTKIAWDLPKFYPPVEPP AAAWGEIRNVGTGLCADTKHG ALGSPLRLEGCVRGREAAAWN NMQVFTFTWRREDIRPGDPQHT KKFCFDAISHTSPVTLYDCHSM KGNQLWKYRKDKTLYHPVSGS CMDCSESDDHRIFMNTCNPSSLT QQWLFEHTNSTYLEKFNRN*A ALLFDDESQFDSSNCQHSCYPR
8179	38547	A	8234	203	314	VPASSPALGSTLEFQLCEPINSG FCLNQID*GFGYL*ARFMSWPY WSLLSPFPLIPLH
8180	38548	B	8235	I	1008	

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8181	38549	A	8236	2	1495	CLVVVTSTDTSIRFQIIPWAGTEMK QE/IJKLKDGSMEEHLKKPLEDY MALFPSPVRILRTKKGREGLIRTR MLGASVATGDVITFLDSHCEAN VNWLPPPLLDRIARNRKTIVCPM IDVIDHDDFRVEYETQADAMRG AFDWEMYYKRIPIPPELQLQADP SDPFECQLVRDITLGDADSDQQH DVSHLARCQADFLFPWSPVMA GGLFADVDRKF/WELGGWAWS HGDPQQPWKESELFPSSCTSPQ VESHWPAGPMPPIPEQYCNWSP AVTCPVTAGRVCLGWGWR*RK *WGTKDLLGARWKSKPF*SP*T NQDVKPNPNDLIEQFQRKEHFC TESAWLGCPCQNGSWLQLSQRS HRERWNHGFMTVISA VSCNLKH GVVCGGRMED PCSRNLKRAV/ EVWMDEYAEYIYQRREPET/GHL SAGDVAVQKKLRSSLNCKSFK WFMTKIAWDLPKFYPPVEP AAWGEQKDMPLSQTYSKKGAGI KSYLGSCUTHWGHRGRQKQG NILIAHQ
8182	38550	A	8237	1126	1603	TIMKITGRAGDAIMGADICH/N KDRKVVRKEPKSDQIVRLLLVK LYRFLARRTNSTFNQVVLKRLF MSRTRNRPLLSLSQMIQK MKL GRENTATAVVVGTTTDDVRVQE VPKLKVCALRVTARSLSLILRA GGKILTDFQLALDSPKG*GTVL LSGPRKGR
8183	38551	A	8238	504	737	QLCWAGGKILT DQLAVDSRK GCITVLLSGPLKGRKVYGHFGK APGTPHSHTKPVVHSKGRKFE RARG RAS*GYKN
8184	38552	A	8239	1	360	MLGFALLPAPPGPGLV/GSG*SP DDQ GRTGPALAPSCLSRSPAT LNSAGSEIHDRPRSGAPPPTPLCR GSAQASTSACSPGANGPEPKPG LGTLRQQLEHIMATNRLDEAG WVACYPTDVR

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8185	38553	A	8240	3	666	MSFRQLFQDLKRYVQDADVR WEYCVRAKRGQTDSLGRLFQ QPGPVPGRHRAHSATSPDHRFP VADLTGQQGV!*GCGPPAAAPWG AG*YPGAPLHAGLGLPLAAAG AHHGHOPAG*GGAGGSATPLRM SVEGCSQRPWTEAPDRPLEHEA VCSVRPRPRCFLGGVGRAGAFL EEEWQHQSVVCVPCQPPWLGT CSSMSGKLSRPAPASSLSSRGKA WGQEES
8186	38554	A	8241	2	443	RTSLEFFFFFF*DGSFTLVQA\GVQWRHLG*LQPURPPGFK*FS YLSSLSSWDYRHALSHILANFV VVVLFCFYETKSRSVTKAGVQ WCDL GSLQAPPGFTPFSCFSLL SSWDYRHLPPHLVNFCIVSRDG VSLCWSGWSRTPDYK
8187	38555	A	8242	1	354	VSLOPVSQEGVQSRTLQGQSSRS SGSG/CPGE LNSPIFGVPHRWD AA*EESRAAGVPWPSGOISGMC SKFRI*NW*DVSWAGWSEDLRS *VDSLHGAKSRRTGDS*SPKGGP PIRVTA P
8188	38556	A	8243	2	241	WSTGLLRRSGS/NQSSA GKP RR SQSES PG/P GRS SGS GC QES GT CH*G*RRRG*GVLAPAPG KRD L PPR VKD QVR HPC VV
8189	38557	A	8244	5	282	AKKESVREPWARVPGALGVAA R*VEQSDFQCQCPAQM GHGLGG IPGC G/PFLGLVVRF LALVASSC PFP RKA GLA AKGE GP RQASLRG LTPL KRG
8190	38558	A	8245	1	302	LSREGVGQK ALGQSSRGSGSVC /LGELNSPISSGVPQRWDTA*EE SWAAGIPWP GGQIDFWHL*QA PCPRK SREGVETRREGVGVLAP SPEKR DPL LRV KD
8191	38559	A	8246	1	200	LSPKG VGS QRALGQSSRGSGS/C PGE LNSPISSGVPHRWDTA*EES WAAGIPWP GGQISGTC SKL HS
8192	38560	A	8247	23	187	
8193	38561	C	8248	1	1764	

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8194	38562	A	8249	115	872	LRRGRTRYPPP*ELPKARHP*WS TGLLRRSGSISLQPVSQEGVSOR AFGQSSRGSGG/SPGEELNSLISS GVPHRWDMA*EESWAAGIPWP GGQISGTCS/RAPGGGGSGGMP GCCGSGVWKFLCASKRAGKGS GHRDTRSGCGHKGLGRRDMRL GCGNKGSGHIRDIRGWGTCPPF RKAGLAAKGEGPRQASLRGLT PDLKLVRCPWAGWSEDLRS*V DLSHGAKNRTGD*SPKGGPPI LGRPLRACSAAVHF
8195	38563	A	8250	85	529	SGSISLQPLSREGVSQRALGQSS RGSGSG/CPGEELNSPISSGVPHR WDTA*EESWAAGIPWPGGOISG TCS/RAPVGGSGGTPGRCGSG VWKFLCAGDVAGVCLTVEAR NCNFLLLYTLKARLSCPCPR KAGLAAKGEGPRQASLQ
8196	38564	A	8251	1	552	MEARETGPWKEGNVERVASVL IKKGTGLPSTRVVTGSSASVMV YGASEAIQHQSSAAKPRRSQS ESLGPEFQQLWEWLPGPRAVK RLRVIIFDEKEPKRYLIWDEKEKG ALTUTMPLAPATFLRVNCWAG GGGLVTERNCKP*WSTGLPRRS GSISLQPLSREGVSQRALGQSSR GSGSGCQGLGL*SVLINKGTGL PSTVRVTGSSASVMVYGAESAI GQHQSSAAKPRRSQSESLGPEF QGLWEWLPGPRAVKRLRVIFD EKEPKRYLIWDEKEKGALTLM PLAPATFLRVNCWAGGGGLVT ERNCKPDQKMKGIEIKRRERLK CGSKIERRKRLRDSEGGWRRVE
8197	38565	A	8252	535	710	KCFPACHHYHNHHHHHHHHHH HQHHHHHYHHHHHHHRITIIIIIF IIIIIIIIINIIINIIITNITIVFMRVR VKRPNNRLCVSNMAVYFTWVQ KKKSSLAFFSSVVTSDLKSKKRR LSGKSLETSSASLMYVGASEAT GQRQSSAAKPRRSQSESLGPEF QGLREW*YGDGGDDDDNDGIV DGGDDSGGGGGCGSGGKQESI SIFD

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8198	38566	A	8253	54	563	AEKESVREPRARVPGARGVAA RPSA/RPR^GRPLLCSTGTPPKH* NCAWHHQACCWLGTGPAAPAA SPPACAAFSWGYGGLPAPIQTA FQAGWIGAPGQRGRSKTTRPGV QSVSNPGEPAPEPRAAASSGLSS GAFFPAPATDPGICSWAEGLVM GKGHHIIRPSISARIPCFHV
8199	38567	B	8254	232	987	
8200	38568	C	8255	1	1812	
8201	38569	A	8256	1	1035	
8202	38570	A	8257	2	664	SLIKLIPPPRFGRNRHLPVIRQN ERTQRGKRRGTRYMFSRPF*/R KHGVVPLATYLCEIYKQRCDF VDIQGEWGTCSKKGMPIIHKC YHG\KTGRSLTIVTPACLLPLFN TTQFRRKILAK\RN\VARIEHI^AL LRARD*LP*NRVKENDQEKEERS PKRGKGTWGST*SRQPVAPPVREA HFLEEPNGEGALSCWEFPFYWI SLGLLGVKKKNKDLWATKK
8203	38571	A	8258	1	747	MSESFLKPLPEVDAGAALLVQP AELYSKASRLDCYQKDSYTH RCQEKRRTCHTTGGHSQKHQSLS SGASVSPTCASAKTRDKINCFDPS PKSEVITLSSNDDSVLSDCQEG KPKPCSGPFATFKMQYDRTE WTALKISNGKLILISTNVSFIR LIGAFKGVVIIHTFGSYVANSEAV TLEASFTADSQFVMIIGSEDGKI HWNEESGKK*LGWMVN'TQA QLPVCNSTPSSMTFASACSNMA FWLPTIDD
8204	38572	B	8259	50	260	
8205	38573	A	8260	1	541	EVWGPGLASEGAVGITHGPFPK AKRNPGKVRSKRDPPIQFQNL RRS*WRSIPRKPGRQTGSRRSL WT/ALHPGAGTAKHPPAA/CA GRET*CKSKSPAGRKWSFHRSS SRRASE*DASQFAVPAGVTSRE PFGSRTTGAPTTGGTPTTRTAR SRTWSSSWVRLSGRTGAVGYS RSPSCSS
8206	38574	C	8261	177	236	
8207	38575	A	8262	1	417	

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8208	38576	A	8263	2	475	GIHTRLNSELLKEEESNKRLEAEIEYQSRLTAAISKHSESVKTERNVKLALE*TQDVSQVKMSSDISEVEDKNEFLTEQLSKKQIKFNTLKDKFRKKRDTI.RKKS LALET L/QNDLSQTQQQIKEMKEMYENAEAKVNNSTGKWSVCVEERICQLQHEN
8209	38577	A	8264	3	518	IFRAPFRICLGILLSPPNTEQAQYKKQLEQ/FKQGYNTASLNKKELTLKDVECKFYKMKTAAYEEVTT ELEEYKEFAAAALKANSMLK KLTKSNNKIAMIS/TQLFMEKEQVKYFLSTLRARRGRGESPQCDENLTSIGL/NRKYIPQMPVRIPTS TSNNCQNYLTVSHMTVSL
8210	38578	A	8265	1053	3733	NGRSCCRSSLKKECTDIESSEFVNRSKSLTSGLEEEEQQRRERSEK KQPQDFHNHHEEVKDLMDENCI LKTDIAIPRQEICTMKNDNIEKE NKYLKDIIAKGNTAALENCILNEEMITKTAFRYQQELNDLKA ENTRLNSELLKEESKKKLEAEIESYQSRLAAAISKHSENVKTERNLKLALETQDVFEQAGLEEAELVLSRLSCGEATEGARRALA AEEAGRWRRGVG/DSWLAPESRLHVLTGSCWWENLELGRHH*LCLWAVKNFQKRFLPGQKKSPFQLMSPQREFQHTL*ITQKQRVMNNFIKYLRLMSSV*CMP LT/IKHSIDKEVRSTSARLPCLGS EERICPAALSGKYKKLLEMINTVLSVFGNEDFDCHGDLKTDQL KMNILKKLKHKFDDLTAEKEAVSSKCVDLAKDNQVLQQELLS MKKVQQQCEKLEKDKKMLEE EILNLKTHMEDNMVELSKLQEYKSELEDERAMTAVEKLEEHLO LNKGNTASLNKKETLKDVECKFSKMKTTYYEVTTKLEYEKAFAVALKANNSMSKKLTKS NKKIAMISTKLLMEKEWVKYFLSTLPTRRQESPVCENLTIVLN S KYIPKMTGRIPTSNP*TLNNWQNYLTEEDMVGSDLISGTWSME EWSLGASSLGTWSAAVGQYLA RWPLCDLSVTVAESPSPCLCGA
8211	38579	A	8266	2	209	

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8212	38580	A	8267	1	1431	MTQKAAASVHELAIRCHWSQR PAVTGDLVQVYSGSEGTAIIFCE TQRSVTE AMNPFIHQNAQCLH GDIAQSQREFTLKDFFREGFKV LVATNVAACGLDIPEVDLVIHG SPPQDV/E SYIHRSGRTGFVTM TLESLEEIQDVSCAWKELNRKL SSNAVSQITRMCLLKGNVRVCF DVPITKSERLQAEWHDSWIFS VPAKLPEIEEYYDNRNTSSNSRQ RSGWSSGQSGRSGRSGSRNYF AVDTASAIAIALMTGTMYPMS VYSGKVLLQTTPHVGQLDKL IREVSTLDGVLEVNRNEHFWTLG FGSLAGSVHVRIRRANEQMV LAHVTRNLRYTLVSTLTQIFKD DWIRPALLSGPVAANVLNFSDH HVIPMPLLKGTDLNPVTSTPA KPSSPPPEFSFNTPGKVNPNVIL LNTQTRPYGFGLNHGHTPYSS MLNQQLGVPGIGATQGLRTGF TNIPSRYGTNNRIGQPRP
8213	38581	B	8268	128	1497	
8214	38582	A	8269	1	618	
8215	38583	A	8270	1	334	LFHSIFGYLPFAEQTLLPGSILVF TYTOPPKIQFANGTKGLPDPLM TPK*QKAPLMPLLVSLGLSAST IALGTRIAGISTSVTTFCSLSNDF SASFSPYLHRCFLPWSSL
8216	38584	A	8271	1	2919	
8217	38585	A	8272	1	4192	MRIPVDASTSRRTPPSTALSPG KMSEALPLGAPDAGAALAGKL RSGDRSMVEVLADHPGEVLVRT DSPNFLCSVLPTHWRCNKTLPI AFKVVALGDVPDGTLTVTMAG NDENYSAELRNATAAMKNQV ARFNDLRFVGSRGRGSFTLTI TVFTNPPQVATYHRAKITVDG PREPRNNECVYGNYPEIPILEEM PDADGVASTPSLNIQEPCSPATS SEAFTPKEGSPYKAPIYIPDDIP PAEFELRESNMPGA
8218	38586	B	8273	385	3930	
8219	38587	A	8274	830	906	

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8220	38588	A	8275	483	971	ATMPGHFYLF CETGSNSVSQAG VQ*HDFGSLQPPPGFKQFSCSLS LLSSWDYRHMPPRPAN/SVFL VEMGFYHVGQAGLGLLTSGDP PASASQS VGITGMSHHAGPTM KLLNPQESEVIFSPRNSHSTLLTP LSRHLPHPI SISTWC IHYAPLHT VSISAEAP
8221	38589	A	8276	1	2088	
8222	38590	A	8277	1	1822	MMTKDGLVFGQLQRGPSPILYVQ GLSRFRSFSVASGDSKRTRHRE KLPLLEAGERDHNCYGPSPQILA FQAICKIAKPGKEQSCSKLVGH TFDPLLI EARKPEERQKLDPDCV KWGGVGNFPPPVKRGDIRIFVS QGGKFSQ APEGPEVTSGSQGLE SKTLEVYVPVFYCTVAEALHNH VQPSHSTLPFPQAEEPHSVATT GPWGVLPGCCQCSLKAQGLFS QLVMNAACTGIHTSGQWAPLW PSTVPEMPSKSSGLES GTPRTCF VLYPAVAKLLP RGTlaysKG CQNSSANHWDGTQIHSPCHAA AAREYGGKSGISDSRSLSPTLFSA SF SNMLKLD FKVFKYGC FECF EATAGANV LIKIRE SKY KNTD DIDILSRQATPVIAQ L AHE HSGH VAGMEVVF GFSNTDFHPLRQT WLQPLSHASLLAAETNTESKND TPOGDQPATW RLNSGYGYAF PACNASAKTI HGLTEVLYTVLV DGNHNLNTKLSLEEENCLQLK CENLQQKLEQMA\ E\ KSLRRK RATQEECLMHSNLKFKEKSAE YTALARQ\ LEAALEEGRQKVAE EIEKMSSRESALQIKILDLETEL RKKNIEEQNQLVFKNEQ
8223	38591	A	8278	1	5103	MDESSVHSVGDHRVDRVSTS QVAERTRCNKMWR IETKS PSG DNEGTTGVIEKKTRL SGQGF CL QLSEGILQNLQAQRKIKFREME DPSSRLCSSL DIALCA SVKPSA GFPQRPKVKPLC VLGS GAGTG DAERSLQSSDPLKKQ QPLARSL RGLCERIVLG GSGCGARGLRG AGGGTALSVPGASRG FEGMFG LDQFEPQVNSRNAGQGERNF ETGLSMNTHFKAPAFHTGGPPG PVD PAMS ALGE PPILGM
8224	38592	A	8279	1	783	
8225	38593	A	8280	888	4915	

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8226	38594	A	8281	94	757	APTGCLACNLLCELGQVTSPL*ASAPKCVTVHN*PLCKALPRR*SSAWELS*MRKRLRLRGVNFLRTDGLCFCISTRATPPSSARARCVSTSLKPASLQLAVSYHHGSRSQGCHLPGAGREVCTSQRSGVRETS PWGCVEKGSPYAE GFP AVISLNP PSSSTAHDLPANKASASQPGSII LQCLSVHCTDDVGDAKARASVPTWRSLHSIDSNRFGTFAALT
8227	38595	A	8282	2	374	
8228	38596	A	8283	260	500	
8229	38597	A	8284	98	828	RWASVFPHPFPYVLPALLEKKTAERRGAFSRNKQTAGPCGGT LQEEGSARTVGDSYGEASAGGFSCNKEEGNQRYREG*VTEML\GVGYHRAALLQLRGLDPS\PALS VT*SRTSGPRPSRLNKTYCIPP RQDCYNNLAACLLQMEPVNYE RVREYSQKVLERQPDNAKALY RG/SGVAFFHLQDYDQARHYLL GCRE*AALKMPNVRRYPPRLTR VRTQQPTHRKEKQLLPWACLV NKEERCSS
8230	38598	A	8285	396	602	GNCGPEKERTCLRSPSWTPMPS\PKQAVPVSSWPPGPHHQ\RCVP SRSSNFSKSSKSNSCDGWNSSSSS
8231	38599	A	8286	3	156	SVVSLSPHR*AIQILSGVAAGW GLSDGPSSSPPSGARDTSPGSSLGL
8232	38600	A	8287	32	515	ARGSWGPGAGARPPGTARRAACCATGCGRSRSSHA\VPSPRRA APSSVHPGGCHGPALPPSPRVTQAADARRAAPPLRAASAAP SRRWSQAPTP/K/RRLGYPPLRP PAHIPGPR/PPLRRMVSRSSEDP PRRLT*TGSETPKSTWRELSSRRSLSLSKAATR
8233	38601	A	8288	30	460	RRCPAQRGEGIWQSGBHVRALLSC SGLHPFQTSQLPVYTVRVKLPT QALAMVDAPPKTLECPRLJSV CCYAGSENFKPVDSLSSIGS GGVGTRGNLLVCELRPWRDKRSIWAGVSRFLRLSPSRPFLA\LG LSSYLTTRKT

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8234	38602	A	8289	2	1094	RMSRISDDSRATASQLDEFQECL SKFT^ARYNSVRPLATLTSYASDLY NGSSIVSISIEFDRCDCDYFAIAGV TKKIKVYEVDTVIQDAVDIHYP ENEMTCNSKISCISW^SSYHK NLASSD^YEGTVILWDGFTGQR SKVYQEHEKRCWSVDFNLMDP KLLASGSDDAKVKLWSTNLDN SVASIEAKANCCVKFSPSSRY HLAFG^CSDH^CVHYY^DLRNTK QPIMVFKGHRKAVSY^AKFVG EEIVSASTDSQLKLWNVKGPI^Y CLRSFKGHFNEKNFVGLASSG DYIACGSENNSLYLY^KALSKT LLTFKFDTVKSVDKDR^EEDD TNEFVSAVCWRALTTQMGESIN VLIAA^*QFRVP^IKVLELV
8235	38603	A	8290	1	667	MRIKATSEDGTIVIAQAEYGSVD IGEEVLKKGFAEKCRLASRTDI CEEKKLDPGQLVRLRNLKSPIPL WGHRSNQSTSFRPKGHLSKEKM TLDLKDENADAGNLITFPKESLA VGDFNLGSNVSLEKIKQDQKLI EENEKLKTEKDALLESYKALEL KVEQIAQELQQEKAABVDTLN HLEYTLKTYIDTRMKNLAAKM EILKEMRHVDISVRFKGKDLSDAI QVLG^SKGALLLQLL^MD^R^Y GQNTVWLRRILKL/SEYVSEGNI LIAQRNEMOQKLYMSVEDFILE VDESSLNKRLKTQDLSVSLEA VYGGQAKEGANSDIELKKFYDW KCDKREEFTSVRSETDASLH\LL ^HGSKEP^RICKVMQTR^*FQIHI VKYCKRFIQRKGSLPQYKLSSTR TVLS/SKKQLIEYLKKIPSVDH LSIK/TDIEKLKSSTQMIE^*KE^* FGKSQMLMALKLRK^KKK^LK KGFAEKCRLASRTDICEEKKLD PGQLVRLRNLKSPIPLWGHRSNQ STFSRPKGHLSKEKMTLDLKDEN DAGNLITFPKESLAVGDFNLGS NVSLEKIKQDQKLI^EENEKLKT EKDALLESYKALELKVQEQAQE LQQEKAABVDTLNHLEYTLKT YIDTRMKNLAAKMEILKEMRH VDISVRFKGKDLSDAIQVLG
8236	38604	A	8291	1	325	
8237	38605	A	8292	1	593	
8238	38606	A	8293	1	2013	

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8239	38607	A	8294	2	1427	LLARGAGRTPAPPLMSCGPW GKFLKCCEVYKSGPYKVQ*EEI TIHSRAEAESTYQIKYEEQLQTLA GKHGDDLRCAK/T/EISEMNQNI SRLQAETEGLKGQQGASLEAAIA DAEQWGELA/IKDANTKLSELE AAMQRAKQDMA/RQLGEYQK LALDIEIATYRKLLGEESRLES GMQNVIHKKTTSGYAGAPARI VSLLQNELLSSLEVGVLKGHPTG KGEELGAPYSECFSGLCRRTVM LTQAPSSVRSRNSRNHTVNSG GSCLSASTVA/PAINDSSAAMS CSTISAQKRTCTACEPARKYK DTASHQEPAVCQPACQLETADP KGGGVLALPQPPSPGMLCWPY CRAHATDYFLANFSEPCFHFL HRAGAAQTQATGDGMEHGQS RELPKRKAPREESSETSEEKSPNK WGPVSKQQKQLLVDIITIIIRPT RGNAYTGLSTRKWKPSEENA LMQPNNKKDEKGTLTQKGL
8240	38608	A	8295	301	462	
8241	38609	A	8296	2	825	YPPSPPGRSAAHVSTLTYRTTP* WPDQRSAAPPTAWAAS*SPSAR RRPAESMVPREPL*YRPSAATS AATPAISPARALGAGACPFLR RRSGPFGRT\$AIRPSSAGKAVL FPPHGRPVWPVGRLARYATAS GWGAHI*ASSGASE/PAVSVLP AGSGASPFSASWDPPAHPAAA ASA AAAVIPAL*RSGDRPPVLSFQ PLFWFLIRGDNSVSFWLLRGLP CPSQA VTRRHRSLQEKLKRNR KSCVNFMQSQVSVKYSNLVK HHHFCIRPL
8242	38610	A	8297	3	251	
8243	38611	A	8298	208	307	
8244	38612	C	8299	18	197	
8245	38613	A	8300	1	1866	

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8246	38614	A	8301	2	2558	FEVLWSDSSITSVTKSSEVTEFI SKLCQLYPEENLEKLICPLAGPD AFYVERNHVLDLDSLRYLASLP SHVLKNDHVRRFLSTSSPPQQL QSPSPGNPSLSKVGTVMGVSGR PVCGVAGIPSSQSQAQOHGQHP AGSAAPLPHCSHAGSAGSALA YRTQMDTSPAILMPSSLQTPQT QEQNGLDWLRLKLHLHKYYPV FKQLSMEKFLSLSTEEDLNKFES LTMGAKKKLKLTQLEKEKSE RRCLNPSAPPLVTSGVARVPPT SHVGPVQSGRGSAAELRREV EQPHIQLPREGSSEYSSSSSP MGVQAREESSDSAAENDRVEI HLESSDKEKPVMLLNHIFTSSA RPTAQVLPVQNEASSNPGHHHP LPPQMLSAA SHITPIRMVLNSVH KPERGSADMKLLSSVHSLLSL EERNKGSGPRSSMKVDKSFGSA MMDVLPASAPHQPVQVLSGLS ESSSMSPTVSFGPRTKVVHAST LDRVLTQAQPALVVETSTA TGTPTSVLHAARPPIKLLLSSV PADSAISGGTSCPNNVQISVPPA IINPRTALYTANTKVAFSAMSS MPMGPLQGGFCANSNTASPSR HPSTSFAANMATMPSPCPAPSSSP ALSSVPESSFYSSSSGGGGSTGN PASNPNHHHHHHHHQQPPAPPOP APPPP G CIVCTSCGCGSCGSSG LTVSYANYFQHPFSGPSVFTEPF
8247	38615	A	8302	2	266	YCGPL*SVWVARNPNGFAFVEF EDPRDAAGVV*ELDGRTLCPG PSWGHRP*DDYCRRGLPPRRP PRRRNLSCSRSLYSPWTLSL
8248	38616	A	8303	37	535	ESWLVLGRRKAGRLIGACGFEP PHFLTLDLEMHDRCPLDCKV YVGNLGNNGNKTELERA FGYY GPLRSVWVARNPNGFAFVEFED PRDAADA VRELDGRTLIGCRV REEVLNGEKKK/SRN RGPPPS/W GRPPSENDNRKEESFPPR\RRSP R\RRSF\RSRSRSLF

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8249	38617	A	8304	2	668	EIAERRITQPAPPGRPSRSPGPGPA GELGGPGTGTGRALCPADNGGLC CGCPLAVP/GPLAVPR/ALKPQR TSLSHPTSVTNNGRGVSQPGPR RHPGLPTQASTKPPQSRRDAAP LGGAGRGGPGSMAAARTPRGG GH*GVGDGPGRPRDASRLGRLF RPRSRADPVPG*P/PVAIGRDLPS PDDNGQRP*GAWKVSE/CPERR RVERLAAIGRLVFL/PDFAVGRE
8250	38618	C	8305	101	183	
8251	38619	A	8307	329	399	RERET*SSINTTIFPGSVLQLPDAS PSKTGTLSIPVTIPENTTSQSQVI GTEGGKNASTSATSRSYSSILP GVIALIVITLSVFVLVGLYRMC WKAHPGTPENGNDQPSQSDKES VKI/FTGKTISHESGEHSA*GK
8252	38620	A	8308	192	537	KFPSTPENGNDQ*PQSDKESV KLLTVKTISHESVILNQNKMDEI TEIEFRIWMMAMKITENQKIEHTS EESEEFNKTIQGMKYEIAIRLNK KTDLTELKNSPQEFPHNLTLEVLT AE
8253	38621	A	8309	1	789	
8254	38622	A	8310	1	423	EDIWFDDVDPADIEAAGPEAA KIARKQLQSEGVSLSLVEKEQ AFAGEELEVVQKEVAEMLKG RILVGHALHNDLKVLFLDHPKK KIRDQTQKYKPFKSQVSGRPSL RLLSEKILQLQVQQAEHCISQD AQAAAMRLYVM
8255	38623	A	8311	1	1077	MGKAKVPASKRAPSSPVAKPG PVKTLTRKKNKKKRFWKSKA REVSKKPASGPGAVVRVPKAPE DFSQNWKALQEMGSKKKPKII QONKKETSPQVKGEEMPAGKD QEASRGSVPSGSKMDRRAPVPR TKASGTEHNKKGTKERTNGDI VPERGDIEHKKRKAKGQPQPH PPR/IDIWFFDDVDPADIEAAGPE AAKIARKHLTRALALCEMVG VGPGEESMAARVSIVNQYDG CVYDKYVKPTEPVTDYRTAVS GIRPENLKQGEELVVQKEVAE MLKGRILVGHALHNDLKVLFL DHPKKKIRDQTQYKPFKSQVKI QDAQAAMRLYVMVKKEWES MARDRPLLTAPDHCSDDA
8256	38624	A	8312	3	640	

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8257	38625	A	8313	1	1274	MGKAKVPASKRAPSSPVAKPG PVKTLTRKKNKKKKRFWKSKA REVSKKPASPGPAVVRPPKAPE DFSQNWKALQEMGSKKKPKII QQNKKEETSPQVKGEEMPAGKD QEASRGSVPSGSKMDRRAVPPR TKASGETHNKKGTKERTNGDI VPERGDIIEHKKRKAKGQPQPH PPR/IDIWFDDVDPADIEAAIGPE AAKIARKQLGQSEGSSVLSLVK E/QAFGLLTRA/LALDCEMGVG GPKGEESMAARVSIVNQYGKC VYDKYYKPTEPVTDYRTAVSGI R/PENLKQGEELVVQKEVAEM LKGRILVLGHALIINDLKVLFLD HPKKKIRDTQKYKPFKSQVKSG RPLSLRLLSEKILGLQVQQAEHC SIQDAQAAN*GCVYVMVKEGVG RAWPETGAPCLTASRPLQ*RRL SSPALLAACPPRLQRQC
8258	38626	A	8314	2	414	
8259	38627	A	8315	1	621	
8260	38628	A	8316	1	885	MGEKPGPLLSSAKPKKNPQE HKDEGDHPNNSFSPCSAHDRRC LQKHFAKIRDRTSGGKMKVN GAPREDARPVNKGTYLVSTGG QTVAFTTGWSWDQDDSESSLGC QEDSTALHPTSTSPGPSETVPPS LLPEATKRLLSLDFESFGQTQR NLSCPCLCPAGVWQEQKTLCEWR DAGGNRQAGVPQAPCMKSN ALIVLGTVTLD/AVGIGLVMV LPG/SPALLQRQAESPGRRTQG /RVTTPTTASAPVAPMTAGAC RSTS PKFETGAPVGAR*RSMGR PGRM PGL*IKAPTWCPCQVGRLL PSLLAPGTKT TQSPA/SGCQEDS TALHPTSTSPGPSETVPPSLLPE ATKRLLSLDFESFGQTQRNLSC PLCPAGVWQEKTLCEWRDAGG NRQAGVPQAPCMKSNNALIVL GTVTLD/AVGIGLVMVLPGLLR DIVHSDSIASHYGVLLALYALM QFLCAPV LGALSDRFGRRPVLL ASLLGA/TIDYAIMATT PVLWIY
8261	38629	A	8317	1	396	

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8262	38630	A	8318	186	2123	CPAHCWQEAMLSAWRLVMSPPG GGPCCTQHPAPACHPSVPLTTPRK AGEPRPWPPCPAWGPIALDSSK PHWRWPKPPIPASCRPLVRRPWGP QRTLTPTLTSHWRASIR*SWNW TPPSSCFPQQLGAPRLSWSWRAPC Q*ERRRNLLKPWT*STSR*PPPDQ GATMAPSTAPAPLSPRSPAPFA VVASSFPETSPERHEAVRASSS LGTRAGGTSALEPPQRVSP/HRP PNPSISIPCMGSKASSPHGLGSP LVASPRLEKRLGGLAPQORGSR SVLSASPVSVDVSYMFGRTHPSP PLAKEIIAVAAAPHPSPPTWWTY PLC*STAANQNRGSPPQRTPGH QNSVQPGAASPSNPCPATRSNS QTLSDAFTTTCPEGPARDMQPT MKFVMDTSKYWFKPNTREQG CPGGAWSISDSRIVPAIELLRK EPGAFVIRDSSSYRGSFGLALK VQEVPASAQSRRPGEDSNDLIRH FLIESSAKGVHLKGADEEPYFG SLSAFVCQHSIMALALPCKLTI QRGCHTLYLSSVSVELTGALA VQKAISTFFERDILPTPTVVFHK VTEQQITLTDVQRKVFFRRHYP LTLLRCGMDPEQRKWQKYCK PSWIFGFVAKSQTEPQENVCHL FAEYDMVQPASQVIGLVTALL QDAERM
8263	38631	A	8319	15	909	LHVSHPGHDARGGLLQPCAA PPLWLCLRIQCCPWRWFQTPSQVF YHAATEHGGKDVPQQCLWE GCEPFQRQRFSTFHLOQANC/R EAQRSTPRAQKAIVNHPAAAL MALRGSRNLVFRDFTEKEG PITKHIRLTAALILKNIGKYSEC GRSPWPRASRYQQGHQDQLFILRS DLPSQVFIRDQLMERRNRRTGR TEKARIWEVTDRTVRTWIGEA VAAAAAADGVTFSVPPVTPHTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVYTKVFALDVAAR HRVQFAMPESDAVAMILQLS

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8264	38632	A	8320	189	4419	KPGLFP*RVY*EYVFRLSQSLGE FHQE*FKRGQY/ATTSSPPFSPW ANIIRKATRC*CRWRRFIMPFW MASMSA/GMLNELQQYCDEW QGGAAVVAQHV APPGIVIEIDS EKFAQCWLNAHFEVNPDCSVSV RAEMYSEYLSTCSKLARGGTL STGFYKCLRTVFPNHTVKRVED SSSNGQAHIIHVGVKRRAIPLPI QMYYQQQPVS TSVVRDSDVPD VSPAPSPAGIPHGSQTIGNHFQR TPVANQSSNLTA
8265	38633	A	8321	27	674	GPQNTPMPPSPSPSVRVQGQPNS QPSFGSGSQPGDPMRKPQPGNF MCLWQSCKKWQFTPSQVFYHA ATEHHGGKD VPGQCLWEGCEP FQRQRFSFI THLQDKHC SKDAL LAGLKQDEPGQAGSQKSSTKQ PTVGGTSSTPRAQKAIVNHPSA ALMALRRGSRN LVFRDFT\DEK EGPVTKHTPTNSCP*Y*KISGY SEC GSADWLKETMENNLSSA
8266	38634	A	8322	16	341	PPGRGSAHPAARQLQTPGSAAP LS*HQGPASRTGPPGPIKARAP SKSRARGLRAA QRARLSARAR AGCA/PP*ARGAARKLQAGPTF QETLPPGTRDRKCCSGDAVVH
8267	38635	A	8323	1	400	MAEGMAMLRWTRLGTWPDD FDEM DSTLAVQQYTQQNIR/AQ DCSN TDKNLE PPEGQDADCHG F*APRWHCSASYVASSEFAGDD RRI*IPLDPWVKFCECWCSGPT PFRE/CPRELN*HLKDGCSCRYL RARN
8268	38636	A	8324	3	179	ISWPSPSLLGQTAALCANGAGP AGTTPG RGPV SARFGRGAA C VCSPPPSPSPLAPLSR*RF AVMW WQEA*RRGPR LPLLSSLPAAAG SGRAARAAAELPGG RAGAR/P L/LLTPAQVQGESARG/AGAEG GRGTPGP/GCPLPAGRSLCQPG PRSPP*TAALCANGAGPAGTPP GRGPV SARFGRGAA CVCSPPS PSPLAPLSR

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8269	38637	A	8325	1	1744	DFQERLSMKDQLIAQSLLKEQQ IVLEMAEMGGLEDLPQPQRGLFR GGDPSETLQGELILKSAMSEIEG IQSLICRRLGSANGQAEDGGSSST GPPRRAETFAGYDCTNSPTKIV EAPGTES/DPRLPTVLESELVQRJ QT/LSQLLNQAVIAHQDSY/V ETQRRAIQEREKQFRL/QSTRGN LLLEQERQRNF/EKQREERAAL EKLQSQL/RHEQQRWERERQW QHQ/ELERAGARLQEREGEAR/ QLRERLEQERAELELRQ/RQAYQ HDLERLREAQRRAAQPSP/HPPSF NGEGLEGPRVSM/LPGVGPEY AERPEVAR/RDSAPTNRLAKS DVPI/QLLSATNQFQRQAAVQQ/ QIPTKIAASTKGGKD/KGGKSR GSQRWESS/A*AGPPLRLGLEG ATGQALAAGSQEIRDTCAILW RGNQKAQLASWLRPPHTGPVVW SPGPKLRL*STLHLLTSTKTVG WGPGALERARARRQRSLATWD QHSRTGTASFDLKQQLLNK/L MGKDESTSRNRRSLSPTCPGRH SPAPPDPGFP/APSPPPADSPSE GFSLK/AGGTALLPGPAPSPLP/ ATPLSAKEDASKEDVIFSKRAV TQANH
8270	38638	A	8326	147	536	WAQEWSGRNTHQQYKILDVML KGFLFKVCAGRQQLMAGPVFDL GTDG*TGVQLKDQ/WSALPRPV LRTRSSLAAPSLLF/YYFDHNS WNLLIRWGIFCNQTGVFNQ GPHSPILSLVRTGEVAREPSVG
8271	38639	A	8327	59	339	
8272	38640	A	8328	43	510	LLLWCGGLRELTIMVEDEGEQM SIWVLDDKDLGAPHLVLVGSMIL TARSRCWTWRSSHATAATSE GEGWGVGVLIAADRPGWASDEG DGEGGGGGGLLTSAEFGELAAV GEAGSAHPMFSFRPRYSTWCLT HIGGGGLELTL*STRSASQSAG VTGMSH
8273	38641	A	8329	98	493	FFYFLFIYFFETESRSVTLAGVQ WYDLCSLQLPPLRKRFSCSLSP SSWDYRHPPPWHANFCFLVVT GFHHLGQAGLELLTS*/IPSSAS QSAGITGVSHHARPGLSLANN PRSQRTSATVCPEQLGLD

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8274	38642	A	8330	3	328	HSAARRPSSRRSSPRPETSCANS VNAGWNQDPTHIVIRFRSMAT AGSTRYR*GLHAAPSPPHRRP RSPPGAE* A/RREARSLKR*SPPC HPTKKATMCRCIYVPLIIK
8275	38643	A	8331	24	593	FEQQWGWA AAAAPPGKAHTR *TGRSPHRPHRTQPR*NPSGTA APGPVPS*AGSSH*AGSG*RAW GPGSSRR*RSCT*RLRSRGRRPR *GPSR*VRSARPSPRA RAPPGS HRPGCGAAAPAPAASAPARAP WAGADSSAPPRTAD*SLPTRVC CSLSALHTGSESGLGPGTQIEG KQNYSVTVWFLAR
8276	38644	A	8332	24	832	FEQQWGWA AAAACSSRSQSTYSL RTGRSPHRPHRTQPR*NPSGTA APGPVPS*AGSSH*AGSG*RAW GPGSSRR*RSCT*RLRSRGRRPR/T MRASFPLSAILRSPKSGRDAHHQ ASHRPFGCAAAPAPAASAPAR APWAGADSKRASSYSRLEVLK VIEAAA WT SAGSFRT*/PENLPI PVNEIMLLSNCPGRMGSVPLKR RLILGVRLGERGPGIAWCTCG PPTSMCTGALDLVSWAGRGM WASQRR/PQGDRVRDKPGTCFL PSAVPVLPCV
8277	38645	C	8333	153	269	
8278	38646	A	8334	615	1275	QKRKTFTNTTKCYNKEKGSWPR WPTGSS*CAQLSWRGMEGTSK YRTF/ILKHPGQEIPS EPTEPPGP/S SLTCRATWSLRAA POPHMKPR EP*ILSIYVAPSPSTIEKPSIGERF AIFITLLMRNGDLGEASCDAVK ALRQPWGKAQVEKNQNLSQLTKC PAMWHFESQNPA LLIVRECLEG WKAYPQSTKEERLLHPEEGAG FTSSSQEKYVVRVGQRLWPTPF FSLQMIDRKERHLIPPNVIIKKR GVGQDGRLEAVSVHSHGEEW KGQVNTEPSETSRSGDPIMNP LHQGLKSDMQSYMESQQSSPS ATHEAQGALDTQASWKKQQQ LRKSRAISSLQADGVQHIGHEA RHCHDVLKDRQTSWPCKMSS LAEEVVAADTWLLDNGTMQA TGRAAQVREQGKGMDLGQYIS CYLMTLSRAIKQKENKVCFC RLGKPRVKTASVQKK

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8279	38647	A	8335	423	998	PPSAVPHDHSSPART* PQSLSVI TAELEPVRAPSILIAFFGHGSAC MCPFRWRYSRFSLKQQRILAHD PVNTFGIDRRHTIKFCLSAKQRP YPTITIRWQLSDNMVYTEKHIRI ISVTTAAAIHPVIGSFPIPG/PIRA RALSTFLPVHIQRLL*GVHFPSF SCRAGAGVL*SASWRQQVQRQ EQPVLRRQQ
8280	38648	A	8336	2	218	HPSPSGLKHRSLSGSPVNPLL LPGSFSLLPAGHSHGDGPSAS QMHI*FQNQTHPVVP*PDPASLPA VQSHQ
8281	38649	A	8337	76	129	
8282	38650	C	8338		410	
8283	38651	A	8339	651	741	
8284	38652	A	8340		612	
8285	38653	C	8341		729	
8286	38654	B	8342		313	
8287	38655	A	8343	705	990	TRSSCWGKEASLGDGNGRNVVA ALHHFTGAAARQHSGSPLERGP HPQL*SPRS*VEGHWLEI/LQA* S*VLPKQPHQPARCWQLLSSH WLPRPALLC
8288	38656	B	8344		588	
8289	38657	A	8345	220	678	MNAIPVASPCMVCVSLIVHLVLS RPM*PW*RPPTRFQWSEVQE/V MELTTMRPRQQPPPPPPPP*QQ QQQQQQQQQQQE*L*LAATPR APGTLAQGSLTSPQIFSA*RLKT DAAGSPIGSPQTITDAELRVTLT VEGKSVPFWAVLPQSFTDSPH
8290	38658	C	8346		411	
8291	38659	C	8347		534	
8292	38660	B	8348		774	
8293	38661	B	8349		705	
8294	38662	A	8350		297	MPGHOKAPLRPAVSKK ESMLE KGKIK*LLKPEGILPISEPPSNRIF ACWGKPAWTACCNSLARR*R AISCCPSHW*KEKPPWRPIRKPP LPARWIH
8295	38663	A	8351	616	988	DPQLQAGSGHIPGRNVCPGERI CWRGTPD/SDPSTPTY*PPEKE VAQGRDLIHASGCLWS*IPLEA LQQPGQCPQFSQVCCIPVPTVE MKQGRQQLASDFQDQQDLEFY EILSWKPGILIIP

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8296	38664	A	8352	1	1668	MELVPEEATAVSARAYTGRWP LDAAARTILVTAPGVGHTNIVL CGQASLDAYIKSICLKKEGRKE GKKKGKRKERKRDKYKGKEKK RKKGRKKGRRKKEKKKEREK ERRKEEKEGKKRKKEKERKKE KERKKLSIGKGVVYCLSSNTQK KVQSQTQKIRVISTILFILAGCIVF VTIPAVIFKYIEGWTALESIYFV VVTLLTIVFGDFDVAAPHSDFHL CWVIVTCKGKYLLPDSPQEKAAT DFSGVAQKRNEPQKPL/WC/W ELRSYPTALMMQERVV^KEKP KAAAPNRRLGLTEKLEF*EV AAAYPEHAVLSMIGDWLRVLS KKTKEE/VCRPLFLKFSPSPNLRL LGVAHHVGEIKAHAAEWKAN VTAEFRETRRRRLSVEIHDKLQR AATIRSMERRRLSLDQRAHSLD MLSPEKRSVFAALDTGRFKASS QESINNRPNNNRLKGPQLNKH GQQASEDNINKFGSTSRLTKR KNKDLKLKTLPEDVQKIKYKTFRN YSLDEEKKEEEETEKMCSNDSS TAMLTDICIQQHAELENGMIPTD TKDREPENNNSLLEDRN
8297	38665	A	8353	1	418	
8298	38666	A	8354	251	394	GAQVPTLLVGVLTVTISTVQNL AISLLGAK^*GEGILSVGRMY RVL
8299	38667	A	8355	107	250	EEGHILLDPRMVDPMMAACTM QLEKLQTLNASL*KQLGGGLYL AKPQG
8300	38668	A	8356	331	893	SITENCENKNPIPHVENKDIGTK YNSLKLPEHIRAEVMQPSKLD* VN/P/LPSTCKERFVMQSHLART VGSSICNL*MSP/CFGIW^QLAЕ ANPAKCFP/GCWKTNSTCSSML CSKVVTPTNGTVV*ITREGPISDD SILRFLLSMETKRMQGLLVISTA QPKGHQSSYQLHKRGPEHIERS SSQPPVAAFGIH
8301	38669	A	8357	2	416	SGFRYGSDIVPSKVDEEQMKY KSEGKCFSVLGFCKSSQVQRRF FMGNQVLKVPFMDLRQYMFSS LKNSKKYAPTEAQLNAADALI DSMSLAKKDEKTDTLEDLFPTT KIPNPRFQRLFQCLLHRALHPLE PLPSIQQ
8302	38670	A	8358	1	2130	
8303	38671	A	8359	1	1152	

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8304	38672	A	8360	1	320	FKGTAAPWPLSFARAAAAGRQA GTDTRPSLRVRFPRERSARQKG RGRSVRLSAKSPPAKVERTKPSG GSRTA*IFRQRSKQGKMGAKG KQAKWLLILRALICFSLSER
8305	38673	B	8361	1	1231	
8306	38674	A	8362	1	2276	GGRPKRLLTGNMVRSGNKAADV VLCMDVGFTMSNSIPGIESPFEQ AKKVITMFVQRQVFAENKDEIA LVLFGTDGTDNPLSGDQYQNI TVHRHLMLPDFDLLEDESKIQP GSQQADFLDALIVSMDVIQHET IGKKFEKRHEIFTDLSSRSFSKSQ LDIIHSLLKKCDISLQFFLPFSLG KEDGGDGRDGPGFRLLGGHGPSP PLKGITEQQKEGLEIVKVMVIS LEGEDGLDEIYSFSESLRKLVCVF KKIERHSIHWPCLRLTIGNSLSIRI AAYSKSILOERVKKTWTVVDAK TLKKEDIQKETVYCLNDDDETE VLKEDIIQGFRYGSDIVPFSKVD EEQMKYKSEGKCFSVLGCKSS QVQRFFPMGNQVLKVAARDDE EAAVALSSLIHALDDLMVAI VRYAYDKRANPQVGVAFPHIK HNYECLVYVQLPFMEDLRQY\ MFSSLKNSKKYAPTR/EAQLNA VDALIDSMSLIAKKDEEGQTPL KDLFPPTTKIPNPSIFRGLFQCLL AQELLHPRIEAFYPPISGRHIWE YAGILPAEGGQRKSSGFPPLS*N* RTLFL*FEAKEKGFKWTAQGI FQQQPWKVGPTAKKLKTGARG EPTFSVSSLAEGSVTSVGSVNPA ENFRVLVKQKKASFEEASNQLI NHIEQFLDTNETPYFMKSIDCIR AFREEAIKFSEEQRFNNFLKAL QEKEIKQLNHFWIEIVVQDGIT

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8307	38675	A	8363	624	1992	GRKVVVLPPPLGNQSTPGGIC LSAQQLPL*RD* SASARCSSPGS *TSPPSYFLPDPRGPGRALQRFS RSPSSPGNPA SAAPSPRSKLLL GPPGAAAATAAAAGAKPELRH RLPSSATTASRVRACHLLAS AAATPAFSPPPPPP PASPSSQRTP KEVQRAGKAAECPAPELLGF GGSRD3AGELGGLSSDACV/PD SSEPGVRRPARRTLAHALTHA STHTRLPGSCARVAVPVALCK GGFT*PIFSPQVVTNTYPGEEGA RLGVLIGREQTVAIILLGGSRSK APITTVAVASAPPVTAAGR TP HASIRIPRMLSK SPPPQAL*K GVMAPAQCPCPARRGQAGLEG GFGKSPTRPHQLTAASSPCNGL IRIRQQGGGGKGRRWRGSSGDP GAWYCFCRGRGGGPSLRTAT LIPGLGGHGGGSGDAASPLLT RDGGPEAHLGKE
8308	38676	A	8364	123	248	
8309	38677	A	8365	1	540	MLEALGALNKPESSRPLIPELHL ASTAAANLGEHPNQQRALKFAS QETPEESANAVPHYHKLCNRVS HVWGNRRGQHIRNTMDNPRP GKTTFV*IIVSPLPALLATHSW DSQVRPAVL Q/P/YSHGTGT P*W RSSSPCAASST*KSPYP*CH*QR LSQSPSA FRPTLRLSLSRSTRCRS WRRK

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8310	38678	A	8366	31	1429	RETRSCWAHYHAESSKKHQAK LKDSRKARRSIELIGPGQSSQKGG DICSLIHLSKKLGYCYSKTGNM GGWEGGMQLRVVSENMGKSS RERAADLPQGSCWHELPGRRLI NTRISLKPRHVWNLSSVLQCVV KKVKVSMQMFMHMPITSAMQGD RLGICVTQFDPKLLERGLVCAP ESLHTVHALISVEKIPYFRGPL QTKAKFHITVGHETVMGRMLF FSPAPPNDQDQEPILDNFNSQEY LFQEQLSKDLTPAVTDNDEA DKKAGQATEGHCPQRQQWALV EFEKPV/YLPSAVPGDWLQARC GHSVPNTCRLAFHGQCSCTG*RT GTTPTASCPG*RCTS*STSMGLV ERAMDDYSVIGRSFLKKETNIQ LFVGLKVHLSTGELGIIDSAGQ SGKFKIHIPGGLPESKKDPDPTP PSKTPGPWPVGGQPGRRRSPSG ANPHKMGWLTRPFKRYVFDTH KRMVQSP
8311	38679	A	8367	3	119	RSPREGGGHGRGPSSGGCRRR PGWAGNEAM*PDRRARVGIE VPAEEEGGAAVAQDGGLGMKR CSLLRDLL
8312	38680	A	8368	3	389	SFATHITAGPQPPAA/PAPKRM ARASWGRNPPRAPVRTSAAA RAAGTRRPAPARVACPLPAGP SPRRPPRAARTRARRPAGP AAQQSAGRRWTPPAPAPSGASF AAPAAAGSASPSPHRSSAPGGGS TQSSLSPSSSALHSSPPSRPWA ARHERSSWS*/PRSLALPTSTEP/ GPGPRRAPVLGTRSCORGAGQL E*EA*GAA*APPPLGWT*LLCV HVTLGNAVSHWVSCGAAPPHG GVGVGYRARSPREGGGHVRPA RTREVPPSPRMGWNEAM*PFK* VSSRWPPRLPSRGMAAPRGA AAGGARRVEWEGASLLGSA PGSARWPRAPAPASQVGARC AAGAPCPLRPRVWRRAVGAE NAPSELAASTPAG/GGRRGAGSG SSDLAGRGAVALRFPGG*GHSR QQHGAEKDGQGFLGSQPPP SCAHQRRGACSGNAAPSSAR RMSASSRSRQPEKATQSRNSA RSSAARPRSRSTAVSRAQVDTA SSCAFWRVFCSSCRFCESAEP TVSTRWW

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
8313	38681	A	8369	3	1130	LDFQHHINYKAMRKLKMVKVQE QCPNITRIYSIGSKYQGLKLLYV MEMSDKPGHE/LGYWHGEW GEVGTGQQPRHEPAASPHVSPG EPEVRYVAGMHGNEALGRELL LLLMOFLCHEFLRGNPRTVRL SEMRIHLLPSMNPDGYEIAYHR GSELVGWAEGRWNNQSIDLNH NFADLNTPLWEAQDDGKVPHI VPNHHILPLPTTYTLPNATVSLR AAVEVLWGADPCLCLPLLTCP IQVAPETRAVIKWMKRIPFVLS ANLHGGEVVSYPFDMTTRTPW AARELTPPTPDDAVFRWLSTVY AGSNLAMQDTSRRPCHSQDFDS VHGNINGADWHTVPGSMNDF SYLHTNCFEVTVELFCDMFPH ENELPHEWENNTDA
8314	38682	A	8370	1	2229	MWGLLLALAFAFAPAVGPALGA PRNSVLGLAQPGTTKVPGSTPA LHSSPAQPPAETANTTSEQHVR IRVIKKKKVIMKKRKKLTLTRP TPLVTAGPLVTPTAGTLDPAE KQETGCPLGLESLRVSDSRLE ASSSQSFGLGPHGRQLNIQSGLE DGDLYDGAWCACEQQADPWF QVDAGHPTRFSGVITQGRNSV WRYDWVTSYKVQFSNDSRTW WGSRNHSSGMDAVFV PANSDPE TPVNLNLLPEPOVARFIRLLPOT WLQGGAPCLRAEILACPVSDPN DLFLEAPASGSQDPLDFQHHNY KAMRKLKMVKVQECPNITRIY/ RIGSKYQGLKVVVEMSDKPG EHELGEPEVRYVAGMHGNEAL GRELLLMLMQFLCHEFLRGNP RVTRLSEMRFILPPSMPNDGY EIALHRS*LVGLSEGRWNQNS IDLHNHFADLNTPLWEAQDDG KVPHIVPNHHLPLPTYTLTPNA TVAPETRAVIKWMKRIPFVLSA NLHGGEVVSYPFDMTTRTPW AARELTPPTPDDAVFRWLSTVY GSNLAMQDTSRRPCHSQDFDS/L NGNIINGADWHTVPGSMNDFDS YLHTNCFEVTVELSCDKFPPEE* ICPKEWENNNKDALLTLEYQVR MGIAGVVRDKDTELGIADAVIA VDGINHDVTTALGPGIWRLA* PPGDAYMVLDLPSSEGYHSVTRN

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8315	38683	A	8372	409	517	HFRSAGVCW*PPPLSVHGPR*H FRSAGVCWSSTPDPVCLGITSR GCRTAKIAAFSFL
8316	38684	A	8373	957	1230	
8317	38685	A	8374	1	2658	MVEEVLLDNILKSVFRLGSILPI TFSFPSDSQGPLLQVCRLSLIEH SRPCLPGYHQWRLQNSKDCL FLPLEASSQRGTQCMQPALFY KVSVDPFWEVSSSQETWGSGIH LRRQSVPYQSSSAVLGDLLFSS EPACKNKSAAVPTAAPSPRDA LSREEEESREA VWPQRSLSHAPM GSAQLELPGGFVYTVRKKLPTQ ASVMLDAPPATKLEHPRSSDC CVGSKNFKPVDSLILGSMGVG SVELDH LAPWLQPFPQESERFC LSGPVPVSPPLSEEINHALPKATV MASLGA VARKDNADSLHVPPP TPLFASRPVTALKWQAPREDL QPFTRVTLHWGKGNDQTFWGL VDTSSELTLPNPDPKHYGPPIK VGAYGGQVINGVFAHIQLRVN PMGHWTRPLVIFPVPERKISIDI LSSWQNHIIGSLIGRKTDGSWR MTVGYRKLNLQVTPIAAVPD VVSMLEQINPSPESECLKMSHQI TMRPELPIMNWVLDSDPSSHLEG YAQQHFIIKWKWIYICDRAPAGS ESTTSPFITQWVHEQSGYGD RD GGYTWAQOQRHLPLTKNDLAM AT/AECPISQQ/QRPTLSP*HGV/I PRGDQPATWWRVVDYIAPLPSW KGQRFFFTRIDTYSGYKFYYPAP NASAKNTICGLMECLIHCHGP HSIASDEGTHFIAKEVQQWAHA YRIHWSYHVPHHPEGWGKVQL
8318	38686	B	8375	1	3258	
8319	38687	A	8376	3	196	DWESCQNQC*PQQPRLHGTHW DPC*DME/CPSPC PQSPCPSPLR DQWTIPCPDPLSPQIMAAGRW
8320	38688	A	8377	248	423	
8321	38689	A	8378	407	683	LSSYCVHAGCYPREAAMRMISF SPSQIRWKPGESWRPPARRGT CTPGAHPPRPPSPRAAGPAHRP/ PPP/PSELPRAPQRPGNRNRRPG NSGPV

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8322	38690	A	8379	11	888	TGKLHTSVICNSTELTSWDSRR LFLKGKPLLSAGAGGVNVMPT APFPAPCKGSLRGNPSRPTH* ^S RSPOLERDTGGASFRVDEGEER GASSGGGS\RDTEGGSGA VPFGE SWRPARRGTCTPGA;HPPRPPS PRAAGPAHRP/PPP/PSELPRAP QIGPEAFTLGQPHGRGLFPPLFK LSKLYWPLGETRSRPRPRPYCQ SPGPGVTERGRRWSAPRPGAP RSPRWRRQSQGPALPRPRVNPC IQHGSEASYAPAL*WALRIPQQ GNTSSADEPADFTPNNQQADQM PCLHSCSG
8323	38691	A	8380	1	3135	
8324	38692	A	8381	44	2279	RQTVGDAQPHHHPPQPPRSPF PFPALPCTPAPQLPPSPCLREEF PSSPMGQTPGTWSSSGPWTSP PHSSRRLASPLAPLSVIPSTSQT MARSSSQSTTRFSPTPTHSQQ ASQAGTLWPWFLRGTMILSP LVGGPHFIRNTRRSMVN TAC*S SRPSLGLERSQTTGATRPGG*R SRGSMPTPILPGSPGSGATPTKPS SPRTGAGPMPCFSTRAVGCGST WPSAQATRCSWASLVEMAISK TAH*CPSCQCRGRIALIDS*PTQA SKGCSSTGYTGKKGPTTVSSAC SG*RASLGGPAGAGTSPALVP GSRDDGTYDSNPSA*VAGASA VGSCAASPLGEEACAATGPGE SFSEGWHEQ/TSLAVGPGTGTAT ELVLPLEG/HSPTSVPCTSRGGP TWAWATYRPPSPPGCGSGTPTSP PWMVSVTPSMGWGTCSWGP KTGTPSCFRAAPPRLAQPRPPT SSPLRLST/ASSSLGPVTQWLL EPHDARIVL LDNQTVTFQPDHE DGGGQETFNATGVLLSRNGSIG SRPASTAGPPSR*SRSPSTS PPP ASRPSTRTARRGSWGSGITIQR TSGCPMAPPFQGALRRCFSTL E*PGRSTGQASLARGMTSCLPT SPLFSTHNCKKTAPGLNI*SPTV TEIAHASMTPWCATQASDFTR GKSVKTTSRRTPPSISTRPPSMV VV*LKPTRGRPR*FSTPAMLRM

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hud	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
8325	38693	A	8382	1	2900	MVWGFTCITTATLEGGQSTAAS SRTSNQDISASSQNHQTKSTETT SKAQTDLTQMMMTSFLFSSPV HVNMETVTQETAPPDDEMITSFP SSVTNLMMTSKTITMITSSTDs TLGNTEETSTAGTESSTPVTSAV SITAGQEGQSRTTSWRTSIQDTS ASSQNHWTRSTQTTRSQTSQTL THRTTSTPSFSPSVHNVTGTVSQ KTPSGETATSSLCSVTNTSMM TSEKITVTTSTGSTLGNPGETSS VPVIGSLMP
8326	38694	A	8383	3	468	SSPLGLHPPRPIQSQCPRPAVSCSR GPSALLCRPLLGPEDAP*GSS WP/EGPLWGPRLYPSVSVGNGH WSGAGVADE/PAAPSPRPAGARR APSGGRPAACRSRRASRSSR PGPPAGRAGR*ACPAAARSAVA AAPRPPGAP*CGSASSATAPAAA APP
8327	38695	A	8384	3	1319	DSSRLCSRRSSRGHTVGLWGQS PGLGTTKGRGGGG*EDPPPGBTPR QQQDPHSASKP/PPAGLPAGVK WGPSISSPPSPPP/PAKRELQGRC PKFGRCSEGRRAAGDPPGS/GCPR AKQTHSLGTAVPVVVYYPVPH ALSPAANRTLN*NIISSQLPGLTPP MVPGE*HGRGHA*PRHPLPK DPPQG/PAQR*RGCSEVQRRP GTLP*GSPP/GNSHNGLPAMPPR *PPTAR/PQFPNPQDPRLQGQSSS EPLPRCPKTLCKTRHPDLRGRG KQPRGWAVQVPPGEVFGGGNGA QLEA*EGARMSASP*PSLESSD TTASPPSQGLFTAQKGWLWGPQR RLGALWLGRRESEKTSWRRLLQ SQVYWSCREEVEKCSRQGARL GQRRGWENVLGKSGSAECLs CPFCASLLAMPSCGPWELSKVA QCFLKLTGHPGPQEGSNNLKVT QQS

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8328	38696	A	8385	1	771	HSLIHSNLTHSLPSPPVQSPAWL PLCLSAPAT*ATA/CRVCLPGSC DSCSDSWQVDDCPESCCPCC APCCAPACPLTLVCTPVSCVSS PCCQAACEPSPCQSGCTSSCTPS CCQQSSCOPACCTTSSPCQACC VPVCKKPVCCPVCCPKVCCKP ICCPVCGSGASSSSCCQSSRQPA CCTTSCCRSPSSSVLLCRPVCRS TCCVPIPSCCAPASTCOPSCCRP ASCVSLLCRPTCSRLSSACCGLS SGQKSSC
8329	38697	A	8386	1	453	AQSLGRARPWRGASSSGRPDS RLE*TPTVCLLA/PEHGVAAATAS LGTPLTQWEGHNGCYQRSLFP PQSMPTPPCPASET/PVFRYRPP PSPGSSPRSIATAHPVPLGS SVNP PHPEVWNLPCWTKRLATSLLQQ KFTFGPKLGITNVDSDSLs
8330	38698	A	8387	39	630	IGTWRFGGSDRQEQQSRQGNCE EANDWPVSTALA/KPRGATGK NKSPGNDPAAAIAATAGAAATA GPGSPCLQN/RPHLLPFIS*APP EG*TPTSQDRPWYSAGAA*ASV KCRTGAVQKQQLL*NNRRFPGS PAPAQTADPGRGGGRGTGS/GV PSTGSSDWQERPWPCCGGMEPP RLRCLLRCSGSIHSPALQSLRN HQ
8331	38699	B	8388	1	2673	
8332	38700	A	8389	10	281	TTSDPYHPAPEIGLG*SPN/GGP MQGDLPGASGKEVSFL*GNVN EDIHNSGCVWQPSCDHLARQP KNKAVTMETKKRQKDGTSSLF SSSCS
8333	38701	A	8390	3	416	EYGQQCQCCHKRPRGPFGFHSPG PRGGSYISDLSGQESPEAGGGFP PRISALRPKNSCSFLRPRGRGS* YPAAGRPRAPGGPALQLSPR/PH PAAPPRAAPQPKPPRDVEPA P/PKLHPPP/GGPAPRRQQDLP GRLQP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
8334	38702	A	8391	98	1286	TMPPTRFLAHLPDQAYVCFCVV EGKERNLSRSKHTSPHSSTPAH LLSKPPRSEVVYHSQVLPGTP RPTSQLHLELVPFARLPGHR GIEREQSSPYSSRRGHHRGYTEE D*VNS**DGVEPYGKAAAAG PQRGRGYCCPWRRQRHGRHR/ RRPPIALQRRO/PARTPSARPPIA LQRRQ/QARTPSPRPPIALQRRQ RHGRHRPRP/RHSAEKTTART PSPPPIALQRRQRHGRHRGHG/H HRSAAKTTARTPSPPPIALQRRQ QRHGRHRPRPPIALQRRQRHGR HRPPIALQRRQRHGRHRWPWP PIALQRRQRHGRHRWPWPITLQ RT*RHRCHRHGHPL/PLQRT*Q HGCHRWPPIALQRT*/PAWTPL AMATHRSTKKITAWTSPRPPIALQRT
8335	38703	B	8392	128	457	
8336	38704	A	8393	348	1355	GNEGKAGTSSCWPDKPAAPAV ASSLAS*GASNSTPSAAGSTVA SASWLVESWSPGVTVVGVT SSKLGPMLLSTSTPDEAWSPESS CLLVAAPGVWLLPEAGFLLGH SQGAAPPSSSCFSTSSFSLSSS SSSSSSSLPMATPCDLGFSKCG SRSPPAKALLEDALTPRGGA* AWMRDRASIGADPVWLCPSLP SSFLCFSLKAVCTSSA/PPCYTT GFLSPTKTQPSKQGLGVCSSQ VSRHPALGOLLQDIAEDKSPPH SGSTICSLWLSSRAPCDRCTSR PSSKVQQYLCQQQDSRSRTRAG WKTPTVVGRHPVKIEKESIRP ANFG
8337	38705	C	8394	154	219	

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8338	38706	A	8395	3	1054	LYLKVCYI*KELFEFSNLYKHPS GEEVWERILRV*DNGGRNIVKL YQAEFIDLGPVSRDSAfnVAQ GVKKGSNRFLPWLAEIWITRWP TVSELEMPDLPWFVNVEEGIKRL REIGMVEWISHFRCTHPSWKGP EDIPLTNALQNRFVRAAPASLK SLVIAL\FCMSDATA GTAVTQL QNLNTMGIIGSRGVRDVQVAL NHQRQVGVA NRQGTPR/QRGT KKRTR*PGQAKRPGPKERGTRS HAYAHTSVTTPKNNRHDTRPS QRTPQQKRDQAQHQTEPTNTP NTSRPSPHVSSFRSKKKRRRPQ HEERNKRTRTEEERARNRAN KDDTKRQPKKTRENRRQLWS
8339	38707	A	8396	140	398	
8340	38708	B	8397	15	192	
8341	38709	A	8398	1	1167	AGTARRAPESSRRRAVAGHPE TMGKLVALVLLGVGLSLVGEM FLAFRERVNASREVEPV/EPENC HLIEELESGSEDIDILPSGLAFISS GLKYGPMPNFNPADPEPGKIFLMD LNEQNPRQAQALEISGGFDKELF NPHGUISIFIDKDNTVYLYVVNH PHMEVHCGRIF*ILREQQRSSGY YLAKTIKTWNFFKSVNDIVVLGP EIQFYATRDHYFTNSLSSLFFEMI L\DLRWTYVLFYR\PREVK\VV KGFCSAING\TVLSQTQKYV\Y V\ADVAA\KNIHIMEKHDNWDL TQLKVIQLGTLVDNLTVDPA\T GD\LAGCHPNPMKLLN\YNP PP\GEVLRIO\NVLS\SESPR VSTG YANNGS\VLQGTLWASVYHGK I\IGTVFHKTLYCEL

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
8342	38710	A	8399	89	1685	KGP L LLSLPCRA G AMAET S AT GACGEAMAAAEGSSGPAGLTL GRSF S NYRP F EPQAFGASSPSW RLDGA F GNSNERAEGCKVPQEG RLLK L LAGULTRP D VRRP I LGRG LVGG Q EEASQEAGLPAGAGPS PTFPALGIGMDSCV I PLRHGGLS LVQT T DFFYPLVEDPYMMGRIA CANV I SDLYAMGITECDNMLM LLSV S QSMSSEEREKVTPLMVK GFRDAE E GGTA V TVGQTVVN PWDL L I I GGVATCSIANQFEFI M PDSAV V GDVLV L TKP F RNP G L LFNAH Q WLG*FLERWD* S *RW WFSRE E VELIA Y QEAMFNMA TLNQNCCRV*MH T FNAHAATD ITGFG I LGHSQNL A KQQRNEV SFVIHNLPIIAKMAAVSKRASGT VWGFFQGTSA\ETSGGITGFCLP R\EQGGLAFCSIEIQILPKYGRGS PKAWIV V GIVEKGNR T ADP D PLTS PRVIEV V LPRGATAAAV L AP\DSS NALLSLAREI E TERVV W TL E P LSTITDG S QELIVKKFP K KAACI VVPAALSR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
8343	38711	A	8400	30	2391	ARGRPLIAARSSRPCGPRLPFK RAGPAPAA PHRGDQE ARWFSG AAPSRLPPAPRFSGPA AFLSAQ GPPSGAMQPTLLL SLLGAVGLA AVNSMPV DNRNHNEGMVTRCI IEVLSNALSKSSAPP TPECRQV LKTTSRKDVKDKE TENENTKFE VRLLLRDPADASEAH ESSSRGEA GAPGEEDIQGPTKA DTEKWAE GGGHRSRERADEPO WSLYPSDS QVSEEVKTRHSEKSQREDEEEE EGENYQKGERGEDSSEEKH LEE PGETQNAFLNERKQASA KKEE LVARSETHAAGHSQE KTHSRE KSS/QFSAA*EAGSQENRPQESK GQPRSQE KSEE GDEDATSEVDK RRTRPRHH HGRSRPD RSVQQG SFPS EEKGHPQEESE ESNVPM ASLGEKRDH HSTHYRA SEE EPD YGE EIKGYPGVQA PEDLEWER YRGRGSE EYRA PRPQSE ESWDE EDKRNYPSLE LDKMA HGYGEE SEEERGL EPGKGRH RGRG GEP RAYFMSDTREE KRLFGE GHHR VQENQMDKARRHPQGA WKEL DRNYLNYGEEGAPG KWWQQG VLQDTK ENRVEARFQDKQYSS HHTAEKRKRLGELFNPY DDPL QWKSSHLE RDNMIDN FLEG EENELTLNEKNFPE NYDW WW EKKPFSEDVNWG YEKRNLARV PKLDLKRQYDRVAQLDQLLHY

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8344	38712	A	8401	73	1922	ILPVPIIP/CRQVLKTKSKCPTRQA DLGHCSDP-CSYSLHITFPADASE AHESSRG-EAGAPGEEDIQGPT KADTEKWAEFGGHRSRERADEP QWSLYPSDSQVSEEVKTRHSEK SQREDEEEEEEENYQKGERGE DSSEEKHLEEPGETQNAFLNER KQASAIIKEELVARSETTHAAGH SQEKTHSREKSSQESGEETGSQ ENHPQESKGQPRSQESEEEGEE DATSEVDKRTTRPRHHPRSR PDRSSQGGSLPSEEKGLPQEES ESNVSMASLGEKRDHHSTHYR ASEEEPEYGEGNKRGYPGVQA PEDLEWERYRGRGSEEEYRAPRP QSEESWDEEDKRNPSELEDK MAHGYYGEESEEERGLEPGKGR HHRRGRGGEPRAYFMS\DTREEK RFFGEGHHRVQ\ENQMDKARR HPQGA\W\KELDRNFLNYGEEG APGKWWQQQGDQLQDTKENREE A^VFKINHFISHHTAEKRKRLG ELFNPPYYDPLQWKSSHFERRDN MNDNFLEGEEENEELTLNEKNFF PEYNYDWWEKKPFSEDVNWG YEKRNLRARVPKMDLKQRQYDR VAQLDQLLHYRKKS\AEFPDFY DSEEPVSTHQEAENEKDRAQDT
8345	38713	A	8402	1	381	
8346	38714	A	8403	1	444	MKLIVGIGGMNTNGGKTTLNSL LRALPNCCVIHQDDFFKVPALA RGVLESLDMEAMLDTVAQAWLS SPQKFARAHGVSVQPEASDTHI LLLEGFLLYSYKPLVDSLYSRRY FLTVPYEECKW/KEKYPQLHSP *SPRPLRWPRVAHVPEV
8347	38715	A	8404	3	421	
8348	38716	A	8405	3	4065	SAPPDVTTYTSEHSIQVERPQGS TGSRATPKYGNALMETGDGV PVSSRVSAKIQQLVNTLKRPKR PPLREFFVDDFEELLEVQQPDP NQPKPEGAQMMLAMRGEQLGV VTNWPPSLEAALQRWGTISPKA PCLTTMDTNGKPLYIYLTYGKL WTRSMKVAYSILHKLGTKQEP MVRPGDRVALVFPNNDPAAFM AAFYGCLLAEVVVPVPIEVPLTR KDAGSQQIGFLLGSCGTVALT SDACHKGLPKSPTGEIPQ

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8349	38717	A	8406	10	580	KQCALLTFCISLPMPSFGFAPAIT VTVVN/PRHPLIRDMLRLRIKED DDKTVLDLAVVLFETATLRS YLLPDTKA^YGDRIERMLRLSLN IDPAKVEEEPEEPEETAEDIT EDTEQDEDEEMDVGTDEEEET AKMS*ALLTFICSLPMPSFGFAP ITVTVVNHFVLCSKTSQVFRS ENWKVVAESSRGDHDDCLD CSVLCWGRTATGAFSCPAQLIF AVSSSSVPTSISSSSCVSSV SSAVSSGSSGSSSTFASGSMF LRRSILSILSPYALVSGKRYPDR SVAVNKTTFARSKTVLSSSSLI RRSMSLISGCRD
8350	38718	A	8407	I	1967	MTMAAAVVARAGAGARAATA AALRGCGTAARGRPCAGPAR PLCTAPGTAPDMKRYLWERYR EAKRSTEGETKKVTTSLNARHY YTHFTENEDEINSSSYASQKK TFeINPRHPLIRDMLRLRIKED DKTVLDLAVVLFETATLRS LPDTKA^YGDRIERMLRLSLNID PDAKVEEEPEEPEETAEDIT DTEPDEDEEMDVGTDEEEETG KESDPPMAYIHTAEGEVITFKS ILFVPTSAAPRGLFDEYGSKSDY IKLYVRRVFITDDFHDMMPKYL NFVKGVVIRKKLVRKTLD MIKIAADDKYNDTWFKEFGPTTKL GVIEDHSNRTRLAKLRLIQSSH HPTDITSLDQVVEK^MKEQDK IYFMAGSS^RKEAESSPFVERLL KKGYEVIVLTERPVDEYCIQALP AEFDIGKRFVQNVVQKGCKEFHE S^ENLRK**CKSVEQRISALCLN WMKDALKDKI^K/ALWVSSA ALTESPVLLVAQPVRDWSWP TLGE/RSMKAQAYQTGQGHLL QIYYAESERKHFEINPQTPTLIR DMLRLRIKEDDDKTWLDAIV VLV^NRQRLGSGYLFTQTLKAY GDW/RLEMRMLRLSLNID^PLMPK VEEPR/EEEPEETAEDITV QDEDNEEMDVGTDEKGRTSKG
8351	38719	A	8408	181	462	GMASADSSKTFGRKGQVVG AVGDSAKESQQGQPPGAPP RAAGL/WRRHHCSF^AD^TTN APGKGNPRPGKGAGGEQGTAGDF TCQMPRTQNTL

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8352	38720	A	8409	3	228	STGVPVSQQNL!PLEKASVLNF GALYTQIGTRCDRQTQAGLESA IDAFQRAADMSPGGLTRRSLG TRWHQGTPH
8353	38721	A	8410	129	311	RCFQPDCHSHSTPGTGPGRSGCL LSSAAPW*KPPAAPRTHSRSH NRGPRRQQHARHQDDP
8354	38722	B	8411	1	789	
8355	38723	A	8412	1	933	TVVLKDFILEHYSEDGYLYEDE IAIDLMDLRQARRTPSRDEAGVE LLMTYFIQLGFVESRFPPTRQ MGLLFTWYDSLTVPVSQQNL LLEKASVLFNTGALYTQIGTRC DRQTQAGLESA/IDAFORAA/GP TRGGRASTYEMTPAAS/PEIPGA SLQREE/QWTGAUTHQQIYQP GTTP*SPQQAQPSRFLFAMDFA ATTSAIGSARPSTNQS*GYFHTG RSWQPVA**ECHILRGNNAENVL HDLLSH***RQN**NQENLQEAF LPELGHQQEQTEVSQHLVPPIG RGCTASGQEEAALPFQPSQLRQ FLVL
8356	38724	A	8413	1	389	
8357	38725	A	8414	1	506	
8358	38726	B	8415	125	700	
8359	38727	B	8416	19	338	
8360	38728	A	8417	1	3335	MAALWNNTCGAWKNMLIPECH SQLRVAANPKVREQRVRLELSF VNSDLQMLKEELFGLNISVGVY QNTDEDGYLYEDEITDLMDLR QACRTPSRDEARVELLMTYFIQ LGFVENRLFPPTWQMGLFTW YDSLTVLVSQQNLLKEKASVL FNTGVLYTQIGTRRYRHTQAGL QSAIDAFQRAAGVLNVLYKETFT HNPSYDMIPAMLSLVKMMMLA QTQESVFEKISLPGIWNEFFMLV KVAQEAAKVGEVYQQLH
8361	38729	B	8418	1	1689	
8362	38730	A	8419	2	722	CPGGSERGQRQPCGCRSGRTE PGFSPC*KSAPRPQAVSLKASP RPSSSS!GPAGISSLPGRECSRSCGT QNILGPFPQLVSG*PL*GR*CQFP AAAEPVAVPL*AEDISA/GPPAV *AP/SGLAHLASG/PGPLPLLLGG AGLV*QSI**GGHGQADEGP*G EMDAKEAGPAAQNCNDLHVCPG ARGAEGAPGEGCIS*QPHADPA L*AASELPKDELLRQCSCGG*RC SPAGSAAPRAGSSA VLEPQ

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8363	38731	C	8420	144	439	
8364	38732	B	8421	1	4747	
8365	38733	A	8422	1019	1880	YCCLPRGGNAGCQTRQDPSCRPGPSQGLSLPPGR/PGAAVECGARSRGWGQQDGPGPSPGKAQVPAEPAPPQTVPGPPPEDPCLGPRNEVPDGG/GARQSHHPGPPRSPGPEGGSPOAAARLVDWWRVSRPQNQLPNPGP*DQPPRPAIPTATPSCGCNGPFGPRAPRPRPLSSEEAPSRAGPEEEAAPTYTPRLRRGRPARGPVCR/PPAGPFAV*PEFRRFALPRASVSGFQS/PVAAGGAPDPGPGRLLGYTDAHGJDLPLTNTTACTGPWPAGPRHCASGAEA
8366	38734	A	8423	240	763	VLVARRPQRPGHEPAVLQQ/PAAGP/VPVPRKPNPSPPSPSAGLRPPGRAGPLTSPRCGPGLPAFTGHR/T/PVGVRPKAAGPRRTYQGRGMGPRPRP RRPVVPVGGERSHSHPSGPPLRSPGPEWGLTSSSCPA RGLEGVSA/TQNQLPNPGP*DQPPRTCHPHGYTORI/PSGPLLSPGPEWGLTSSSCPARGLEGVSAPRISSRIQGRRTSLPEPAIPTATPNGYIGSGFPAG
8367	38735	A	8424	2	609	PYSISIVSTGPSADS VYT KVR LL EGETLSVQCSYKG YKNR VEGK V WCKIRKKCEPGFARVWVK GPRYLLQDDAQAKVVNITMVALKLQDSGRYWC MRNT SGIL YPLMGFQLDVSPAPQTER NIPFTHL DNI LKSGTVTTGQAP TSGPDAPFTTGVMVFTPGLITLPRV*PPPD LPPRQATASLLPAPPARDPGGPWGPRQ
8368	38736	A	8425	1	252	

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8369	38737	A	8426	3	1581	ALHCAIRHEDKWPVAVRANGH LLLNEKMSKSTGNFLTLTQAI DKFSADGMRMLAIDAGDTVED ANFVEAMADAGILURLYTVWE WVKEMVANWDSLRLSGPASTFN DRVFASELNAGI\KTQDNEYEKM MFKEALKTGFFEFQAAKDKYR ELAVGRDAQ\KLVLFRFIEVQTLL LAPFCPHLCEAHLGHSGWKGPG LQLWNCFPWACGRVPV*WPKFL IHSSQYLMEVTHDLRLRNKY MMPAKGKTKTDQPLQKPSHCT IVVAAKEIYPPWATLPPCLFLTV KHFEQQLTGKTGLDNKAIASE LGSMPELKYMKKVMPFVAMI KENLEKMGPRILDLQLEFDEKA VLMENIVYLTNSLELEHIEVKF ASEAEDKIREDCCPGKPLNVFR EPGVSRFLLVN/RPQPIPMAHFL NPKLEIRQGD\TVPIIIRRLMKM NRGI*RPFPKVKGWRI**SHCW GPRRSSCPWEKEYTREDPPPE ACLFSD/VDLMSKKIHLTENGIR VDIGDTINLSGSLNSCTLEIYPG FLGILLL
8370	38738	A	8427	1	1052	MIKNIGPQYLTAPSFLGEQEKGDEE EEGHIVDAEAEEGDADASDAK RKEQEEEVDYESEEEREGE ENDDEDMQEERNPHRGARKT QEQQDEEVGL/GH*GGPVSPRP DAAPETHPQPGAPGAEAVER VQAVERIHPFIDDYQYD\TEESL WGQVTVKLPLMKINFDMSSLV VSLAHGAIVYATKGITRCLL\NE TTNN\KNEKEVLNTEGINLP FKYAEVLDLRLYSNDIHAJAN TYGIEAALRVIEKEIKDVFAVV GIAVDPRHLSLVADYMCFEGV YKPLNRFG\IRSNSSSPLQQMTFE TSFQFLKQATMLGSHEDELSPS ACLVVGKVVRGGTGLFELKQP
8371	38739	C	8428	154	219	
8372	38740	A	8429	1	1584	
8373	38741	A	8430	200	277	

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8374	38742	A	8431	3	877	LYLKVCYI*KELFFFNSNLKYKQPS GEEVWERILRV*DNGGRNIKL YQAEFIDLGPVSRDSA FNVAAQ GVKKGSNRLPFWLAEIWIKKW PTVREVEIPDPLFLNVEEGIQKL REIGMG*WISHFRPTHLSWEGP EDIPLTRPSQNIFVRAAPASLKS PVIALIYMSDLMVRTAVTQLQ NLNTMGIJGSQQGRDRVAPLNH QRQSGHGYHNGQQRESGQNNS LTGVELWHWLINHVVSRESEVD RKPTTFLNLVYQKTSRSNRK TSLNYKNRESRPLNQFPDLSQF
8375	38743	A	8432	1	282	
8376	38744	A	8433	1	281	SVHTGHHHYHHRHHHHHHHQ HQLHQHQHQCGGHHHHHHHH HHH/HYFQ*ATWEMLLWVGHS HL*RQP*KQHEHRDDVSQAGS VCPCASRGFHRI
8377	38745	A	8434	64	302	
8378	38746	C	8435	133	262	
8379	38747	A	8436	1	1962	MFSIPTGQLRAAASGARRHRGR GSIGGGPFHAIQGPVETDTTAQH ETVAPPDLAHPSA RGP RPY/G RHALDEPFLHISGALF*DSSLAV *EPPESRLDARPGARNNSRCPIT A/RPPDTDMGTPSAQGAKSSA FAQLPPPHNSTRRAPAGDMPPS MPGATELLACASVPAG*TSELRG GGFASSLSGSPCSKGSPASSDA WPRLRQRPWPVTFPEAQPLEVPG GTEHGCPSPWEPLNSAAQTPLFF PPLHPTAPSCPLGLPGSPPGPTSS TGDYIPT*DQS GTSKLYCPLQQ GGAEAAHCV/PA/PEQPETNSKR KGETPTPN/DKEGETPTNEKKE KHQQQT KRRNTNTKRRGEETP TPNEKKEKHQHQTKRRRNNT KRKEGETEPAQGGTNPGRVQQ SPAAL*CFSY*SECQQA C P S D E S AGARFTAGSAPDKGL/PPGPSS WAPSS*HLI LATT VHL VTRPC* PPSCTGPGSHLVVGGPRPSAHH HSDLLF*SSAGKPDWS PCWTMS AMGILRPRGRASGAPGSATPFP GEFQEAHAPPVQPSTAQSLPAP CLPLGA SGGP R OH PPD V S R G G DRGLQQSVLSDAAP*PGVRGNP PRGARWGARA AWPAGPSAPHS PCPQPVPGRDPLVY PSPGTEAQ MSCLTPQFLQILLCDFF

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8380	38748	A	8437	438	699	LLEGKLTNRKDIIHTKTPSVCHH HRGPKVVDKTTKMGKKQSRKAE NYKNQASAPPPKDRSSYQQRN KAGHRMTLMS*EKKASENQTS PS
8381	38749	A	8438	I	1334	MDGRLYSVTIQPSSVLNLQLL SGPKSAVLVVTILMCSETNLSF NEFSFHKTTSPPEKMSIRKPOEK SADGKQFLQNDRKNPKLGNQT TLLRNNDVSGLLSRTKRNIVPPG WYSVYVTNNYVFKKPSKAK VSESTTKNDPVKNJHIESSHNI LNKIAMNSNLQVVVKRLEDTIS IAKKSWNQNQPLSEGYYKASKKLI EIDGKDQHADRNMTLTLNRMT CKEQSLSKSVVASGNIINSHCM PTVDLNNKRLENLKKSSIIDMG RLISSVENVPAKYEGTESSSVSN YSSPIKLMFLSEVKSEGVKYTL TSVGTSHSNVVLPSKEPTTHHV TEEKTTETNEDISNANSENHYHSS HYDTDTFQRELNKFSHAKETA GSSTMFIGDINSDKPQEEPKDNS SSATDPsf/NKKTR*TKKNRSPS CETD*ATNWKTTKA*N*SNKH
8382	38750	A	8439	115	523	QFFFSLSQALKLDQAIHISMDF HSVSELFAQSQRRLGDPAMDLL VLSQGHQTNILDIVHHKEALT KVTEENRQHVAEKGTE/SAEADD VRIT/VNRNSFTTSLEIHHFHPI* RDMKSQMZHFLQQEILFFQKSS RN
8383	38751	A	8440	1	461	
8384	38752	A	8441	3	319	
8385	38753	A	8442	112	480	IFSSLNVAYPWIPEKKVDGSKC PIQQQLERKIKNFVLYLK/RQL TKCEFKN*RLENFIRVNNEKY VCT/SYHTKLLFNNLHMALILIV FKYQSFFSLHSCCNQQPAHKVLE PALELQDEDGMVH
8386	38754	A	8443	I	528	

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8387	38755	A	8444	2	811	GIHTRLNSELLKEEESNKRLEAE IEYQSRLLTAISKHSESVKTER NVKLALE*TDQDSVQVKMSSDI SEVEDKNEFLTEQLSKKQIKFN TLKDKFRKKRDTLRKKS LALET VHNLLSQTQQQIKEKMKEYEN AEAKENNSTGKWSCVEERICQL QHENPCIEQQQLDDVHQKECLPS RKEKFKSEPPAFLSGNQVKSSS CSLQTLPFPDLDILENPKDST KKLLELINKFRTVTGYKLQKQS VAFLNDKNEQSKEENQECNPVI
8388	38756	B	8445	1	1581	
8389	38757	A	8446	617	2972	EQNKPYQWLQRKNSKRERSE KKQPQVKEGNNTNKSEKIQLSE NICDSTSAAAGRLTQQRKIGK TYPQOFPKKLKEEHDRCTLQE NEEKTNVNMLYKKNREELERK EKQYKKEVEAKQLEPTLQSLE MKSKTARNTPNRDFHNHEEMK GLMDENCILKADIAIRQEICTM KNDNLEKENKYLKDIIKVKETN AALEYTIKLNEEMITETAFRYQ QELNDLKAENTRLNAELLKEK ESKKRLEADIESYQSRLLAAISK HSESVKTERNLKLAERTRDVS VQVEMSSAISKVKAENEFLTEQ LSETQIKFNTLKDKFTRDSDL RKKSLAETVQNDLTQTTQQQT QEMKEMYQNAEAKVNNSTGK WNCVEERICHLQRENTPWLVQQ \\LDLVHQKEDHKELK^LISQRGF IESGKKDLVLEEKSKKLTNECD HLKESLFQYEREKTEGVPKKEN EELRKLFELISSLKYNVRIRKK NDELEEEATGYKKLLEMINTM LNFGNEFDCHGDLKTDQLK MDILIKKLKQKFDDLTAEKEAL SSKCVNLAKDNQVLQQEFFLSM KKVQQCEKELEEDKKMLKEEI LNLKTHMENNRVELSKLQEYK LELDEKAMQAIVEKLEIHLQEQ AQYEKQLEQ/FKQGYNTASLNK KELTLKDVECKFYKMKTAYEE VTTELEEYKEAFAALKANS

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8390	38758	A	8447	1	2794	AVYLSRGCVCCIRCISLLKEPH EEGVCMCSFRSVATQKNDIRPDF QLGKMDSKIKELEPQLTLYQN PKTLKFQGKKSVKFALSPSMAL RK*PFKMFSI*SIFIALQFLHIGYY KPILFEPNQTWPQGHVAWQDT CSIVAI/SANITQKVHPVI/W/SSIP PYGVALSSLTTGTAAPPLCTQL GV*IPLDCAQATFISHDKMVISL KGYLFLSSCLGNSSLKKYTEKL QEPPASAICEAADKEEPSQKK RVDT/S
8391	38759	A	8448	184	427	WAIAIQRHVVYDQEWAIDPC NM**VENAETLPQGPFLNISLES SARRRATSRDDNRFRPHRSRR SRRSRSNDNALHLASE
8392	38760	A	8449	1	903	MAQKFMAPNRAARTLRDICTDR EAYPVQESMGSGTRGQRKEDM GGAALSTGEGGARDVKAPLPE ATLCSQMGPTRPSGLCDLAG STLAGRWMHQSFDFDGGMEAS KLPGQEGVRIQPMSETRRRAT SRDDNNRFRPHRSRRSRRSRSRD FSLHLASEREAISRLKDPRPLRA REDYDQFMQRQRSFQESMGHGS RRDLYGQCPTVSDLALQNAF GDRWGPYFAEYDWWCSTCSSS ESDNEGYFLGEPIPQPARLRYV TSD\DCCTNTAPTASPNLPH*VA EDSCTAGKDQRAKTCIISLY
8393	38761	B	8450	1	322	

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8394	38762	A	8451	I	2460	MEEKSKRRGVLSLLALAKFG DEPLPLGSPNSCKYKLTTLKELG WREVFVSSLQFCLCTSVASQMLS QYFEYTQPHPGDICHPCETCALQ KVFLTSSGQSSTSSSQFVLQ INAQTILEKTPTHISTPTPTPTLA NPTAVGLEEDREQDVGTSSRG GAWDTRIKRELEKMSEKCGGQ INGGDIAVFASRAGHGVCHWPP CFVCTVCNELLQIYFYQDGK IYCGRHAECLKPRCAACDEIIIF ADECTEAEGRHWHMKGFCCE CETVLLGGQRVIMKEGRPVYCC CFESLYAEYCDTCAQIIIGEAF GSQ/HWSFC/RCGHLCFGEWG* PQLLWMLC*LELTKGPRDAIMS SLHSWHLRKGVRRRRRKEDK SPEVLP*KSISSGTLSH*R*RPH* SLFLGSRVSL PSGECRGPQPPYS HSLRLYSQQALPTGRGPSSSQFP FCQFYCCYKKSLLCDCLSKSPA LEKAMRGIDQQGQMTYDGQHW HATETCFCAAHKCKSLLGRPFL PKQQQIFCSRACSAGEDPNGSD SSDSAFQNARAKESRSRAKIGK NKGKTEEPMLNQHSQLQVQSSN RLSADVDPDLSQMDMLSLSQQT PSLNRPDIWRSREEPYHYGNKM EQNQTQSPQLLSSQCNIRTSYSP GGQQGAGAQPEMWGKHFSNPK RSSSLAMTGHAGSFIKECREDY YPGRLRSQESYSDMSSQFSSET
8395	38763	A	8452	2	942	NKNPKNHYPESYVSLKNDFTK LTSHRRHRGVQEQLVQLCHFV CEHGHIVITLSSGFIVYRTRAN YSSSAQGVGIAAAAALDAVLIRA HQRTQGCHHELSALLAFAEKGSE KKEEEEGGOVSRSSSLKVQAQE LSATEDKGHISPFWEAVYHYA SGECRGPQPPYSHSLRILYSQQA LPTGRGPSSSQFFCQFYCCYK KSLLCDCLSKSPA LEKAMRGID QQGQMTYDGQHWHATETCFCC AHCKKSLLGRPFLPKQQQIFCS RACSAGEDPNGSDSSDAFQNA RAKESRRSAKIGKNGKTEEP C*TSTASCK

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8396	38764	A	8453	I	937	VHQYYSC PEEKVPVYVNSPGEK LRIKQLLHQLPPHDNEVRYCNS LDEEEKRELKLFSQQRKRENIG RGNVVRFPVTMTGAICEQCGG QINGGDIAVFASRAGHGVCWII PPCFVCTVCNELLVDL IIFYQD GK Y GRHHAECLKPRCAACD EIIFADECTEAEGRHWHMKHFC CFECE VLGGQRYIMKEGRPYC CHCFESLYAEYCDTCQAQHIGID QGQMITYDGQHWHATE TCFCCC AHCKKSLLGRPLPKQGQIFCS RACSA GEDPNGSDSSDAFQNA RAKESRRSAKIGKNGKTEEP
8397	38765	B	8454	214	551	
8398	38766	A	8455	I	1140	
8399	38767	A	8456	I	2525	MLNIQSVP GIGQGHYSRYLHSN PMHSGFISNIHMRKP KFREIJF ADECTEAEGRHWHMKHFCCFE CETVLLGGQRYIMKEGRPYCCH CFESLYAEYCDTCQAQHIGE IF GSQ/HWSFC/RCGHL CFGEWG* PQLLWMLC*LELTKGPRDAIMS SLHSHWLRKGVR RRRKEDK SPEVLP*K S SSGTLSH R*RPH* SLFLGSRVSL PSGE CRGP PPYS HSLRLYSQ ALPTGRGP SSQQFP FCQFYCCYKSSL CDCLSKSPA LEKAMRGID DQGQMTYDGQHW HATE TCFCAAHC KSSL GRPFL PKQGQFCSRACSAGE DPNGSD SSDSAFQNAKESRRSAKIGK NKGKTEEPMLNQHSQLVSSN RL ADVDPLSLQMDM LSSQT PSLNRDPIWRSREEPYHYGNKM EQNQTQSP QLLSQCNIRTSYSP GGQGAGAQPEMWGKHFSNPK RSSSLAMTGHAGSF IKECREDY YPGRLRSQESYS DMSSQSFSSET RGSIQVPKYEEEEEEEGGLSTQ QCRT RHPISSLK YTEDMTPTEQ TPRGSMESLALS NATENQDDCS FVNRLKGSNNRPGR RQELMV T WNFIQERNGSGMDQ CDDGGG KILD P V I L T V E L TGF AKGWKM FSVKDQSVNVLG FAGCLSADG GAKRQEHL SRFSMPDL SKDSG MNVSEKLSNMGTLNSSMQFRS

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8400	38768	A	8457	7	302	PLPSSPEQPAGRKGTVGLPCALT EIYFRVTIY/FYVEIEKLLIVAK QEGLSGNNHKP/VERKYMTYLS AQDIHELIQVQVQNGHLQMCGK SETGNEASPVS
8401	38769	A	8458	1	241	MTYLSAQDHIELIQVQVQNGHLQ MCGKSETGNEASP/G*GRGVNP WP/RHARSRMRALTRSSASCCR CSGASSICTGTSLSTGG
8402	38770	A	8459	31	454	QRSAWRSQIWSASRSV*SVFVR RASSRCLRNTGSGPGHPDR*DC RT/ARRCGWTRRRMASPAAC GRSRCSCSACVI/LNIVELKEVVV GNHLESISFLVMGYCEQDLASLL ENMPTPFSEAQVKCIVLQVLRG LQYLHRNFIIHR
8403	38771	A	8460	1	914	SYHHLRHHHHHLPHHCF/HHN NHYHHYHHYHHHHHHCHCHYH YHHLHHHHHHHHHHHHHHCHYYH NNNNNCCHHHHHHYHHHHHH*Y HHYHPHHHHHHHYHHHHHYHH HHHHHHHHHRHHYHHHHHHQHH HYHHLHHHHHYHHYHHNNYHR HHRYSCNNNHHYHHHHPHHY HHHHHC*HHHYLYHHHHHHNNH HHHYHHHHHHYHYHYH/HHH HHHHHHHHYHYCHDHNHYHYH HHHHHYH/AHFHHHYHHYHYHY HHHHRHRRHHHLHHHYCHRPHH YHYLSCCETSHTLFPQNAISSFD CKYLDGQDDDEFVYYKLCTLY
8404	38772	A	8461	102	420	DTGPGEGAAGGC GGIVVGEGV AAPAAPGHS*VG/GNQPYLSPV CSRGSPTGRAAARGLSGCWP WWSPRSGSAPSQCSSAWSAW SAGAPRFAPSAPGHPEGRCPA
8405	38773	B	8462	121	215	

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8406	38774	A	8463	44	1584	AVLDRGPRVGSSSPGGMSTC LSSPLFATAAELGGVGLCSAGRDX GPRRKVYLSVDEKKI.RCCQPKS GRSVAERAAGHSAEGWRPVH VGPGLLGLAL*GP*AWGFQGR KGGI^KGAYTAKCMMGSDKAQ ASGIATGGGHSGAEAVG/PQQ/ QGTVLSEFGGGGLSFRRMPGSL ^GPSVPCKCGHPGPRCPPHAV EGTDTVATVAAT/GPPLAPSHG TSWQS GSLQ*DTGPGEAAVA AVVGVEGAEELPAAPGH*VG VISHICHPFVAGGSPGTGRAAAA RGLSGCW PW WSPRSGSAPSQC SSASWSA WSAGAPR SAPSAPGH PEGRRCPA*GWNPQGSKSSLKS SELWTPIPYVPYAVP*HTCGYA AGPAPVQT PCR GGWNGAQVGL DPVGGHDG DTPHGS/APRLPGRV GGAP*AAVAISTDPPATASLG PAPGGPACCP SL*ACAPASSASP APARSSWPPAPASC GSAAPWW HQTHGHGS LWWEHSCRLSHRS PSPGAPCW/PPF FRASPD RGTA
8407	38775	A	8464	1	541	MKSLEEKIGCLLKFLGLDDQTC CKEDLHILFSNHGEIKWIDFIRG AKEGHILFKEKAKETL GKADAK NNGNLQLRSKEVTWEVLEGEL EKEALKKITEDQQESLNKWKSK KGCRFKGKRKGSKAAQPGSGK GKVQFDKKT KFASDDAHDEN GSTGPIKRGREETDKE^PASKQ PKTENA

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8408	38776	A	8465	1	1326	PAALGGGVAVAVCEPVARLL WAGTLKIAVMAENGDNKEKMA ALEAKICHQIEYYFGDFNLPRD KFLKEQIKLDEGWVPLEIMIKF NRLNRNLTDFNVIVEALKSKA ELMEISEDKTKIRRSPSKPLPEV TDEYKNDVKNRSVYIKGPTD ATLDDIKEWLEDKGQVQLNIQM RRTLHKAEGSIFVVFDSEIESAK KFVETPGQKYKETDILILFKDD YFAKKNEERKQNKEAKLRAK QEQAQKQLEEDAEMKSLEEKI GCLLKFSGLDDQTCREDLHIL FSNHGEIKWIDFVRGAEGIILF KEKAKEALGAKADANNGNLQ LRNKEVITW\EVLEGEVEKEAL KKIIEDQQESLNWKWSKGRRF KGKGKGNKSCPSPGSGKGKVQ FQGKTTKFAASDDEHDHEN ATGPVKRAREETDKEEPAKQ QKTENGAGDQ
8409	38777	A	8466	2	331	CSTSLMIREMQVKITMRYHLTP ARMAIIKKSRPGVCQPGFTASY CSSWRNRGLSRAMAQLSPRPLS TLQ/PLLAVDRGS/PVLAGSHRL PAQC/CMTDSSSTLGSAAAGSW QQ
8410	38778	A	8467	1	209	MNSHFLKEDIQMANKHMEEKCS NPLLMIREMQIKPTVRYHILTSAR MPIIKKSKINSRCWHGCGEHGT LLHC
8411	38779	A	8468	2	370	CSTSIIIREMQIETTMRYHLP RMAIIKKISRCWQGCQGEQETLL HSWKPOP/LWRSSSGTARERQF LHPPLLKARIEITPPESLAVLKIP MEGTWMELEAVILSKLTQKQK TKH^MLSLTSGS
8412	38780	A	8469	2	194	CSTSLMIREMQIKITVRYRLTS ARMAIIKKSKINSRCWHGCGEH RTLLHCCNLWKERNVSYVSA
8413	38781	A	8470	341	496	

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8414	38782	A	8471	46	711	SIJHLFLIFCIGLDVRLGKDFMT NNLKGNNAIKTKINFWDLKLKN FCKAKRNSQ^RANR*QTEWEKT FIICTSDDKGUTSRIYNKLKQISKK KTNNPIIWKADMNRQFSKED ^I QMANKHMKKCSTSLSMIREMQI KTTVRYHHTSARMAIIKKSKN ^S RCWHGCCEHGTLHCW ^K /SKS LYEKDTCTRMFIAAQLAIK ^T W NQPKGPSINAWIKDWCSKTN HNK
8415	38783	B	8472	36	1199	
8416	38784	A	8473	3	184	FFFFFLRRSL/DSVAQAGVQWR DLSSLQAPPNGFTPFSCSLSSLSS WDYRRLPPR PANFLY**RRGF TMLARMVYSIS*PRDPLASASQS AGIQKNSFFFLETRVS ^A FVAQA GVQWCDLGSQP ^P PGPK*FSC LSSLSSWDYRRLPPR PANFLYF
8417	38785	A	8474	3	295	AAAFFVVETEFRSVAQAGVQ WRDLDSLQAPPNGFTPFSCSLSP CSWDYRRVPPCPANFCIFSRDG VSPC*PGWSRSPDLVIHPSRPPK VLGLQAMS
8418	38786	A	8475	1501	1879	IRNTAHAKIIELCLLPFLTEL*CNF FFFFLRRSL/DSVAQAGVQWRY LGSLQAPPNGFTPFSCSLSSLSSW GYRRLPPCPA/NFFVFLV\ERGFT VLARMVLMS*PRDPPASAQSQA GITGVSHHARPTLK
8419	38787	A	8476	1550	2469	FFFFFFLRRSSPLPRLQCSGMI LAYCNLRLLGSSNSVASASGVA GITGTCHHTQ*IFVFLVETGFHH VGQAGLEFLTSDLPTSAQSQA/ RDYRRDDHTRPEKCF/C^KTHIL WHSPSWSS/EERGSQFQSQDS*K SSRYPKKLLGMWVIAINIYGTR T*K^EKFKTREYIGTHSIHRGNH GVNTYHVASEKLH/*TYRMRK KAKNFFFFFFLRRELASVAQAG VQWRDLG\SLQSPPPGFTPFSCIP ASLRSDYR/VLPPCLANFFL YFFS/MRRGFTVFSRIMVYSIS*PR DQIPASASQISAGITGVSHRARIL KIIFLFFFSETESRSVAQAGVQ WHDLGSRHRPPPGFTPFSCLSFP SSWDYRGPPPR PANFCVFSRD GVSPC*PGWSRSPDLVIRPASAS QKCWDYRREPPRPA
8420	38788	A	8477	1	2268	

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8421	38789	A	8478	1	2312	MAGPPSGPGRPEVCGAGRTRV AKARFRRRAFASLGWSSGRE VVTFGDVAVHFSKREWWQCLDP GQRALYREVMLENHSSVAGIG EDAPWGPFPCLISQHPPSQASIR GPCVYTADVPVTGIAVIPPAA VCFSRLKDCDTRTEDKEFLHKE DIHEDLESQAEISENYAGDVSQ VPELGDLCDDVSERDWGVPEG RRLPQLSQEGDFTPAAMGLLR GPLGEKDLDCCNGFDSSRLSPN LMACQEIPTEERPHPYDMGGQS FQHSVDLTGHEGVPTAESPLIC NECGKTFQGNP\TLFSVKQSHT GEAISFM CDDDCGKTFSQNSVLK NRHRSHMSEKAYQCSEC GKAF RGHSDFSRHQSHHSSERPYMCN ECGKA FQS QNSSLKKHQKV\HMS EKPYECNECGKAFA RSSNL I QH QRIHSGEK\PYVCSEC GKA FRRS SNLIKHHRTHTGEKPFECG*CG KA FQS QAH RLK HQ R VHT GEK P YEC NDCG KPF SRV S NL IKH HRV HT GEK P*KSSACGKA FQS QSSSL QH RR H TGEK PHVCN VCG K\AF SY*LQCS ESTR F\HT GR GR PYRC SV CGKA FSH SS ALI QH QGV HTG DKPYA CHEC GKT FG RSSN LILH QRVHTGEKPYE CTEC GKT FTSQ S STLJQH QRIH INGA EAP/YKCNOC GKA FM QSS KFS IHP QK V HIG EK PSPC VEC GKG FS QSS HFF QH RY
8422	38790	C	8479	194	458	
8423	38791	C	8480	214	378	
8424	38792	A	8481	107	345	GPLTCRYWEIIHSQE PGPRSL E MVLFSPSQN*SPVWSKEKNL*P *RDMR*/YAKPPGRCK*K*IQQ MTQMRGRNIQEKAASP

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8425	38793	A	8482	1	1454	MHEEEGESGDSR VYMSTQCTH VTLNKFLLGFIVSESVSGLNQES MKEVLRGQSLSKHNPIREAGLET LQSGRQLERRGRGLSGMARPLSL AAAGAPDLLFTALCSLLIEAQP LRPFDLQTTLTAAECHYTGKKF SLNEGKPVLRKNSQNTNWEPG TIITWGRGYACVSPGDQSPVWV PTERLKLRVNSDKESHIREKTSK SETAFIPQAQDLYANRFLYLLLT LSVPVSPQTDLPAT*NSYWA YVPFPPLIRPLTWMDPAEIYT NDSVYMPGATDDHCPTPRREE GTAFNVTMGMKYPPCLGHAH VDGCIGHLQAQIWAAYLPERLAT REQGHLISSLSLSPRLQMKGGVVI GDTPNFQYKPVGKPCPKNFEFGP SKILIWEDCVNSHVVVVLKND YGLVIGWAPKGYFK\NNCSSGG RECLEATYFISHWEDKDHHTPL HRRVSSFFPL*WEDKGTTPRPH MIFPILSI.EHSELWKLAIAMSGL
8426	38794	A	8483	49	1393	AEPATHLPPPSATAPQPERNSC CISQQSFSVP*SP/SPDSDRPRGRH /SPPPP/SPCPFFFFCLPPPKSTTAM PTRCQCPCPPPIPTVAAPFLPPSHF LRTLPAAPRPTQPPPPLSH/TTHPP EQRTLGPKFRLFSTPSPKNLEYL MNKSGRSPGCLLREATGTADL ARSIASLTAPOTDASGISGGRST LRQTRCSSGRLRTHPRLSMRAS LPLRPRRRACLPQCRDKELLITK RKYRKKKDFAAGLEDTVTEFQG REENPRHTFIYSLPLGLQKHQV LTVDIGFGGTAIMTGIARVPLA GAAGGGPGVGRAAGRGPAGVP IPQAPAGLAGPVRGVGGPSQV MTPQGRGTVAAAAATA SIM APPPGMRPPMGPPIGLPPARGTP IGMPPGMRPPPGIIRDCCGSLT PLGDVCLKGSLARVL CRAIVQI YSICVLLTTSEQQLSIRIHPQNA V

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8427	38795	A	8484	49	752	AEPAPTHLPPPPSTAPOPERNSC CISQQFSVVP*S/SPDSDRPRGRH /SPPP/SPCPPPPCLPPPKSTTAM PTRQCQPPPPIPTVAAFPPLPPSHF LRTLPAAPRPTQPPPLSH/TTHPP EQRTLGPKFLRFSTPSPKNLEYL MNKSGRSPGCLLREATGTADL ARSIASLTAPOTDASGISGGRST LRQTRCSSGRLRTHPRLSMRAS LPLRPRRRACLPQCRDKELLITK RKYRKKD
8428	38796	B	8485	511	1349	
8429	38797	A	8486	3	431	ADAVGGPGGPGMAGCDGLPG GFGSDIRPRLWLWLGPRWLWS* RGTVNIILASVPKKLLM/DCYA LARDRTATLGTFDAISKTAQN WIPDLWKETVFTKFPYQEFTDH L/VKTHTRVSKQKTQPVAVATT AARQTMEGQAPVEY!
8430	38798	A	8487	1	470	
8431	38799	A	8488	3	314	
8432	38800	A	8489	1	458	
8433	38801	A	8490	1	855	PTRPLVLRVGATARALPRPSRS CSPSAVVPSAPSSCPPQRRTPK PEPEPEQVIKNYTEELKVPPDED CIIISMEKLSTASGYSVDVTDKAI GSLAVGHLTKCSHAFFHLLCLLA MYCNGNKGDSLQCPCKTIYG EKTGTQPQGKMEVLRFQMSLP GHEDCGTIIJVYSIPPQHQGP/EH PNPGKAVALSLPEGFPQAQCYLPEQ RPGPAKSLRAP*RWAWKIRRLI FTVGHVPAPTGETDTVVWNEI HHKTEMDRNITGHGYPDPNYL QNVLAELAAQGVTEDCLEQQ
8434	38802	A	8491	1	3797	MEYYAAIIENDEFMSFVGTWMK LEIIILSKLSQEQQTKHMRMFSLID FGFSNLFTPQOLLKTCWCGSPPY AAPELFEGKEYDGPKVDIWSLG VVLYVLUVCAGLPFDGSTLQNL RARVLSGKFRIPFFMSTGLVPEL DKRLKAGCLSAECEHLIRHML VLDPNKRLSMEQICKHWMKLN GDADPNFDRLLIAECQQLKEERQ VDPLNEDVLLAMEDMGLDKEQ TLQSLRSDAYDHYSAIYSLLCD RHKRHKTLRLGALP

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8435	38803	A	8492	1	2563	MGDFNTPPLSTVDRSRMRQKVDK DTQELNSALHQADLIDIVRTLH PKSTEYTFPSAPHHTYSKIDNIIG SKALLSKCKGTEIIITNSLSDHSA IKLELRRIKKLTQNHSSTEKLNNL LLNDYWVHNEMKAEIKMFSET NENKDTTYQNLWDTFKAVCRG KFIALNAHKRKQERSKIDTLTS QLKELEKL.NQEEVESLNRPITG AEIVVAINSLPTTKSPGPDPGFTA KFYWRYKEELVPFLKLFQSIE KEGLIPNCSYEASILIPKPGRDT TKKENFRPISLMNIDAKILNKIL ANRIQQHKKLIHHHDQVGFPG MQGWFNICKSINVIOHINRTKD KNHMIISIDAEEKAFDKIQQPFLM KTLNKLAQNLKLISN/SQQLSLR IQNQCTKITSILIHQ*QTNRREPNH E*TPIHNCFKENKIPRNPTYKGCG EGPLQGELQTTAQGNKRGYKQ MEEHSMMLMGRKNQYLENGHT AQGNL*1/QMPSPSSY**LSSQN WKKLL*SSYGTKKAGPHSQVNPNP KPKEQSWRHHTT*LQTILQGYS NQNSMV LAPKQR*RPMEQNRA LRNNAAYLQLSDL*QT*QKQA MGNGFPPI**MVLGKLASHMEK AETGSLPYTLYKN*FKMD*RLT H*S*NHKNP RRKPRQYHHSVHIRH GQGLHV*NTKSNGNKSQN*RM GSN*TKELLHSERNYHQSEQAT HKMGENFRNLLI*QRANIQNQ

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met htd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8436	38804	A	8493	I	1839	MPRALAFQAPVNQAEQAGTA MNISVPQVQLINPENQIVEASSN LWELSAETTFFAISLLPFLLIINS MPDGTLNLDSDGEEPSPEALV RYLSMRRHTVGADPRTEVME DLQKLPGFPGVNPQAPFLQVA PNVNFMHNLLPMQNLQPTGQL EYKMSGLPLSPRLPLISWSVLP LFLA\EQSLLQQPTILQLLNGMGP LGRRASDGGANIQHLAQQLLK/ RPRGSPSLVTMTPAVPAVTPWD EESSDGEPDQEAVQRYLANRSK RHTLAMTNPTAEIPPDQLQRQLG QQPFRSRVWPPHLVPDQHRSY KDSNTLHLPTERFSPVRRFSDG AAISQAFKAHLEKMGNNNSIKQ LQQCEQLQKMYGGQIDERTL EKTQQQHMLYQQEQHHIQLQQ QIQQPAQSQQVTIQVQEPMVDML SNMPGTAAGSSGRGISPSAGQ MQMQHRTNLMATLSYGHRLPS KQLSADSAAEHLRKWETREKG LEDDSSVSSNTGGDVTEGKST ESADFGFSNLFTPQQLKWTWC SPPYAAPLFEGKEYDGPKVDI WSLGVVLYVLVCGALPFDGST LQNLRARVLSKGFRIPPFMSTG YFHLLGSHCNVVLNAKDVKGF
8437	38805	B	8494	I	3879	
8438	38806	A	8495	I	4065	MGKKQSRKTGNSKKQSASPPP KKRSSSPATEQSWTENDFDEL EEGFRRSNYSELREEIQTKGKE VENYEKSLEECITRITNTENCLK ELMEPKTKARELRKECRSLRSR CYQLVERVSAMEDEVNEMKDT HRLVKVGWRKIYQGNQKQKK AGVAILVSDKTDKFPTKIKRD EGHYMMVKGSIQQEELTILNIY APNTGAPRFIKQVQLSDLQRDLD SHTLIMGDFNTPPLSTLDRSTRQ KVNNNTQELNSALHQA
8439	38807	A	8496	1490	1813	TGNLQNQGRKFQPTIHLTKG*YP ESMMNSNKKTRKKQTTPSKSG RRT*TDTTSQKTFQMVKPNT*KN AHHHWPSKCKSKPL*DTISHQ LEWQSLKSQETTGAGEDVDK

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8440	38808	A	8497	1614	3085	AGEGNKADKQLQQSLRIQNQC TKITSILIHQQQTNRREPNEHSTPI HNCFKENKIPRNPTYKGCEGPL QGELQTTAQGNKRGYKQME HSMLMGRKNQYHENGHTAQG NLQI/OMPSPSSYQ*LSSQNWK LLSSYGTKKIGLHHQVNPKPK EQSWRHIIAT*LQTILQGYSNQN SMVLVPKQRYSRMSQEQRALRN NAAYLQLSDL*QT*EKQAMGK GFPI**MVLGKLASHM*KAETG SLPYTLYKNQFKMD*RFKR*T* NHKNPQRKPRHYHSGIHRHGQQ L/LCPKHQKQW/HTKAKIDKWD LIK/IELLHSKRNHYHQSEQATY KMGGENFRNLLI*QQRANIQNLQ* TQTNLQEKNKQPHQKVVEGHE QTLLKRRHLCSQETHEKMLIIT GHQRNANQNHNHEIPSHTS*NGN /QLKSQETTGAGEDVEK*EHFY TVGGTVN*FNHCGSQCGDSSGI *N*KYHLTQPSHYWVYTQRTIN HAAIKTHAHVCLLRHYSQ

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
8441	38809	A	8498	2	2013	LNQEEVESLNRPIGAEVIAINS LPTKSPGPDGFTAKFYWRYK EELVPLLLKFQSIEKEGILPNSC YEASIIILPKPGRDTTKKENFRPI SLMNIDAKILNKILANRJQQHIK KLJHHDQVGFIPGMQGWFNICK SINVIQHINRTDKDNHMIISIDAE KAFDKIQQPFLMLKTLNKLQAQN LLKLISN/SQQLRIQNQCTKITS ILIHQ*QTNRREPNEH*TPHNCFK ENKIPRNPTYKGCEGPLQGELQ TTAQNQNKRGYKQMEEHSMLM GRKNQYLENGHTAQGNL*I/QM PSPPSY**LSSQNWKLL**SSYG TKKGPHSQVNPKPKEQSWRHH TT*LQTILQGYSNQNSMVLAPK QR*RPMEQNRLRNAAYLQL SDL*QT*QKQAMGNGFPI**MV LGKLASHMEKAETGSLPYTLY KN*FKMD*RLTH*S*NHKNPRR KPROYHVSVHRHGQGLHV*NTK SNGNKSQN*RMGSN*TKELLHS ERNYHQSEQATHKMGGENFRNL LI*QRAANIQLQ*TQTNLQEKN KQPHQKMGKGHEQTLKRRHL CSQKTHEKMLIITGHQRNANQN HNEIPSHTSQNGD/QLKSQETTG AGEDVEK*EHFYTVGGTVN*FN HCGSQCGDSSGI*N*KYHLTQP SHYWVYTQRTINHAATKTHAH VCLLRHYSQ
8442	38810	B	8499	1	2860	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
8443	38811	A	8500	3	2202	EGRNKDVI*NQREQRHNIPESL GHIQSSV*REI*NTKCPQEKGK IQN*HPNITIKRTRKARANTFKS *QKARNN*NQSRIEGNRDTKNP SKN**IQTTCREYYKHLHANNE NLEEMDKFLDTYTLPLRNQEEV ESLNRPITGESEIVAIINSPLTKKS PGPDGFTAKFYQRYKEELRIKY LGQLTRDVKDLFKENYKPLLK EIKEDTNKWKNIPCSWSVGRINI VKMAILPKVIYRFNGIPIKLPTF FTELEKTLKFIWNQKRARVAK SILSQKNKAGGIMLPDFKLYYK ATVTKTAWYWYQNRIDQWN RTEPSEIMPHIYNYLJFDKPEKN KQWGKDSLNFNKWCWENWLAI CRKLKMDPFLPTYTKINSRWIK DLNVRPKTIKTLLEENLGNTIQDI GMGKDFMSKTPKAMATKAKID KWDLIKLKSFCATAKETTIGVNR QPTKWEKIFATYSSDDKGLIFRIY NELKQIYKKKTNNPIKKWAKD MNRQFSKEDIYAAKRHMKKCS TSLAIREMQIKTTMRYHLTPVR TAIIKKSGNNRCWRGCGEIGTL LHCCWDCKLVQPLWKSvwRWF LRDLELEIPFDPAIPLLGIYPKDY KSCCYKDTCTRMFTAALLTIK TWNQPKCPTMIDWIKKMWHIY TMESYAAIKNDEFMSFVGTVWM KLEIIILSKLSQQGQTKQRIFSLI DGN

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8444	38812	A	8501	437	2163	KQKCNISHLWNAVKVERIKYL GIQLTRDVKDLFKENYKPLLKE IKEDTNWKWNIPCSWVEEPIP* ^K WPYCPR*FTDSMPSPSSYQ*LSS QNWKLL*SSYGTKKEPASPSQ S*AKRTKLEASHYLTNSNYSTRL Q*PPGKRGPEVQGHNADENN HTEDRQGNRRHEHSIDOLAVT DVHSTTAETFLSTRGGFSKID HMLGCKTNLNKYKEI Q QSIFS NHNEIKQEINSRKRTRKSTNLW ELSSALLMNGSEKKTQVNLDNI WKLMAKMQHITLMCESESRK NKIPRNPTYKGREGPLQGELQT TAQQNKRGYKQMEEHPMLMG GRINTVKMAILPKVYIRFNAIPI KLPMTTFFTELEKTTLKFIWNQK RARIAKSILSQKNKAGGLTPD FKLFYKATVTKTAWYWYQNR DIDQWNRTEPESEIMPHINYVIF DKPEKNKQWGKDSDLNFNCWC ENWLAICRKLLKDPLFLPTYTKI NSRWIKDLTVRPKTIKLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLKSFCGKET TIRVNQRPTKWWKIFATYSSDK GLISRIYNELKQIYKKKTNNP KWKVDMNRHFSKEDIYAAKK HMKKCSPSLAVREMQIKTTMR YHLPVRAIIKKSGNINRCWR GCGEIGTLLHCWWDCKLVQPL WKSIVWQFLRDLEIIPDPAIPL
8445	38813	A	8502	1	2001	MPHIQVMLMQEMDSHLSLGKLC PYGFAEYSPTSSCFHGFVLSCV GSSRKATQRVDALVRQVIVN GGIVLDQFAVHDRVVALADLIDL LVDLSAMMLCGVPTTGDPFVA FALGHPPDFDHLLLPKHLVDRY LLLEPLLGPVQLLSHSAVSHLD LHQFCSDFSYGIQLTRDVKDLF KENYKPLLKEIKEDTNWKNI CSWVGRIJMIMKMM\MPR*FID SMPSPSSYQ*LSSQNWKLL*SS YGTKEPVSPSQALA
8446	38814	B	8503	152	3166	

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8447	38815	A	8504	15	2745	HPTVNIRQINETESQQGYPGIEL SSAPSGPNRHLQNNSP/PPNNQNI HFFQHHTTPKPLTT*LSTLDRS TRQKVNKDTQELNSALHQADL IDIYRTLHPKSTEYTFSSAPHHT YSKIDHIVGSKALLSKCRTEII TNYLSDHSAIKLELRIKNLTQSH STTWKLNNLLNDYVVHNEM KSEIKMFFETNEKENKDPTYQNL WDAFKAVCRGKFIALNAHKRK QERSKIDTLTSQLKELEKQEQT HSKASRRQEITK
8448	38816	A	8505	2853	3925	AVGPSVRTPRPYLCVVKDVKHD VVPILRPSATSLFMPRAAGQGG QKAGGTEKSSGP*KDDV*RLQP PNGFRIIH*VQ*TCRKCPHLSK RNTFQFQN*R*NLLVPA LPNIPH SSVEEGVGSI*ARSEDLEGAQLP *LLARLFTCRSNTYRGKFTEA* GGE*QSICYSTRRANYPKY/HM HPIQEDPDSSKS*VTYKET*TP TQ**WETLT/PPLSTLDRSTRQK VNKDTQELNSALHQADLIDIVTT ELSTPNQKNLNHFFQHHTTPKPL TTYLEVKLIPQQM*KNRNYNKL SLRPQCNCQTRTQD*ETHSKLLN YMETEQPAP*LLGT*RNESRN KDVL*NQREQRHNPESLGHQIS SV
8449	38817	A	8506	2	376	IPYLP*STYMETGMIVVVQGIY GYHHYMQDRIDDNGWCAYR SLQTICSWFKHQGYTERSIPTH EIQQALVDAGDKPATFVGSRQ WIGSIEVQLVLNQLIGITSKILFV SNTRKNKKVGNIVS
8450	38818	A	8507	I	1008	
8451	38819	A	8508	218	343	
8452	38820	B	8509	306	1434	
8453	38821	A	8510	3	659	

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8454	38822	A	8511	3	1990	EPHRIASPRFRQAFDSGTDRTL*FLSDIEEEEELTRGDPEQRHVPLRRKSEWKAADRAAIDSRWNLWQAHVSDLEYRIRQQTDIYKQIRANKGLIGLGEVPPPEHTTDLFLPLSSEVKTDHGTDKLIESVSQPLENHGAPIJGWHISESLSTKSCGALRPVNGINTLQPVLADHIP,GDCSDAAEQLHKKQRLNLVSSSSDGTCAARTRPVLSCKRKRLVRPNISIVPLSKKVHRNSTIRPGCDVNPSCALCGGSINTMPPEIHYEAPLLERLSQLDSCVHPVLAFPDDVPTSLHFQSMLKSQWQNKPFDKIKPPKKLSSLKHRAAMPKGSLPDSARKDRHLVSSFLTTAKLSHHQTRPDRTHRQHLDVGAVPMVERVTAPKAERLLNPPPPWHDPNHSKMRRLRDHSSSERSEVLKHHTDMSSSYLAATHHPHSPLVRQLSTSSESPA PASSSSSQVTASTSQQPVRRRRGESSFDINNIVIPMSVAATTRVEKLQYKEILTPSWREVDLQLSKGPSPDEENEEPASP DVSSHSLSSEYSHGQS PRSPISP E L H S A P L T P V A R D T P R H L A S E D T R C S T P E L G L D E Q S V Q W E R R T F P L A H S P Q A E C E D Q L D A Q E R A A R C T R R T S G S K T G R E T E A A P T S P P I V P L K S R H L V A A A T A Q R P T H R
8455	38823	A	8512	119	739	ADD RDHLHI QTWC A K A P F L Q PGSSW L S T K G K K M / P E T P A S D E PPLRQP A V R F E F L Q H A P P D S L Q P LGSPGH S * GPSSDTGQPAAGRW PRRQP * AA V Q D L G P Q T R G S A S P E S Q T V L P A A P S A P G S A R P H G S M S A S A P S T A S P Q M S K P C A A A C L R G S G A G G G T V G P C L E P G G S A P P R A L P R C A A G S A R P G A A A G P P G A G T T R A V P
8456	38824	A	8513	1	343	MRMC LRI PTLMTK CTN W H V T G H L C R P T / M R E P T P E P / W T G D T T TA * M E T R W P A E Q P A L A E R R L F R AAPR G A F A G I A A P S P A A P P Q P G S L G I L P E P T P A Q A W A A R N Q L R G R I K E R G S

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8457	38825	A	8514	3	405	KKFPNAGERVCTIL/VDPSIPSTA YPSYGVPHS*GDSLSPHL/SSSS RPSSISCPNGPWKGCS**PCRA QCAQPQAT*ESCIHS/SSNCIPP AWEGETPSKKNKINGNPWSKIR DKTSGGEVEVWGLVAVAPVM
8458	38826	A	8515	100	1397	PPASTYLMIELRKAPWSAALQ RKYFDLGIVWTAPISMALTMLN GLLIKDDSSPPMLLHQVNKTQL DTFNLYQSCFMQSVFDH/PEILFI HRTYNPRGKV/CIYLPGWTSG AAGGSSCPSLLCHPC/ARRDT/ CRPVPDVPSIQEVS*SSMGESLYH PGGSSFPSTAYPS/SWSQLRSF SQPSTFVSSSRPSSICPLNGPW KGCS*PPCRAQCAQPQAT*ES CIHS*ATASLQPSCPSFTHTGCS TTASGWLTAGEAELRAATTSR ASRSPPTSSASSLVPPHLRNKV WLLCSVTCSRLLQTQTRQTSRAC VRPTIMLPQTPSKAPNWSSW* NPTSSTPSMPMSAQGQQPNCAW ASLLWSRNPHTSLALAQKR*TY RSWKIPIRCSPSPLAAAATLTR PSTCPAAATS*PCSVPAARCSSPT CCRLSGRQAVLPV
8459	38827	A	8516	1	326	CLTOMYFLIS/FANVDTFLLAIM ALD/RLLAICSAALRYCSIIITPGIYS HFYCDAYLLMKIACSIHVQNQH VFLGAVVFL/APCALILVSYIRI AAA/IIRIPSPTRRRKACSCIC
8460	38828	A	8517	2	669	TISYPQQLTQMYFLISFANVDTF LLPIMALDHYVAICSAALQ*CSIIT P/ELCQGLPVLA*AGSSLISPVHT VIMSRLAFCSSAQISHFYDAY LLMKIACSH*T*NOHVFLGAVV LFLAPCALILVSYIRIAAAILRIPS PTRRRKACSCICSSHLSLVTLFY TVLGICI*PPDSFSQAQDAIATIMY TVVTSMMLNPFIYSLMNKEVQEA VRRLFSRGSHSSWCW

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8461	38829	A	8518	1	3594	MVAAAAAATEARLRRRTAAATAA LAGRSGGPHCVNGGRCNP GTG QCVC PAGWVG EQCQHCGGRFR LTGSSGFVTDGPGNYK YKTKC TWLIEGQP NRIMRLRF NHFATE CSWDHILYVYDGSIYAPLVAA FSGLIVPERDGNETVPEVVATS GYALLHFFSDAAYNL TGFNITY SFDMCPNNCSGRGECKISNS SD TVECECS ENWKGEACDIPCH TD NCGFP HRGICNSSDV RGCS CF DWQGP GCSVP VPAN QSF W
8462	38830	A	8519	1	471	ALCAPQPGKCFCTTGSSG/DE CQLCEV/ENRYQANPLRGTCYN TLLIDYQFTSLSQEDDRYYTAI NFVATP DEQNRDL DMFINASK NFNLN ITWAASFSAGTQAGEE MPVVSKTNIKEYKDSFSNEKFD FRNHPNITFFVYVSNFTWPKI IQ VQTEQ
8463	38831	A	8520	1	4289	
8464	38832	A	8521	1	3488	MDYGVLT RLTGSSGFVTDGPG NYKYKT KCTWLIEGQP NRIMR LRFNHFATECSWDHLYVYDGD SIYAPLVAAFSGLIVPERDGNET VPEVVATSGY ALLHFFSDAAY NL TGFNITYSFDMCPNNCSGRG ECKISNS SDTVECECS ENWKGE ACDIPHTDNCGF PHRGICNS SD VRGCS CFSDWQGP GCSVP VP NQSF WITRE EYSNFK A/L PRASH KAVVNGNIMWVVGGMFNHS DYNMVL AYDLA SREWLP
8465	38833	A	8522	4794	5740	YICNWYKMKDSSFPSL VQSPRS PGSCGLSGWG WG GCP RVASAGS ACSCNSA VPAR RTQEACR REL GGRSTIFTDVQGQWGAPG TVN EGNSACPTL RVTVA AW LSLF VLCRVCAASVPSL VRLR WGPQ CSGPWGAWAPPWAAR VS QPG AGPGRGAEAQLLPAASIQWPC HQAPHLLL VLAL VT SQGP SRCR GFCLAGPCQGGPGG LIL FCHW NVPLQFSSLFFFF *DGVSLLL PR LECSGSISGHCNLR LPGSS DRPA LGS* VAGDYR CLPAC SAN FFV LVEKG FH VGRAGLKL MVIH LPRPPR VRLQ A

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8466	38834	A	8523	594	2868	CWTSRNRRIPGSCHPMELPRPF RGKAKVQNHQLVHINKALIN RGSITFWLDDGAIQAWHCPVK TYYQYTPVSSKAMY/DAFWNG/KFRDC/AFHSLWNEDPFPVCEYQ GQSSDLPQPVPNAGGGSGGGGS GGGSEGGGSEGGGSEGGGSEG GGSEGGGSGGGSGSGDFDYEK MANANKGAMTENADENALQS DAKGKLDHSVATDYGAADGFIG DVSGLANGNGATGDFAGNSQ MAQVGQGDNPLMNNFRQYLP SLPQSVECRPYVLSAGEIGAA CASRSGYDNKGKVRDYG YTDCK RSEDLDPRLRHQILGGKKAIQFTL QGFPTLPEGAPAGNSGSLAVHK TAQSSYRHALLILTPMSGTRF PPIPGPVVNIRVPFPVAPSSCERJC YSWSWVPGPSPVHCQSDGSVP1 SYAPLASQYSSFLFFRNRPYA PYDYL SVMTPSRTLREQIRIYA PSAPRLPPPEVYCSNSTIVYVRN NPSGPTPGFAGGTLEGRSGGP FRFYAKRAKGDVLKPFSLNLPL QTLIRFMVDIACGMELYSSRNFI HRDLAARKCMYEFWRTRGWET TAAAYGGGGTFFRKESQKLQ QSAKKRDAELANGALGIELNN DYTLLKKVMKPLITSNTVTEIE RANVFKMNGKWLFTDSRGSK MTIDGINSNDIYMLGYVSNLT GPYKPLNK TGLVLQMGLDPND
8467	38835	A	8524	302	409	
8468	38836	A	8525	199	359	ARRQQSVVKSYRWEEDQHCG ELQGSE*VSDGLFKPP*S*HGW VEEERQKEON
8469	38837	A	8526	1853	2032	VKQSTALLPHAVAC*PKVISSG ARGLKSILVLRIVVMVMSMLP QLALSGWGFRVLPG
8470	38838	A	8527	118	445	AAGGEPGDAPWVPGVWEPPES VCRGPPPSSTFPHPVLSTFGASG PENSRCDSWLSPLQH*AA*VASG NNGPQAAQGSLSGIPDAATLSG I*RASILHVSVVEIISPGFR

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8471	38839	A	8528	1	770	MRVLGIETSCDETGIAIYDDEK GILLANQLYSQVKLHADYGGVV PELASRDHVRKTVPLIQAALKE SGLTAKDIDAVAYTAGPGLVG ALLVGATVGRSLAFALGRFGDP CTPYWRASVSARCWKAPNFR CALLGSAAYAVNHGTGLSKKP TTLGSDHSKTPAQLAKRAGEA RRNGWQGALFPWESARSGEEE TP/VICRH*HSHRAAAKSGLGA GGTSSGGRYRLGGYSILADHGG *KFHCA*RHGATSGDGKVLD
8472	38840	A	8529	3	834	VGRVEIADQYQDLAILWNCLG SDHIASSRQRPFPRGAKAVQNH QLVHLQQSSHQPWLPHFLAG* WGDSGLGGGS EGGGSEGGSE GGGSEGGGGGGSGSDFDYE KMANANKGAMTENADENALQ SDAKGKLDSVATDYGAAIDGF1 GDVSGLANGNGATGDFAGSNS QMAQVGDGDNPLMNMFRRQY LPSLPQSVECRPYVFGAVRHDV RRIRVTGTRVTPPEEVDTSVH SRGAHIRRSGFAPKRSVRVTTD TCIKRNSTCGVKSLWDGGGF
8473	38841	B	8530	1	811	
8474	38842	A	8531	1	1044	
8475	38843	A	8532	3	1472	GVVGERAGMARPGRPREGGGS G/GYSRPVPPAGGPGP*RGRTRI/ SGLANGAGPVVFQFLTELTRLF QKCRTSGSVYITLKKCQREGS RAMLPGFPYTPVSSKAMYDAY WNGKFRDCAFHSGFNEDPFVC EYQQQSSDLPQPQPVNAGGGSG GGSGGGSEGGGSEGGGSEGGG SEGDSSEGDSGGGGSGSGFD YEKMANANKGAMTENADENA LQSDAKGKLDSVATDYGAAID GFIGDVSGLANGNGATGDFAG SNSQMAQVGDDGDNPLMNFFR QYLPSLPQSVECRPYVFGAGKP YEFSIDCDKIKILRGVFAFLLYV ATFMLPVIANIAIPQKRPFMQQT RCEVQCREDIEVQKLSYDKIL ASINKPGVNGWQKRRTVNA GEAHDDQQALDYALYHRLRIMTP AHDERSSIAAKGLTGEGYKGH VFWDTEVFLLPFHLFSDPTVAR SLLRYRWHNLPGRARRKDGN GWAGGAPISVGKARAACK
8476	38844	A	8533	609	855	

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8477	38845	A	8534	369	1278	GHTACEWYSQGRHPGPPELSPFL *GPG*NAGHVISMMPAARPMEMPC LGTGGLDVLLHHLRPDLPAAAL PGSAWPGEALPLPGQVSGRG RSAACLQPGAWPGRGAAPVRR RPRPAAGSVREAEELLESPHLA AHRDC*LARKLNSSGGYIPQAELY GKHAGLPLPGARALS CGC RAR APVPAALPHPLLDHQDPGPAGR IVGIGAGTQTLDGSAPRTSRLA GSTQMPEARPGLAGWGVAVG WSRG*SR*TRGSAS/SPPRRCAL LLALPGAAVSGDLRARNPGRSL PPKAPSGRGGPLLPHRSTPRR
8478	38846	A	8535	3	2494	YQRQSSSPEDPAETASPTYALIA ACQSEIQLQTQQPCDMAPGPL DCDPVKGSRRKRMFLMNAPPV VALQPKWEASVPPGSFRPECF SEADKGVESMSPTMHKELPAL AACGLVADFDPVGEETEADFG PLVLDSDSDDSVDRDIEEAIQEY I/KGGGSRCKRELAHSS/APTAL CSPKLVPGS GG/GGPGSQVGSS KDQGSASPVSMSRADSFEQSIR AEIEQFLNEKRQHETQKCDGSV EKKPDTHENSAKSLSKSHQEPA TKVVRHQGLMGVQKEFAFCRP PRLAKTNVQPRSLSRKSVTTTTT QEKEGSTKPATP/TRPSEAVQN KSGIKRSASTARRGKRVTSQV APEASDSSDDGIEAIIQLYQVQ KTRKEADGDPPQRVQLQEEERA PAPPAHSTSSATKSALPETHRKT PSKKKPVPTKTTDPGPGDLDAD IISPKIPKETKAPPPTSPASRSKF VEWSSCQADTSAELIVLDFIK TILP/APMEGSDGSLSA SPLFYSP NVPSRSDGDSSSVDSDDSIEQEI WTFLALKVQSRSL LARGAAGQ APERVEKQAPAGAEELPKSKRD SCEGSRKKPPSVFGSRAERTKP RPSCSSVDSDDSI EIRKFLV KAKESGVPGQAQPCLWKPTLA GEEGLRSPA KQEGLTS AIVAGIS AALGPEHTWVPGATTTPTPSVA PVLVPAVPTHWKKLA PACCGP

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8479	38847	A	8536	I	2463	MHKELPALAACGLVADFPVGEETADFGPLVLDSDSSDVDRDIEEAQEYL/KGGGSRCKRELAHSS/APTALCSPKLVPGSGG/GPGSQVGSSKDQGSASPMSRA DSFEQSIRAEIEQFLNEKROHET QKCDGSVEKKPDTHENSAKSLS KSHQEPAVKVVHRQGLMDVQKEFAFCRPPRLAKTNVQPRSLR SKVTITTTQKEEGSTKPATP/TR PSEAVQNKGSIKRNASTARRGK RVTSAIQAPEASDSSDDGIEEAIQLYQVQKTHKEADGDPQRVQLQEERAPPAHSTSAAKSALPETHRKTPSKKKPVPTKTTDP GPGDLDAHDSPIKPKETKAPP TSPASRSKFVEWSSCQADTSAE LIAVLDFIKTILP/APMEGSDGS LSASPLFYSPNVPNSRSDGDSSV DSDDSIEQEIWTFALKVQSRSL LARGESCPOAAQGPLSPGLSS QTGSPKAPLSKTLDP/LGCKRK HRGGVSKAQPARPRDGRAPLG WDLSIQTASEAPGGEAARVP GDTRTSQQGKTDEARHLDKK KSSEDKSSSLSDKDLDTAIKD LLRESQGPAPSPGSLSDNSSSVDDDDSIELIRKFLVEKAKESGVPGQAQPCWKPTLAGEEGELRSP AKQEGLTSIAVAGISAALGPEHTWVPGATTPTPSVAPVLVPAVPTHWKKLAPACGGPGQSLIDID
8480	38848	B	8537	I	3345	

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8481	38849	A	8538	1	1339	MTKKSPGPDSFTGHWCVISPS GYERSRLKVTLPREEGRGALPFL VSVAISSGSCSDNNAAAVPTVLE GATTVISAAAVLRLDPHDGAREII LEAMTISAVAIAAEI^WTSQCG LCLHPGMFMPYRIGDGIRDLLP LVLSATICAEFFKGDSKKPSKK RVKRKPYSTTKV^SGSTFNENI RRYAVHTNQCRRPHGSRVKKK RYPQEDDFHHTVFSNLERLDDL QPTLEASEESLVHKDRGDGERP VNARVVQVAPLRLESSKYSGIT CQENNLDAKKA/TP/CRTPYMT SLTRTPHTTSLTRLSTA/SANEA ADKGIANEADAQGIANEADAH GIMPARNPPRASPRTSPRASPRT RTPPRASPRTTPRASPRTPT GSPRRTPPRASPRTTPRASPRT TPPMASPTRTLPTALLTRMPCT ASLMRTPYTTSLMRVPVYMTSL MTPYKAR
8482	38850	A	8539	1	3090	MHKELPALAACGLVADFDPGVG EEETADFGPLVLDSDSSDSDVDR DIEEAIQEYLKVGVSSKDQGSASP VSMSRADSFQEQSIRAEIEQFLNE KRQHETQKCDGSVEKKPDTHE NSAKSLSKSHQEPAKTVVHRQ GLMGVQKEFAFCRPPRVLAKTN VQPRSLRSKVTTTTTQEKEGST KPATP/TRPSEA/VQNKSIGKRSA STARRGKRVTSAVQAPEASDSS SDDGIEEAIQLYQVQVKTHKEAD GDPPQRVQLQEER
8483	38851	A	8540	1	2919	MHKELPALAACGLVADFDPGVG EEETADFGPLVLDSDSSDSDVDR DIEEAIQEYLKVGVSSKDQGSASP VSMSRADSFQEQSIRAEIEQFLNE KRQHETQKCDGSVEKKPDTHE NSAKSLSKSHQEPAKTVVHRQ GLMGVQKEFAFCRPPRVLAKTN VQPRSLRSKVTTTTTQEKEGST KPATP/TRPSEA/VQNKSIGKRSA STARRGKRVTSAVQAPEASDSS SDDGIEEAIQLYQVQVKTHKEAD GDPPQRVQLQEER
8484	38852	B	8541	1	1122	
8485	38853	A	8542	1	1074	
8486	38854	B	8543	1	1017	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met Ind	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
8487	38855	A	8544	1	1436	MNL PRAER LRSTP QRSL RDSDG EDG KID VL GEE EDE D E VE DE EEE EAS QKF LEQ S L Q P GL Q VAR WG GVAL PRE HIE GGG GP SDP SE FG TEFR APP R SAA S E D A R Q P A K P PYS Y I A L T M A I L Q S P H K R L T L S GICA FIS GRF P Y Y R R K F PA W Q N SIRH NL S L N D C F V K I P R E P G R P G KG NY W S L D P A S Q D M F D N G S F L R R R K R F Q R H Q L T P G A H L P H P F P LPA AHA AL H N P R P G P L L G A P A P P Q P V P G A Y P N T A P G R P R Y A L L H PH P P R Y L L S A P A Y A G A P K K A E GAD L A T P A /A L P V L Q P S L A T V K P V G Q F C S N S S G I R R T V G N G C A P T K G A V L G G H L S A A S A A A A V S G G G R G L W A D I A R A L W A E R D L T S FF SIA HA Q F P G R V R R A L L E P G S R Q P H S P T G V Q K R P L L A N P A G L Q G SK SSET T E N R G /C P M S C Q L L A G L R S N S P L S V V R K R L R A D L P S F I A N K R P G R A A T A A E P R R D F L
8488	38856	A	8545	1	1287	MNL PRAER PRSTP QRSL RDSDG EDG KID VL GEE EDE D E VE DE EEE EAS QKF LEQ S L Q P GL Q VAR WG GVAL PRE HIE GGG GP SDP SE FG TK FRAPP R SAA S E D A R Q P A K P PYS Y I A L T M A I L Q N P H K R L T L S GICA FIS GRF P Y Y R R K F PA W Q N SIRH NL S L N E * F V K I P R E P G H P G KG NY W S L D P A S Q D M F D N G S F L R R R K R F K R H Q L T P G A H L P H P F P LPA AHA AL H N P R P G P L L G A P A L P Q P V P G A Y P N T A P G R P R Y A L L H PH P P R Y L L S A P A Y A G A P K K A E GAD L A T P G T L P V L Q P S L G P Q P W E/R G Q G S G V A T G R I G C I F S I E S I M Q G V R G A G T G A A Q S L S P T A W S Y C P L L Q R P S S L I R T I L Q Q Q Q H Q E E D C A N G C A P T K G A V L G G H L S A A S A L L R Y Q P V A K G L W A D I A A A P L G G E G T S P V F L

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8489	38857	A	8546	202	823	AQNPTAFGVKHTSSGGEETFPN IRGIKKSPPLSSSSIRLSKNILST TGKTVHQTRDDQPRDFKKR NRVNESHQKSSNMNAAGPSWNK VQHSKNSSGKRQSKSQVPHASS QPRSSLTAVTQPTEEKLIESIPE ARRKRNPPLGFRCCQGASRNKLFL DFQSMKIIKENADEDSASDLSDF SGKNSSHSSFSPTRSQSSS*RN RVNESHQKSSNMNAAGPSWNKV QHSKNSSGKRQSKSQVPHASSQ PRSSLTAVTQPTEEKLIESIPEA RRKRNPPLGFRCCQGASRNKLFLD FQSMKIIKENADEDSASDLSDE RIPPPSPLTPPDNLNRAEIGSSL L
8490	38858	C	8547	219	1013	
8491	38859	C	8548	252	452	
8492	38860	A	8549	25	443	
8493	38861	A	8550	20	1371	RLRGPAVGAGGGSVTLRL/PRS EQAAKKEAGLNTMIPLEKPGSG GSVPRRHRLGPSSGG*AGRA RTTPPPQARGLLTIEIAVVRTEP FQERLQPVPRAWSWAGKGKSSG EKMYKEKILGKNNLQQSS*EKRR K\SQDCRMEEIIHEIAVLELAQDN PWVINLHEVYETASEMILVLEY AAGGEIIFDQCVADREEAFKEK DVQRLMRQILEGVHFLHTRDV VHLDLKPQNILLTSESPLGDIKI VDGLSRILKNSEELREIMGTPE YVAPEILSYDPISMATDMWSIG VLTYVMLTGISPFLGNNDKQETF LNISQMLNSYSEEEDFDVLESA VDFIRTLLVKKPEDRATAEECL KHPWLTQSSIQEPSFRMEKALE EANALQEGHSVPEINSDTDKSE TEESIVTEELIVTVTSYTLGCRQ SEKEKMEQKAISKRKFEEPLL
8494	38862	A	8551	I	1275	
8495	38863	A	8552	I	4173	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
8496	38864	A	8553	2	5115	PDQFHNMMDLRRGGPHDGVТИPR TSDTDLVTSDSRSTLMVSSYY SIGHSQLVHWDIKEEVDAGD WIGMYLIDEVLSNFLDYKNRG VNGSHRGQIIWKIDASSYFVEPE TKICFKYYHGVSGALRATTPSV TVKNSAAPIFKSIGADETVQQG GSRRLISFSLSDFQAMGLKKGM FFNPDPYLYKISIQPQKHISIFPALP HHGQEERRSKIIGNTVNPIWQAE QFSFVSLPTDVLEIEVKDKFAKS RPIIKRFLG
8497	38865	A	8554	202	260	ARVIIQPVLKQRFPLELGRHH QDSEAHAPPPGPAAASRGGI*V AWPAPRAGVVVSLLGCRSSWTA AMELSAEYLREKLQRDLAEAH VLPSPGVGQVRGETAASETQ AGERVPSRRAPAHPCL
8498	38866	A	8555	72	578	GSKGSVAGARA VVSLLGCRS RWTAAMELQRRI PRAEAAGP WRRSMWRWRTRP STAVPVA SE SWWCRPSSRG NRCFQRHSLDPS MTHCDMVITY GLDQLENCQT CGTNYIISV LNLLT LIVEQINTKL PSSFVEKL FIPPSKLL FWRYHKE KEVVA VAVA HAVYQAML
8499	38867	A	8556	299	939	LPSPGGVQVRGETAA SETQVL YRAMRRV TAANQAFFSEAEVT AAKERGIVLPLRC CDPSQTIHCD MGWITY GLDQLENCQT CGTNYII SVL NLNTL LIVEQINTKL PSSFVE KL VIPSSKLL FWRYHKE KEVVA VA AVLSRPMLQLGR NIPCFG RTAY*V*Y WGRKWT CGPLN N PGTVCNF PEACSEIK HEAFKNH VFNVDNA KFVDLN

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, #=possible nucleotide deletion, ^=possible nucleotide insertion)
8500	38868	A	8557	1407	2783	SSAASHSSPGAA\$RARATAGS RRRSPPIQSCHPPASACGQSGQS ETHRLAMRNRTPPS*GFSK/H MRRSSLASS*RG^KSVAVIL*CS ASGILPTDVHILSP\$PGSSETCHR PHPGH*EP\$DCQLKQLPASALG*S *QEQLSHNSPRSA*A/QYA/ESSG NSFFSSKVGD*RFTTTVA/PGGG GRRTLPGKPSPEHFLP\$ELPPP RSPAQVCDQTLVAPHDHNTAG TPGDQVCLTVSTSRSLVLS GCFFLHII\$TSLVQAGVRHLSLV S\$AAEPTSYL*VGPKLMAPS*K\$ LKIRTRKPRADDSPGT\$RYSSA HTRTRKPRADDSPGT\$RYSSIAH TRMWKPRA\$DSRH\$RYST\$TCR SPGQMTLHAPADTLHTPG/PR KPRAD\$PGTSRYSTAHTRTRK PRADDSPGT\$RYSTAHTRTQKP RAD\$TGT\$RYSTPLAS\$RRHRI AASASWALVVLICLT
8501	38869	A	8558	92	1817	PLRN\$TLCRGKGKHGP\$LEGG\$SR RRDRGRASERRQTQERGKTL CSSHPWWLKANASA\$APAVWSQ AHRTQKPRADDSPGT\$RYSTA TRTRKPRADDSPGT\$PDTALQTP GRRSPQMTPGTSRYSTGRGSP GOMTPGTSRYSTERSPGQMTL QTPADTAQDAEAQGR*LQAPA DTALHTPGRSPGQMTLQAPA DTALHTPGRHSRGKMTLQAPA DTALHTPGRGSPGQMTLQAPA DTALHTPERSEPQGQMT\$PRRP DTALHTPGRGSP\$QMTLQAPA DTALHTPGRSPGKMTPGTSRY SIAHTRTRKPRADDSPGT\$RYSTA AHTRTQKPRADDSPGT\$RYSTA HTRMRKPRA\$DSRH\$RYST\$TC RSPGQMTLQAPADTLHTPG/P RKPRADDSPGT\$RYSTAHTRTR KPRAD\$PGTSRYSTAHTRTRK PRADDSPGT\$RYSTAHTRTQKP RAD\$SRHQQI\$HRM\$QKPRADD SPGT\$RYSSIAHTRTRKPRADDSP GTSRYSTAHTRTRKPRADDSPG TSRYSTAHTRTQKPRADDSPGT SRYSTRAGCCPPGLASSAWAGL RLKTRKGWTW

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
8502	38870	A	8559	13	299	EKGQDILQNLFWQLRHGPIMSS^PSASNTGWGSSS*SIVPSSTVSSWSTAMKLSSSLSEELAMTFHSTENIVVLGVVQWLTPVVPALWDSEAGRSP
8503	38871	A	8560	337	1879	VHVGAARRGFGVYPVPLSTVS GTQNCGPCLQTVVSTYQRV*PI SVIMVS*RLSRKETFSGRAVPLI LEPOSLSASRTVHAIMM/HNQS MYVFGGCTQSSCNAAFNDLWR LDLNSKEWIRPLASGSYPSPKA GATLVVYKDLLVLFGGWTRPS PYPLHQPERFFDEIHTYSPSKN WWNCIVTTHGPPPMAGHSSCVI DDKMIVFGGSLGSRQMSNDVW VLDLEQWAWSKPNISGSPSHPR GGSQLFKDAWLLHMHSGPW AWQPLKVENEEHGAPELWCHP ACRVGQCVVVFSQAPSGRAPLS PSLNSRPSPISATPPALVPETREY RSQSPVRSMDAECVNGRWGT LRPRAQQRQTPSGSREGSSLSPAR GDGSPRLNGGSLSPGTAAVGGS SLDSPVQAISPSTPSAPEGYDLK IGLSLAPRRGSLPDQKDLRLGSIDLNWDLKPASSSNPMGMDN RTVGGSMRHPPEQTNGVHTPP HVASALAGAVSPGALARSLAEIKAMSSKGPSASGRH
8504	38872	A	8561	25	313	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met codon	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8505	38873	A	8562	1	1409	MIERVLEGKWA LSRAEGLHRH QC LEFLIHLV FQLMKVV NEMCP NITRIY NIGKSHQGLKLY AVEIS DHPGE HEVGEPEFH YIA GAHGN EV LGRE LLL VQFVC QEYLAR NARI VHLVEETR JHVLP SLNP DG IDINNNFP DLNTL WAEADR QNV PRKV PNHYIA PEWF LSEN ATV AAETRA VIA MEKIP FVLG GNL QQGEL VVAY PYD LVRSPW KTQE HTPT DDHV FWR LAYSY ASTH RMLTD ARR VC HTEDFQ KEEG TVNGAS WHT AGSL NDF SYL HTNC FELS IYVG CDK YPHE SQL PEW ENN RES LIV FME QVH RG IKG VL RDS HGKG IPNA SIVE GIN HDIRT A T DGDY WRL LNP IG EY V VTAK AGR FH CI H P RTCM GY DMGA HK CLNF TLS KTN LA RIRR DH WRS FGKA APS AL PS G *KL RG RK RR QRG
8506	38874	A	8563	3	749	KTDH ILGH KTKL KTRK IEII SGI LSDH SGIKL QINNK GNFG NHTS TWKL NNNN MLNDQ *VNEE IKKEI *NH PET NDNG NATY QNL *DTG KEV LRG KL /PI STY IK *VE KLQI NNLT MHL KELE KPE QT KR KTR RKE II KIR AE INE IEAK KTP PKFN ETNS WFLEN IHK TNEH ILAR LRK KD PNK IREE KED II DT VE IQR II RS YYAK K WEN LEET DK FL DTY NL PRL N NEEV Q NLS RP ITT VPI
8507	38875	A	8564	1	842	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
8508	38876	A	8565	1	1203	VPELFGNCRQLI.EEVEVAT*PRRFRDSPGGSVQGLWTSLLRAAEMLFPVHLVRPRM*ILERFVPHALDYLLGSRLFKEPLPLKQVNPSRSLDHQLR AREHFINYLTQCHCYHVAEFELPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIORYKQKKELEHRLSAMKSAVESGQADDERVRGYYLLHLQRW\VDISLEEIESIDQEIKILRERDSSREASTSNSSRQERPPVKPFHSHFGTWLHSQSTFGAGYSKGWPTRYRTVS\DWYE QHRKLWSTYPDQGIAKAAPEEFRKAAQQQQEDQ\KKRRKRM\RTKQLPQSPGVGMTGSDTH*GPMGTDRTWADLP TTPODISGVH\TPLPRKTMQSSPPPVSWLQLCTTEGKDAKSCFAFSKVSSDLSVYLYP
8509	38877	A	8566	1	995	GTKELLLT*LGGSPLLLT*TKPLGVDPLLKGGVTFQGFNEKAVFAALRPSTYQGPAGKPAFAGAMSLAGAQGSLWSVEGGNKLVCSDLKLTKANVIHATVTSTVLHSTE GKALYQVAYENEVGNSDFYDIVVIATPLHLDNSSNLTFAGFHPPIDDVQGSQPTVSVLHGYNSSYFRFPRP*AFPLSNILTTDFPSFFCTLDNICPVNISAFRRKQPQDAAVVWRVQSTKPLFRTQLKTLFRSYYSVQTAGVGRANPLYGFRPHGFPRFALHDQLFYLNALEWAASSVEVMAVAAKNVAFAWLYNRWYQDLKDQKDLMHK
8510	38878	A	8567	1	372	

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8511	38879	A	8568	1	1699	MHAKSIKTQALADMEKI.KVVV RDKNVVARIIPOMTSKGHGV TTSSAKLKSQGKDSVAVKR RSGLMIGERFRMVPYPSFGPQVL MEIPKDADKLLCPSCAAVVLG QKKHETQTLSKELPVQDNVV PKEDPGTWERTVKEGILEEV MCWLQSRVEGDWAKEERKIFH EGELAEAKAGRGGLASCTCCPL TPGKMGAPWTFTLLCGLLAAT LIQATLSPATAVLILGPKVIKEKL TQEIKDHNTASILQLPLLIAM REKPAGGIPIVGLSIVNTVLIKII WLKVITANILOLQVKPSANDQE LLVKIPLDMVAGFNTPLVKTIV EFHMTTEAQATIRMDTSASGPT RLVLSDCATSHGSLRIQLLHKL SFLVNALAKQVMNLLVPSLPNL VKNQLCPVIEASFNGMYADLL QLVKVPISLSIDRLE/F*PSVCH QG*HHSALPGGQVVGTLGKGD QVVHNSAASLTMTLDNIPFSL IVSQDVVKAAVAVLSPPEEFM VLLDSVLPEAHRLKSSIGLINE KAADKLGSTQVKILTQDTPEFF YRPRPCQGGPTDRAGSVSLQ
8512	38880	A	8569	1	1060	MGLPAQGVGGNTLAKL ^{LA} /DD IAKGGKRNKSEASVVRNAADA PKVLQDLSARLMLGDFELRNRCN SPCTLLIGIVVLINAAETLVFLVS DHMEDQGSSLNVNVA ^L SYFQQ QDPEGQKEETAGIDLMMMASDI LQPKGDDVARISWYLDRIIYT QETPNVIERCPKPVIAAVHGGC GGGGAAAPMPRPLASSLSSVM GQTVSQEAAPPGSQGWFWWS FSIPGLYLLGVDLTACDIRYC AQDAFFQVKVEDVGLAADVGT LQRLPKVIGNQLVNELAFTAR KMMADEISSKSPVALQS/TKVN LLYSRDHSVAESLNVASWNM SMLQTQDLVKSVQATTENKEL KTVTFSKL
8513	38881	B	8570	331	1200	
8514	38882	A	8571	3	379	TSLTFHSPEVPSS*PPSTR*AGA ARGPRPPGAAGRPR*SC*GPPGT RRWQS*GGTSPPLGPVPGGRSGA ASCGLPDCEL*PLKRSQAQRNQ CPV*SSPRSWSRSEPCAAARG WPPSACRHGNRR

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8515	38883	A	8572	384	1718	SQLPRGLLPESCAADPGA**PPS CTR*AGAARGPRPPGAAGRPR* SC*GPGT/PALAKPPSCPVTS AAPTQARPMLPKPQGAAWSTQK LPIPTSASPTQKSPITPSASSTQK LPIPTAAWSTQKLPIPTAAWST QKLPIPTAAWSTQKLPIPTAAW STQKLPIPTAAASSTQKLPMPTAA SSTQKSPITAASSTQKLPIPTAA WST*KLPITRAWSQKLPIPTA ASSTQKYTIATAASYHAKATDA WST*KLPIPRAAWST*KLPIPTA AWSTQKLPIPTAAASSTQKSPIT AASSTQKLPMPTAAWSTQKLPI PTAAWSTQKLPIPTAAASSTQKL PMPTAAASSTQKLPMPTAAWSTI TTMGATTG/GPSTDQTQNVVFLH PRCPEQASSQRSGAGAD*GLSN PKVSSAEAPSCAKDEPEVEKGR GPAPWTSQRWRRAVGRPRG
8516	38884	A	8573	302	543	KLHLGWGKTPG*HWGLY*NLP RLNGPNLMPSLRVRVRNKR QVTISAGCALQMEQWMHGMT RHPTISTRPTAAREVRI
8517	38885	C	8574	253	396	
8518	38886	A	8575	1107	1751	LQDLSQYFGGSQQLIKT*IG*TTSI ITNSNI*TTLLEM/SVKGIAEQLG TNCOAMAWEENRIALDMILAERG GVCIMIKTECCAFIPNNTAPNGS ITKALQQLTALSNELAASSGVN DPFTGWLEKWFQKWKGITASIL TSLTAVMGVVILVGCCVIPCICG LVQRHRGPPLVVIETKPLGLER LAGLPVGHALKLGSGIQATPQN GENADRREAFPAAS
8519	38887	A	8576	1	1365	
8520	38888	A	8577	3	263	QLILKDKFITQSAA迪KEKLQKS TLGPERNLKTLNLAT/CCFL** RSGGAGGTGQTR*EKGHHFSH GPRASGLWRLWNAESLGKSNA
8521	38889	A	8578	365	470	
8522	38890	A	8579	1	1278	
8523	38891	A	8580	23	257	
8524	38892	A	8581	1	1812	

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8525	38893	A	8582	265	699	LLGSTVLFHDPQLLIELYHSSHG PKVPFLGIREAKNSRSENTRLAT ILGAGLLPSWKWFTTILGAL*A RTPR*HFGNH/VTDIQS/RIEAVK LQMEPKMQSKTKIYRPLDRPA SPRSDVNDIKGTPREEISAAKPL LRPNSAGSS
8526	38894	A	8583	2	181	
8527	38895	A	8584	1	69	
8528	38896	A	8585	1	674	MDLNYTLEQMDLTDIYRTFHPT TTEYTFYSTGHGTFSKTDVG HKMSLDKFKKIEMISNTVSDHS GIKLEINSERNLENHANTWKLN NLLLNECWVKNMKMEIKKL ELNDNNDTTYHNLWDRAKVVI RGKCIALNTYIKKSERAQTDNL RIKNKNHMIIIDAEKAFDKIQH PFMIKTLISKISIRGTYLNLIKD/S *QTHSQHNAAEWGKIESIHSENW NRG
8529	38897	B	8586	1	415	
8530	38898	A	8587	1	516	
8531	38899	B	8588	110	382	
8532	38900	A	8589	140	253	QNKACQHPPKITRVHQHQWIQT KKKSSIYLKKEFRLVLKLIREA PEEGKAQCCKEVQKLIQKVQGEI IDEIDTINKKQPQLQETMDTLTK MQNAQESLSNRIEQEEHHSKSL ENIFGSIMEENFPSLARDLDSQI QEAQRTPGKFITKRSSPRHIVIR LSKVKTKERILRVVRQKRKIVIL KS*PGNMTKQGLSTSPKNHTSS PTMDPNQEEILDPEKRIQEVSY
8533	38901	A	8590	89	194	
8534	38902	A	8591	2	633	

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8535	38903	A	8592	298	2648	GSSKILLFNQNEDDKINFELFFF FVASALVLVQKAFSRSSWSSMA LADKRLENLQIYKVLQCVRNRK DKKQIEKLTKLGYPELINYTEPI NGLSALHHLASVNSNDIMVSFLL DLGAHPDVQDRMGCPTTMRA AELGHELSMEILAKAKADMIV DNEGKVLEGTGGTSSPLAHIA VALHIPRRDTQGVLFYCLPTKR HYRCALIALEHGDVNNSNTYE GKPIFLRACEDAHDVKDVLCTF LEKGANPNAINSILKLFAYNG DVGLISINGNTPHLHYAAMGGFA DCCKYIAQRGCDLKWKWNLDHK TPRAVAKEGGFKAASKEIRR/C RENK**TSQARSQKSQIPLWAL RLHDWSVERE AFLREAFAVLD RGDGSIISKNDFVMVLEESRJM QAQNSWLPFAHLHEKTRGGV NIN*ILLKEPDILNKSFVLGSYGP KKKEKGGMGKKGKGKFVPLPLP ICVIPEYAFPRRQDGPPPYYMIE TYKVNVDSSRFNRDHPPEHQI DDSVVYIDDESEKFSNINIITKA GDLASLKKAFESGIPVDMKD YYKTPLMTACASGNIDVVFKFLL EKGYASPSGQQDIVELLVESGA LIDAASINNSTPLNRAIESCRLL TVKYLLDIGAKFQLENRKGHSA MDVAKAYADYRIIDLKEKLDN LPKPAENQLKGKTPPLKTEG PEIKKEEEELLSSIYVGPTTSEGK
8536	38904	A	8593	3	838	MGRGWTQAVGPRWSGGSCTL YSVGAAGRGGQGHQSRCRPPG PPSASSAPCLA WGAA GRARRE GLRQNAERSSPLTAPAGR*PC GAGPCRR*SR*R\PLVCLR ASPGTGAACGRCCCPPP*P*P NPWHFTVSKAFSYMPSTTA/RL VRGPRLVGPVPVAPYIIPP/PGS PASRGSRCRGRSRSPRPRPSV LSCHGVSL*TGPSLPGWLLQIW QRSAQMS/P/PPKGPP*GSREGPP PP/GPALLPAAAPGGQGHRAPA AGSCGRRAAAARRMEWVRNSPP
8537	38905	B	8594	1	2700	

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8538	38906	A	8595	1	1240	FPPYATNEIGKVGTGLNRRELGH GALAEKALYVPVIRDPFPFTIRVT SEVLESNGMRRIGQPPASSRPV RRVRAPLPPPYLEVRAPLPASRP SGEVLCVTFDSLESGIKSDQV1 TAINGIKDKNFMHLHYEFPPYAT NEIGKVGTGLNRRELGHGALAE KALYVPVIRDPFPFTIRVTSEVLE SNGMRRIGQPPASSRPVRRVRA PLPPPYLEVRAPLPASRPSGEVL CTVTFDSLESGIKSDQVITAINGI DKKNFMHLHYEFPPYATNEIGKV TGLNRRELGHGALAEKALYVPV PRDPFPFTIRVTSEVLESNGSSSM ASACIGGSLALMDSGVPSSAV AGRNM*DWSPKPDPEKGIRKII VC*QIFLGIEDYNGDMDFKIAG TNKGITALQADIKLPGIPIKIVM EAIQQASVAKKEILQIMNKTISK PRASRKENGVPVETVQVPLSKR AKFVGPGGYNLKKLQAETGVT ISQVDEETVFNCNLHQHPVLMLE GKRLSFTEICKDDQEQAIRNLG AVILPAHNNWKSEILGVMGKII
8539	38907	A	8596	152	305	DNQNQGKLKCS*PCNFVHRAPY AVEITVLRFHCVTVQVAQRE RTFLILIK
8540	38908	C	8597	414	611	
8541	38909	B	8598	1	403	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met ind	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
8542	38910	A	8599	1	1702	MDSDEGYNYEFDEDEECSEEDS GAEEEEDEDDEPDDDTLDLG EVELVEPGLGVGERDGLLCG ETGGGGGSALGPAGGGGGGGG GGGGGGPGHEQEEDYRYEVLTS EMILQHMVECIREVNVEIQNPA TITRILLSHFNWDKEKLMERYF DGNLEKLFaecHVINPSKKSRT RQMNTTRSSAQDMPCQICYLNY PNSYFTGLECGHKFCMQCWS YLITKIMEEGMGQTISCPAHGC DILVDDNTVMRLITDSKVKLKY QHLITNSFVECNRLLKWCAPD CHHVVKVQYPDAKPVRCKG QFCFCNCGENWHDPV\QCKWLK KWIKKCDDDSSETSNWIAANTK ECPKCHVTIEKDGGGNHMVCR NQNCKAEFCWVCLGPWEPHG\ SAWDTV*NEDDAKAARDQ ERSRAALQS*LYCNRYMNH MQSLRF*EHR*YAQ*VQTME MQQHNMSWIEVQFLKKAVDV LCQCRA*TLMYT*VF*AFY*LKK NKPSFHIFENNPKARFDENATE GLSG*VLGTRKF*PKDSLQDIKQ KVPRPSTRYCESRRKG*FVTSMC HEGYEKDLWEYIED
8543	38911	C	8600	118	219	
8544	38912	C	8601	16	408	
8545	38913	B	8602	1	996	
8546	38914	B	8603	1	1302	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
8547	38915	A	8604	983	2127	DNWKSIRGSCWQDPRELLTFM APCIGVVVMQTTR*K^NTLAGH PSAGVCWCVTSAAAC^IGAWD ATSPLSSTFATAPLPRCCSQAS PAPRAEPLHGQPGAPPHALKRP PGLPW^PQEARNQYRHNQAYA YSIQGDGAEDDDERIVRFHTRV INHKRKKNNSPRIVQSNDLTEAA YSLSRDQKRMLYLTVFDQIRKSD GTLOQEHGDGICEIHAKYKAEIIFGL ISAEASKDIRQALKSAGKEV FYRPEADAGDEKGYESFPWF RAHSPSRGLYSVHNPYLIPIFFIG LQRNRTQFRLLSETKEITNPYAM RLYESLCQYRKPDGSQIVSLKID WIJERYQLPQSYYQRMPDFRRRF LQHIFVLRERPETVLIIDLQRTK DAVRELDNLQYRKMKKLLFQE AHNGPAVEAQEEEEEEYGVNLD RAYDVVKERRTVTKPNPSFMR QLEEEYQQGILLARPKRATYIYGS VYRRRCGYADHKVEIKHPGWAS ISRGVLVCDECCSVHRSLSGRHIS IVKHLRHSAWPPTLQQSGFPGP SRRAAPRAARGPTPRTEEA AAMALTFLLVLLTATLCTRLH RNFRGESIYWCGTADSQDTVA GSPDHGLAFAYHRLVRFLLW VLCPGWAFFLVNSSRGGVFNPI LHPCPRHGQARFAGVGRAEDV TFLYHPCAHWPWLKLQLALLAY ACMANPSLTTPDSLTDQDRVDIE
8548	38916	A	8605	1	224	RKQEWSKQKENIQHFQAEEE ANILLRQRQYLEECRRFKRR MLLGRHNLEQDLVREELNKRQ TQKDLEHAMLLRQHESMQELE FRHNTIQKMRCELIRLQHQTE LTNOLEYNKRRERELRKKHM EVRQQPKGLKSKELPNKKSSFQ GYLQNSQTRQYKALRNHLLET TPKSEHKAVLKRLKEEQTRKLA ILAEQYDH SINEMLSTQAVSLLF LGQNKFSAFPLPPP*AVSEQLCA HSLV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Motif	SEQ ID NO: in USN 09/540,217	Nucleotide location of last codon for peptide sequence	Nucleotide location of last codon for first amino acid of peptide sequence	Amino acid sequence (X=Unknown, -=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
8549	38917	A	8606	1051	1875	SDQLTAHILLNLCVVAELQFLHR FMLSFIPIHHHLRLFTAPAAQDASL VPLKGDLILGVKLSGDGRGKPA AQHLFLSGLSSSSQQQLPVLPsq CQSLCVHHHPAVVVNLHDIIAGAC VSCLPDLGPRQSCGSILAARSC GQSPGVWCLPSGSGRSSTILC H*GRSWTGPAPS**TPISSPRRSP GPCAASPARGCPAAASPAGS PGTEAAPAAPAPGPGYSQPPGAL SSRCDSPCPRLRAPGAHGHTP RCPSVVARCRGVPRPGSSCMS TSLTRSCSKL
8550	38918	A	8607	714	2148	MPAVAKSKFINRSKRMCPCV LRSASPIQEGERKISANENSLAVR STPAEDDSPGDQSQVKSEVQQPV HPKPLSPDSRASSLSESSPPKAM KKFQAPARETCVECQKTVYPM ERLLANQQVFHISCFCRYCYN KILSLGTYSALHGRIVYCKPHFNQ LFKSKGNYDEFGFGRPHKDJI GQAKMKTEEII.ER\ PQLANAR ETPHSPGVEDAIIAKVGVI.AAS MEA KASSQQEKEDKPAETKKI RIA WPPPTELGSSGSALEEGIKM SKPKWPPEDEISKPVEPEDVDL DLKKLRRSSSLKERSRPFTVAA SFQSTSVKSPKTVSPLIRKGWS MSEQSEESVGGRVAERKQVEN AKASKKNGNVGKTTWNQKES KGETGKR/R*GKVHSLEMENEN AFV\ENGARLPIEIDDNNQLPLPKQQ SSTKNPSLLEFGPSFVDNHILLK EFTTQNQNKSQDVELWEGEVVK ELSVEEQIKRNRYYDEDEDEEE
8551	38919	A	8608	1	4479	MCFSPKKLYKHEIHKLKDLITCL KPSIESPI.RQNRSRSIEEQKQE ENGDSQLILEKIQL.PQWSISLN TDEHGNLVNLVCDIKKPMVDV KIHLNQTDPPDIDINAMVALDF EYPMTOQENYENLWKLIAYSE VPMKLHRELMSKHPRVSYQY RQDADEEALYYTGVRQALIAEP EWIMQPSIDIQQLNPQSTAKKV LLSYNNQYSQTIATKDTQRQARG RSWVMIEPSRAVQKDQTIVLEG GRCQLSCNVKASESP

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8552	38920	A	8609	1	9009	MDEFAPGKHLATSGDGLFGDHNYGRRTYHTLEVKAEEHPAVSDPFQQRQSLRALSPLEDLPPSSGLRSGLTKELELMIIIGNEIPSIPDGALRDLSSLQVFKFSYNYKLRLVITGQLTLQGLSNLMLRHIDHNKIEFIHPQAFNGLTSRLHHLEGNLLHQLHPSTFSTFTLDYFRSLTIRHLYLAENMVRTLPASMLRNMPLLENLYLQGNPWTCDCEMRWFLEWDAKSRGHSCRGCAIISLSHEIQLAKGFCEMLL
8553	38921	A	8610	1	4971	MKASGILKCKKDKEYEGGQLCAMCFSPKKLYKHEIHKLKDTCLKPSIESPLRQNRSRSRSEEQKQEENGDSQLILEKIQLPQWSISLNMTDEHGNLVNLVCDIKKPMDVYKIHNLNQTDPPDIDINAMVALDFEYPMQTQENYENLWKLIAVYESVPVMKLHRELMLSCHKHPRVSYQYRQDADEEALYYTGVRQAQILAEPEWIMQPSIDIQLNRPQSTAKKVLLSYNNQSQTIAKDTQRQARGRSWVMIEPSRAVQK
8554	38922	A	8611	1	1283	LSFTTCSTFSTNYRSSLGPAQAPSYG/SRPVSSVASVYAGTGNSGSRIVSCTSFRGSMESGGLAGAMT/GGLAGMMGIQNEETMQSLND/*LASYPDRVRHLETKNRKL ESKIWEHLEKKGPQVRDWSHYFKTRNQRAQS LAITVDNACIVLQINNTHLAADDFRVKYETELAMCQSVESNIHGLCKVNDDTNVTRLQLETEIKALK EELLFMKKNHEEEVKGLQAIQASSGLTMEVDPKSQHLAKIMAAIRAQYDELA WKNGEELDKYLSQQIEESTTVVTTQSAKAGAAEMTLTELRCTVQSLEINLNSMRNLKASLENSVERVKACYTLQOMEQLNGILLHGS ELAQQTQAKGQCQAQYEALLNIKVKLEAEIATYCHLLEDGKDFNLGDALDSSNSMQTIPKTTTHQRVDGKVVSETNDTKVLRH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, -=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
8555	38923	A	8612	2	1365	RPQSI SPVLSLSPDSMSFTTRST FSTNYRSLGSVQAPS YGARPV SAA SVYAGAGGSGS RISVRST SFRGGMGSGLATGIA GLAG MGGI QNEKETM QSLNDGV ASY LDR VRSLE TENRRLES KIREH E KKGPQ VRDWSHYFK IEDLRAQ IFANTVDNARIVLQIDNARLA A DDFRV KYETELA MRQSVEND I HGLRKV IDDTNITRLQLTEIEA LKEELLFM KK NH^EEEVKG LQA QIASSG LTV E^DAPKS QDLAK ^IMADIR^AQY^RAGL GKN REE\ LDKY WSQQIEVSTT VTTQS AE \V GAA^ETTLTE LRTV QS LEID LDSMRNLKAS LENS LREVEA/R RTPLQMEQLQR GSLLH LSE LA QTRAE GQR Q A/QYE ALLE HQ GSS LAA E\ATY RLL EDGED F N L/GDAL DSSNSM QTIQ KTTTR I VDGKV VS\ETN\ DTKV LRH
8556	38924	A	8613	170	399	
8557	38925	A	8614	141	287	LPSRRAGL GTCSPPC LSLPP PASR APVRPEPLR* APPA PRRP VP ST TQG
8558	38926	A	8615	356	574	
8559	38927	A	8616	552	770	
8560	38928	A	8617	158	368	
8561	38929	A	8618	1136	1410	
8562	38930	B	8619	1	631	
8563	38931	B	8620	321	2234	
8564	38932	A	8621	170	444	
8565	38933	A	8622	325	722	LIELRH LVFFV LLLF RD LQHIMA CNMRDA VRFV CFLV IFREG L SRSSGA /DDRFLAGP *LLSRGAG LGTC SPPC LSLP TPWA /AAP ASLT VTPP PA PRRP VP STT QGLRS ASARHGTGRQLHLQPRCGIH
8566	38934	C	8623	1	1449	
8567	38935	A	8624	326	626	LPSHGAGL GTCSPPC LSLPP PLW AP /AAAEP P RQAPPAP WCPV PS TTQGLRN ASTRRT GRQLH MII WPFPA SLKSSP ATLPCEHCAP TT LTFSCSSNMQT
8568	38936	A	8625	2009	2227	
8569	38937	B	8626	182	1513	
8570	38938	A	8627	497	761	NHTSCLPLGP GTTA EELPSLVA GFGTCSPPC LSLP PTW APVR PE PPR * APPA PQR PV P STT QGLRN ASTRHRT GRQLHLQPRCGIH

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8571	38939	A	8628	218	855	GAGLGTCSPPCLSLPPTQRAPVRPEPPRRA PPAPPAPRPPVPRPVSTTQGLRSASTRHRTG RQLHLQPQCGVLRSAGLSSALETRTNPAADKHL WQSIIISLQLKS DLLKEMLGSQTGNGNVQDV LRYLVKSETQKAIVVSLDCVRKRYYRSSL QLKLCDCWGQALFSSALTLDPKEVVV RDLEELSNYKTITLEGSGIFDSVARV RESESEAEGT
8572	38940	A	8629	350	615	
8573	38941	A	8630	186	566	RILLSPAACRSGTMIFPSIHP SQCRMIGLGWKK*SSVHNATPW APVPEPPGRAPPA PGRPVPLTTQGLRSASARR RTGRQLHLQPQCGIH HWVKPA GLSHEGPRLRSSSQ SDQEPTNSGHSGMCL
8574	38942	A	8631	656	874	
8575	38943	A	8632	415	634	LPSRGAGLGNCSPPC LSLPPTPWAPVQH IKPPRRA PPPTPRHPVPS TTQGLRN ASAWRRSGRHLHQ PQC GIH
8576	38944	A	8633	2	264	NKQPIW PSRHLKPYHEPDAKE EIPGGS*GPTSCSH VETDAEEDP NCHEQHLSNTATHL GTDQEAVIDGRRK PEESRTTS HICRCRS

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8577	38945	A	8634	1	1743	MGQVWALVHSTLETFHTDEE GEYNEVTEQVCLPAKAGSAV DLCCTKAVSLLPGESPKVPTG AGGPLPAGMTGLLLGRSSLNIK AVQVQTGVTDSDYNGEIQIVTS TSVPWKAKPGDHIAQLLIVPKK FARFEGTASSGKTKFLPRFRISF LMAAIVKPKPEIPLKWLTDKPI WTEQWPLSKEKLEALEDLITQQ LKKGHIAPTFSPWNSPVFIUKKK SAEQDCEWFVFTILAVVNLQLK PAKRFIIWKVLPQQPNQQPIWIP SRYLKPYHKPDAKEEIPGSQG FPVAMSRLTLRRTPTVTSNTH RTQPPTWGQIEKLPQMAEENLR KAGQPVTISNWILPRITKFKPIE GAENVFTDGSSNGKASYSGSK GPLTEGNQMADRVLVAKVISNA RHFHNLTNVNASGLKRRYSIT WKEAKAIIQRCPTCQVMLSAAE QHLQKSAAKTEAEKLVWWRD PITKSREIGKIIWGRGYACVSP GPNQQPIWIPSCKHLKPYHKPDA GEKIPGESR/ETPGCSHVKTDAE EDANCHEQHPSNTATHLGTDQ EAVTDGGRKPEESGGTSHNE*F NDSGDIHCLQQGL
8578	38946	A	8635	820	1344	PDGITRDAGRGDRLRSVSWETL RGCPAVRKDSIGWIRLSRTLKK NVHLCPLPRGQQGLFVCPTVSS PQHISSHRGFWNISKDAPMSWP GSYSCHNVVAPVGQQGQ*SRRA RMLRGLLSKAGHHHSFCTDQAID LEITKFTFTWTID*VTLGQ*FMLS ES*SSCKPNNSCCPVQCLVHSGG
8579	38947	A	8636	3	760	

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8580	38948	A	8637	I	1354	MGISCPGSSKMLNSRALPVLKL TQGALRDCKERANYTNFNIYK AVESQGKFCVLYNGQQSPEY VMIPCTSVPSTIQQEVPEDRGMR MVMKNNPKPSKMQSLKSSKH LTNSVIVIAVGIFFSVTLQARDP QLDDAIEQLRGVCIRAWEKITS GGEQYPSFSAIKQQPKEPYIDFI ARLQESLKKMIADSAQDIVLQ LLAFDNANPDCQALRPPIRGKA HLVDCIKACDDIGDGSSNGKAS YFGSKSKVFQTSYTSQAQKELV AVIEVLTAFDMPINVISDSSYM VYSTQLIENAQLRFHTDQLMT LFTQLQTAFRSTMHPFYITHIRA RHITPLPGPLTEGNQMADCLVA TAVSNARHFHNLTVNASGLK CRYSNTWKAAKAIQRRPTCQ MVHSSSFTGGVNPQGLEPNSL WQMDVTWVHPSFGRLAYVHVC VDTFSHVWATCQSGES
8581	38949	A	8638	596	1820	
8582	38950	A	8639	275	1495	RLGSSLLEYT/LPDQQGNIIATFE PPFPKFKAHSVDYIKACDGIG GPLTEGNQMADCLVANAISNA RHFHNLTNVASGLKRRYSIT WKEAKAIICQQCPTCQMVHSSSF TGGVNPRLGEPNDSLWQMDVTH VPSFGRLAYVHVCVDTFSHFV WATYQSGESSACVS/KHPLLQC FVVVGIPIFKTDNAPGYTSQA LATFFSVWNKHTGIPYNSQGQ AIVERMNLNSLKQQLQKQKGNN RDYR/TTP^MQLNALLTLNFLS LPKGQMFSAEQHLQKPAAKT KTEQLIWWRDLITKSWEIGKIIIT WGRGYAYISPQGNQQPIWPSR HLKPYHEPDAIKRKLQEDPEDP PSCSHVKTDAEEDPNCHEQHPS NTAIHLRSQEAVTDGRKRKEE WSGTRTWWRPWSCR
8583	38951	A	8640	232	789	ERPWPGEQNSEGFCPKGLEPR TCLRGPAASAAAAGAEGRQDP GGPWCSAPAAGDGLGSPGVQSPG GGSPRGAQVAMSGSRRRAEP GVWGALQ^HRR*ARRMHSFPP SL/PLL*NG*SPLFLVSKLTGSP LRSASIPCRAARSC^KHPDSPG RGPGRARQSPALHPALPSLARRA APGRSFPLTSRK
8584	38952	A	8641	I	149	

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8585	38953	A	8642	1	2541	
8586	38954	A	8643	1	989	MQRGGQQATGSSANA W G I L Q P K W V Q T G P D N K R M A R N V L K Y E R L L A E S P N H V V A E A V I Q R P N I P H L Q T R D T Y E G L C Q T L G S Q P T L Y Q I P S L Y C S Y E T N S N A Y L L L Q P I R K E V I H L E P Y I A L Y H D F V S D S E A Q K I R E L A E P W L Q R S V V A S G E K Q L Q V E Y R I S K S A W L K D T V D P K L V T L N H R I A A L T G L D V R P P Y A E Y L Q V V N Y G I G G H Y E P H F D H A T S P S P S P L Y R M K S G N R V A T F M I Y L S S V E A G G A T A F I Y A N L S V P V V R V V Q / W P G T S * A F D N Q C O N A L F W W N L H R S G E G O S D T L H A G C P V L V G D K W A N K W I H E Y G Q E F R R P C C
8587	38955	A	8644	2	505	A W L K D T V D P K L V T L N H R I A A L T G L D V R P P Y A E Y L Q V V N Y G I G G H Y E P H F D H A T S P S S P L Y R M K S G N R V A T F M I Y L S S V E A G G A T A F I Y A N L S V P V V R V V Q / W P G T S * A F D N Q C Q N A A L F W W N L H R S G E G D S D T L H A G C P V L V G D K W V A N K W I H E Y G Q E F R R P C S S P E D
8588	38956	A	8645	298	401	K K S S L V R R S W R M K E L K K K I G Q Y * R K L G R L K G K A I
8589	38957	A	8646	1	417	F R A A P A P E S G G E S V F G E T H R A L Q G A M E K L Q R / R L W K E K V D L K E R V E K L E L Q F I H L S G Q T D T I G R K Y I S Q G A V S E T Q H W E / K E D I V R L A Q D Q E E M K V N L Q E L R / E Q V L Q L V G D H K E G H G K / F L T I A Q N P A D E P T L G A P I A Q E L G C
8590	38958	A	8647	2	430	A A V K P L G S A E T A V P I A R L G C R R F S R S R C R R R G S L L S F S A A K V A F F N S A G A N A Q E E Q R V C C Q P L A H P V A S S Q K P E V A A P A P E S G G E S V F G E T H R A L Q G A M E K L Q R / R L W K E K V D L K E R V E K L E L Q F I H L S G Q T D T H N K I S Y
8591	38959	A	8648	1	2769	
8592	38960	A	8649	1	314	F V N L F E I P V R V V E F G A T C R A V A E P E Q Q R * S P S A R P R P C P L L A S V A A A L A A A A A A A G G E A A Y C L S P R R R * G A V S A R P A G E R P E P H E W D N R R S D F K R R R G R D G
8593	38961	B	8650	46	307	
8594	38962	C	8651	1	4584	
8595	38963	B	8652	438	532	
8596	38964	B	8653	832	927	

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8597	38965	A	8654	320	1136	RIMETIANI.SSQSPVSLPLRVLGA AEYLEMEED/DLDSEQEAPRM PNIPGDLESREP(QVAFNSAGA SAQEERVRVCCQPLAHPVASSQK KPEVAAPAPESGGESVFGETHR ALQGAMEKLQVTTLWKEKVD LKERVEKLELQFIHLSGQTDTIV SERLGHWRGELPGHPRGPSI*A MSSCRKVHQPGGSVRD/AALGE EDIVRLAQDQEEMKVNLQELR/ EQVLQLVGDHKEGHGK/FLTIA QNPADEP TLGAPVAQELGCAD EQGGFYPRSPPLDC
8598	38966	B	8655	97	235	
8599	38967	A	8656	1	2104	
8600	38968	A	8657	3	1107	FMTTDERKLFNHLKSPHLKYW VPFIWFGNLATKARNEGRIDS VDLQLSMLTEMNRYSRWSCLLF GYDWVGIPLVYTQVVTLAVYT FFFACILIGRQFLDPTKGYAGHD LDLYIPITLLQFFFFYAGWLKVA EQLINPFGEDDDDFETNWCIDR NLQVSLLAVDEMHMSLPKMK KDIYWDDSAARPPTYTAAADY CIPSFLGSTVQMGGLSGSDFPDEE WLWDYEKHGHRHSMIRRVKRF LSAHEHPSSPRRSYRRQTSRSS MFLPRDDLS/HSQGPTGCALKK PPQGLTHLE/DNPASQKEAPRCT SAWESCPPSGRPARQALYRA*P HSPV*ELPPSKCH!GT*GIDHSSR STSAHIRGLPP*FRYLHLEL
8601	38969	A	8658	3	397	
8602	38970	A	8659	346	474	

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8603	38971	A	8660	1	1344	MHSTWLCPARLLKELPFPQGL FPRLTIRASRTPPAALERVTRD PCAATCLDRGSLKGILGHSPFQ SPPVTSHCAENPNTLKAPPYV GATSALVLSLGGPVTPWLSVEL SIRTFASSGLIYMAHQNQADY AVLQLHGGRLHFMDLGKGRT KVSHPALLSDGWHTVKTDYV KRKGFIITVDGRESPMVTVVGD GTMLDVEGLFYLGGLPSQYQA RKIGNITHSIPACIGDVTVNSKQ LDKDSPPSAFTVNRCYAVAQE GTYFDGSGYAAALVKEGYKVQS DVNITLE^FRTSSQNGVLLGIST AKVDAIGLELVDGKVLFHVNN GAGRITAAYEPKTATVLCDGK WHTLQANKSKHRITLIVDGN GWR^KSHTPQSTPVDTN^NPIYV GGYPAGVKQKCLRSQTFSRGC LRKLALFURGPQVQSFDTSRAFE LHGVLFLHSCPGTES
8604	38972	A	8661	3	92	
8605	38973	A	8662	2	158	HTFPFTSSSPHLVMMIQPSSSSP PPPLPPPSS^SPPPLPPSPPPPLL FFL
8606	38974	A	8663	21	471	DGPQDQPPHQPSSSSSPPPLPPP PFPPPLPLPPSPPPLLLFCSDAE LLCCHTGVELFFVIFAYCSG/PE TEPAISPRYASSSGLNGFLPLPRT PPAYA*IPSSGIHFNPSSLAIKPST TTTVRTPTTIHHSRRPTTTQS STTAPSLHLP
8607	38975	A	8664	2	105	
8608	38976	A	8665	3	265	RKDLYANTVALSGGTTMYPGIA DRMQKEITALAPSTMKIKIAPP ERKYSVWIGGSILASLSTFQQM WISKQEY^DESGPSIVHRKCP
8609	38977	A	8666	3	757	NTPVAMYMAIQAVLSLYTSGRT TGIAMDSGDGVVAHTVPIYEGET LPHAILHLDLAGWDLTDYFMKI LMECSYRFITMAEQEIVCDIKE KLCNIALDFEHKMATGASSSS EKSYEVPDGQVITIGNEWF/*VP EALFQPS/MGMESCGIQETTFNS IMKCDVDICKELYAKMVLSSGT TMYLGIADRMQKEITALGRPST LRFRFIAPP/ERRKYSVWIGGSI LASLSTFQQIMWI^SKQEYDES GPLHPSTANCF

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8610	38978	A	8667	3	171	CPLCRGNHWKVHCPSGR/MVP* VRSPQPDDPTTGQRVPGASASS CHHPh*APGTFNH
8611	38979	A	8668	1	325	SPSRTCYQCGLQGHE*KDC/TSE KPPPRPCLLCQGNHWKVHCPR/ VTKVLWVRSQPDPATGLRV PDD*EHTIRRAYALGKSAVTSK PPPPYPARSRLNVRRLCSLATN
8612	38980	A	8669	3	377	
8613	38981	A	8670	1	423	
8614	38982	A	8671	1	1659	
8615	38983	A	8672	1	1449	MVNNDTRPKVQVEYKGETKIF YPEEVSSMVLTAKMKEIAEAYLG KTVTNAVVTAYFNNSQHQAA TKDAGTIAGLNVLRINEPSAAD IAYGLDKKVGAEARNVFIFDLRG GTFDVSILIIQDGIFEVKSGDTHL GEEDFDNRIVSHFIAEFKHKYK KDITIRDVKLDKSQIHDIVSIGG YTHIPKIQKLLQDIFNRKELNKS INLDEAVAYGAAVQAAILSGD KSENVQDILLLDVNPPLSGIEL AGGVMTV/LPVLIKHSTTIPTKQ TETF*TQIYSDNQPGVYEGERCAM TKDDNLKKFELTGIPSAPHGV PQIEVTFIDANGILNVAVDKS VGKENTTTNDKHLRSKEDM NIWSAEKYKAEDKRQRDKVSS KNSLESYAFHMKAATVKDEKLQ GKINGEDKQKILDKFNEVIKWL DKNQAAKKEFEHQTELEKV CNLIISKRYQSAGGMPPGMPGG FPGGGAPPSSGASSRPITEEVN

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8616	38984	A	8673	18	1388	TRLQLLGFLWLPSLLEPGLHPS NHGPRGPAGVIDLGTITYSCGVF FQHGKVEIIANIDQGNRTTPSY VAFTDTERLIGDAAKNQVAMN PTNTSF^LPNGLIGRVRFD^DAVV QSDMKHWAPFMVVNDAGRPK APS*NTKGETKSLVYPEEGVFLW V*PKMKIEICRSLTLGKTVTNA VVIVPSVYFNDSQRQATKDAG TIAGLNVLRI^NE^PTAAAIA^YGG LDKKGLEQKRNRNRAHLTWGG GTFDVSI^TIED^GIFEVKSTAG DTHLG/GEEFDNFNRMVNHFIAE FKRKHHKKDISENKRAVRRRLTA CERAKRTLSSSTQASIEIDSLYE GIDFYTSITRARFEELNADLFRG TLDPVEKALRDAKLDKSQIHDI VLVGGSTRIPKIQKLLOQDFNG KELNKSINPDEAVAYGAAGVQA AISGDKSENVQDLLLLDVPL SLGIETAGGVMVTVLKRNTT
8617	38985	A	8674	2	1559	RYLNWIGTPTKGMMSLKAFAQVQQ PHKSYWLKTLLPDNMEALQIR K*VPNILGTCAVSWLKGPCSDV AVKKFFIISLGNYWEQN*L^*EH GYKVW*HSNSYLEPISPAQTPK KRTTSYFSTLLCLRLRSCLSLFK RIECYEVNYQPLDEELDR*EPAP QSQGLDLSPSPFDIL*DHIQSRTV YYLMNIHVTPRSIYLCRHGESE LNIRGRIGGDGSLSVRGKQVG WATHTOMGWLGCPWRWAAGFP ILPSRPYPNAGVTLAAPVPTHDS VLPALPTRAGGQDETEPGLKAG PTGLPSAPPLEMGGGAPGKALS WMATPWCLPFCYVEVALTCAA PTVYQAVVVWLPYHYLKCSPT AGQMRQCSLDMRPERGRDVSE GTRDHVRELREFNLWLIPPCQG LLPTSHMKRTIQTAEALGVPYE QWKALNEIDAVRCMG*ISCVW G*LESQIPLRDQDKYRYRYPK GEVRFAGWPNA*DYSPVSSLQL NVLLICHQASMRCLLAYFLIKS SGTTLISALGMFDGI
8618	38986	C	8675	16	206	
8619	38987	A	8676	157	413	ALVCS/SSLAIREMQIKTTMRYH LTPVRMAJIKKSGNNCRWRGC GEIGTLLLHCWLDCKLVQPLWK SVW*FLRNLLEIPFDPAIPLL
8620	38988	B	8677	877	2126	

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8621	38989	A	8678	1	1731	
8622	38990	A	8679	2	1675	
8623	38991	A	8680	1	2142	MIILIDAEKAFDKIQQQPFMLKTL NKLIGIDGTYLKITRAINYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRKYLGIQLTRD VKDLFKKYKPLLNNKIKEDTNK WKNIACSWIGRINJMKAFFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGLAVDIPVNNDKL MVLEVLRALARQKKEIKGIGLQG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFQ FTIATKRKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNP CSRIGRINJMKAFLPKVIYRFN DIPIKLPMTFFTELEKTTLKFIW NQKRACIAKTIILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSHIYNH LIFYKPDKNKKWGNDSSLFNKW CWENWLAIKRKLKDPLPTY KIHSRWIKDLNVRPKTIKTLLEEN LGNTIQQDIGHMGKDFMTKTPKA MATKAKVVDKWDVILKLSFCATA KETTIRVSROPTEWEKIFAIYPS DKGLISRIYKELKQIYRKKITNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM
8624	38992	A	8681	1	1242	

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8625	38993	A	8682	14	1785	FDQVEERVSVIEDQMNEKRE EKFRERKVRIRNEQSLQEIWVDYV KRLNLHLLIGVPESDWENGTGLE NTLQDIIQENFPNLARQANIQIQ EIQRMPQRYSRRTTPRHILNA HKRK*ERYKIDTTLTSQKLELK QEQTYSKASRRREITKRAELKE IETQKTLQKINESRSRCFEKINKID RLLARLIKKKREKNQTDVKND KGDDITDPTETQTTIREYYKHLY TNKLENLEEMDKFLDTYTLPRL NQEVEESLNRPITGEIEAINSL PTKKSTGPDRFTAEIFYQRYKEE LVPFLLKLFQSIEKEGILLNSFYE ASTILIPKAGRDTTKKENFRPISL MNIDAKILNKILNRIQQHIKKL IHYNQVSFIPGIQGWFNICKSIN VIQHINRTKDKDNHTTISIDAEGA FDKIQQQPFMLKTLNKLGDGTY LKIMTAIYDKPTASTILNGQKLE AFPLKTGTRQGCPPLSPFLNVL EVLARAIRQEKEIKGIGLGKEEV KLSLFADDIMIVYLENPVAQT LLKLISNFSKISGYKINVQKSQV FPYTNNRQTEQIMSELLFTIAS KRIKYVGQLTRDVVKDLFKEN
8626	38994	A	8683	1	5127	
8627	38995	B	8684	1	1461	
8628	38996	A	8685	2	1879	
8629	38997	A	8686	I	1299	MKLPEEGSGSIICCSAIAFVLQL PLVIHRQTGYGEDLQQPTPDLQ LRDLTDHSSPAMEQSWMEND FDELNRSRLQKANKLENLEETD KFLDTYTLPRLNQEETESLNRP TGSEIEAIINNPTKKSPGPDGV TAKFYQRYKEELRTVKNHNMI SIDAEKAFDNIQQPFMLKTLNK LGIDATYKLKIIRAIDDKPTANII NGQKLEAFLPLKTGTRQGCPPLSP LLFNVILEVLARAIRQEKEIKGI QLGKEEVKLSSLFADDIMIVYLEN PIVSAQNLKLINNFSKVSGYKI NVQKSQEFLYNNNNRQTEQIM SELPFTIASKRIRYKYLGIQLTRDV KDLFKENYNPLNNEIKKDTNK WKNIPCSWIGRINIMKMAILLK VIYRFNAIPIKLLMIFTTELEKAT TLKCI*NQKRAHIAKPILSQKNK
8630	38998	B	8687	1	2187	

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8631	38999	A	8688	1	1698	MMGDFNTPLSTLDRSRMRQKVNDIQLNSALHMHMDLIYRTLHPKSTEYTFPSAPQRRTYKIDHIVGSKALLSKCKRTEITNCLSDHSAIKLELRKKLTQNHSITWKLNWNWLLNDYWVHNEMKAEIFKFMFETNEIKDTTYQNLWDTFKATLNQEEVESLNRPITGSEIQAMINSLGTKK/SPGPDGFTAKFY/P/E/HDCISRKPHRLSPKSP*ADKQLQQLSRLIQNQCSKITSILHQ^QTNRERPNHE*TPIHNCIKDNKIPRSPTYKGCEGPLQGELQTTAQRNKRGHKQMEEHPMMLMDRKNOYHENGHTAQGNL*IQCHPHQATNDFLHRIGKKYKVHMEPKKSLLHQCVNPKPKEQSWRHHHTT^LQTILQGYSNQNSMVLVPKQRYRPMEMHNRALRNNATYLPLSDL*ET*QKQEMGKGFPI*QMVLGKLASHM^KAETGSLPYTLYKN*FKMD*R LKC*T*NHKHPRRKPRQYHSGHRHGQLLHV*NTKSNNGNKSQN*QMGSHTKELLHSKRNYHQSEQATYRMGENFCNLII*QRANIQLNLQRTQTNLQ/RKKQPHQQVG
8632	39000	A	8689	1	5073	
8633	39001	A	8690	128	1407	EKKASDDQTPSYRRKFKPKAKKLNTLKKI^TN/RJTRINREKCLKELEMELKARELREECRSLRSCDQLEERVSVMEEIQTIREYYKHLYENKLQNLEEMDKFLDTYTLRRLNQEEVESLNRPITGSEIVAIINSPLTKKSPGPDGFTAKFYQRYKEELIPFLLKLQFSIEKEGLPNFSFYEAISIILPKQGRDTTKKENFRPIFLMNINAKILKILANRQQHIIKLIHHHDQVGFIPGMQGWFNICKSRNVIIHHINRTKDKNHHIISIDAEKAFDKIQQPQFMLKTLNKLGIDETYLKIIIRAIYDPTANIIINGOKLEAFPLKTKTRQGCPLSPLLNFNIVLEVILARAIRQEKEIKGIQLGKEEVKLSLFADDIVYLNPIVSAQNLFELISNFSKVSGYKINVQISQAFLYTNYRQSAKS
8634	39002	B	8691	1	1443	
8635	39003	A	8692	1	1878	
8636	39004	A	8693	1	1479	

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8637	39005	A	8694	I	2091	MVFLEKISVGISRLSKQHPPFIR VALPLDADPTVSRIGSFQWVLG LADFNEAVDPRDVQMCPEFIP SGGFVVFVLTSGVKPQTFTVTSITA LKGEPTQMRRNQKTNSGNMTK LGYLTPQKNHTSSPAMSPNQEQQ IPDSPEKEFRRTEASLTEGGTI NPISIWAVGNGSSKNIYHILGK GRKIFSSSGIKQKSIASGERQNFI QRNDQTAAFVHENPLFCSHR CWYPGKQECKLKEMLMEKAK ARELREECRSLRSRCDQLEERV SVMEDEMNEMKREGKFREKRI KRNEQSLQEIWDYVKRPTLHLI DVPETLNAHKRKQERSKTDTLT SQLKELEKQEQTHSKASRRQEIT TKIRAELEKIEETEKTLLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDAIIKNDKGDTSDPTEIQT TIREYYKHLYANKLENLEEMD KFLDYYTLPRLNQEEVESLNRP TGSEIVAIINSLPTKKSPGPDGST AEFYQRYKELLISNFSKVSGY KINVQKSQAFLYTNNRQMESQI MSELPLFTTSKRKIKYLGQLTRDI KDLFKENYKPLLNEIKEDRNKC KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLRLMTTFTELEKTTL KFIWNQKRARITKSVLSQKNKA GGITLPDFKLYYKATVTKTAW WYWQNDRIDQWNRTPESEITP
8638	39006	A	8695	I	3514	MELTKAARELREECRSLRSRCD QLEERVSAMEDEMNEMKREG KFRERKIKRNEQSLQEIWDYVK RPNLRLIGVPESDVENGTKLEN TLQDIIQENFPNLARQANIQIQEIT QRTPQRYSLRRATPRHIIVRFTK VEMKEKMLRAAREKDSTRTRQK VNKDTQELNSALHQADLIDIYR TLHPKSTETYTFPSAPHHTYSKT DHIVGSKALLSKCKRTEITNYL SDHSAIKLELRIKNLTKSRSTTW KLNNLLNDYW
8639	39007	A	8696	I	2091	

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8640	39008	A	8697	1	2781	MGKKQRKTGNSKKQSAPPK KERSSPATEQSWMENDFDEM REEGFRRSNYSSELREDIQTKKGK EVENFEKNLLECITRINTEKCL KELMELTKARELREECRSLSR RCDQLEERVSVMEDEMNEMN DGENGTKLENTLQDIIQENFPN LARQANVQIQEIQRTPTQRYSSR RATPRHIIVRFTKVEMKEKMLR AAREKDFKPTKIKREKEGHYIM VKGSIQQEELTILKIYAPNTGAP RFTKQVLSDLQRDLD
8641	39009	A	8698	1	1584	MSISGTVRMSAKSKGNPSSCP AEGPPAASKTKVKEQIKIIVEDL ELVLGDLKDVAKELKEQHWW HPISGDTATSICTVLESEKS SKIK VTAFDVWLHLWGKGTDKQKD SSNFCRLLKCPCLTALKRAVVL ARSWRCENGQTASSGSLTPDP RAANREAPPSSGRRLTPHTASDG ENGTKLENTLQDIIQENFPNLR QANIQIQEIQRTPTQRYSSRKATP RHIIVRLTKVEMKEKMLRAARE KEIQTaireyykhlyanklenl EEMDKFLDAYTLPRQNQEEVE SLNRPITGPEIVAIINSPLTKKSP GPDGFTAEFYQRYKEERHINRT KDENHMIISIDAEKAFNKIQQP MLKTLNKLIGIDGTYFKIIIRAIYD KPTANIIILNGQKLEAFPLKTGTR QECLPLPLFNIVLEVLAIRQ EKEIKGIGQLGKEEVKLSLFVDY MIVHLENPIISAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMSELPPFTIASKRKYLGIQ LTRDVKDILFEEND

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8642	39010	A	8699	1	1722	MAGYPSEMKLPEELSGNSNCCS AVFTVLQPLLLIPRQTSQGVDL RQTPITDQLQLRVTLVRKRNKNQ KRTSTPKPHLYVTHKDORSKKL TQNHSITWKLNNNLLNDYWW NNEMIAEIKMFFETSENKGTY QNLWDITFKAVCRGKFIALNAH KRKQFRSKIDTLTSQLKELEKQ EQTHSKASRQEITKIRAEQKEI ETQKTLQKINESRSCFEKINKI DRLLARRIKKKREKNQIDAIKN DKGDITADPTEIQSSTIREYYKHL YTNKLENLEMDKFLDTYTLPR LNQEEDESLNRPITGSEIEAIINS LPAKKSPGPDRFTAEIFYQRYKE ELHINRRTKDKNHMTISVDAENA FDKIQQPFMLKTLNKLVLEVLA RAIRQEKEIKGIQLGKQEVKLSL FADDVIVYLENPVSAQNLKKLI SNFSKVSGYKINVQKSQAFLYS NNRQTESQIMNELSFTIASKRK YLGIQLTRDVKDLFKENYKPLL NEIKDDTNWKWNIPCSWVGRIN IVKMGILPKVVYRFNAIPIKLM TFFTELEKTTLKFIFWQNQKRARI AMTILS*KNKAGGITLP
8643	39011	A	8700	3	1033	
8644	39012	A	8701	1	1068	ANKLENLEETDKFLDTYTLPRL NQEETESLNRPITGSEIEAIINNV PTKKSPGPDGVTAKFYORYKEE LRTVNKNHMIISIDEAKAFDNIQ QPFLMLKTLNKLGIIDATYLKJIRA IDDKPTANIILNQGKLEAFPLKT GTRQGCPLSPLLFNIVLEVLR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYYLENPVSAQNLKKLI NNFSKVSGYKINVQKSQEFLYN NNRQTESQIMSELPTIASKRK YLGIQLTRDVKDLFKENYKPLL NEIKDDTNWKWNIPCSWIGRINI MKMAILLKVIYRFNAIPIKLLMI FFTELEKTTLKCII*NQKRAHIA KPILSQKNKAGSITLR
8645	39013	B	8702	69	1055	
8646	39014	B	8703	1	2301	
8647	39015	A	8704	1	3189	

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8648	39016	A	8705	92	1139	ASAADTQANRVWSGGPPANSR PAAIRVLTVRKTKNKGKHPH QNPICTSPSSSKTEIQTITREYQQ HLYTNKLENLEEMDKFFFDTYT LPRLNQEEVESLNRPITGSEIEAI INNLPLT/KKSPGPDGFTAKFYQS VGSSGQGNQAGEGNKGHSIRK RGSOIVPVCR*HDCISRKPHRLS PKSP*ADSQLQQQLRIQNNQCAKI TSILIHQ*QTNREPNEH*TPHIHG FKQNKIPRNPAYKGGERPLQGE L*TTCAG*NKRGYKQMEEHSM MGRKNQYHENGHITAQGNL*IQ CHPHQATKNFLHRICKNYFKV HMEPKKGPHCQVNPKPKEQSW RHHTT*LQTILQGYSNQNSI
8649	39017	A	8706	1	2199	
8650	39018	A	8707	1	2238	
8651	39019	A	8708	3	1889	RSMRQKVNKDTQEELNSALHQ DLIDIYRTLHPKSTEYTFPSAPH HTYTKIDHILGSKALLERIKNLNTQ EIITNYLSDHSIAKLELRIKNLNTQ NRSTTWKLNNLLNDYWVHN KMKAEIKMFETNEKENKDPTYQ NLWDAFKA/EIQTTIKEYYKHL YANKLENLEEMDKFLDTYTL RLNQEEVESLNRPITGAEVIAIJN SLPTKSPGPDGFTAECFYQRYK EELVPFFLKLKFQSIKEQGILPNSF YEASTILIPKPGRDTEKENFRPI SLMNIDAKILNKILAKRIQQHK KLIHHDQVGFIPGMQGWFNIIHK SINVQHINRAKDKNHNMIISIDA EKAFDKIQQRFMKTLNKLGLID GTYFKIIIRAIYDKPTANIILNQ KLEAIPLKAGTRQGCPLSPLLFN IVLEVLLARVIRQEKEIKGIGL GK EEVKLSLFADDMMIVYLENPIVT AQNLLKLISNFSKVSGYKINVQ KSQAFLYTNNNRQTESQIMSELP FTIASKRKYLGIQLTRDVKDLF KENYKPLLKEIKEDTNKWKNIP CSWVGRINIMKMAILPKVIYRF NAIPIKLPMTFFTELEKTKIFIWN QKSAHITKGILSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN

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8652	39020	A	8709	1	1779	MGDFNTPLSTI.DRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFPSAPHHTYSNIHDIV GSKALFSKCKRTEIIITNCLSDHS AIKLELRJKKLTNQHSTTWQLN NLLLNDYWVNNEMKAEIKMFF ETNEKDTTDQNLWDTFKAVC RGKFMALNAHKRKQRSKMG TLLSQLKELEKQEQTISKASRR QEITKIRAELEKEIET/QKTLQKIN ESR/TEIQTTIREYHKHYANKL ENLEEMDKFLDTYLPRLNQEE VESLNRPVTGSEIEAIINSLPTKK SPGPYGF/TAEFYQRVYKEELHIN RTKDKNHMIISIDAEEKFDKIQ QPFLMLKTLNKLGIIDGTYLKILR AIYDKPTANIIANGQKLEAFHLK TGTRQGCPLSPLLLNFNIVLEVLR AIROEKEIKGIQLGKEEVKWSL FADDMIVYLENPIVSTQNLFKLI SNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSELPTIASKRK YLGQLTRDVKDLFKENYKPLL NEIKEDETNWKWNIPCSAGRINI VKMAILPKVIYRFSAIPIKLPMT FFTELEKTKFIWNQKRAHIAKS ILSQKHKAGGITLP

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8653	39021	A	8710	1	2093	MEITINCLSEHSAITLQLRIKKLTQNCTTWKLNLYLLNDYWVNNEMKEEIKMFFETNEKDTTYQNLWDVFKA/CRGKFIALSAHKRKQERSKTDILTSQLKLEKEQEQTSHSKASRRQEITKIRAEELKEIETQKTLQEINDSRSSSEKLNKI DRPLARLIJKKKREKTQ/DIAKNDKG/EINTNPTEIQT/TIREYYKYL YANKVENLEEMDTFLDTYTLPRLNQEEVESLNPITGEIEAIINSLPTKESPGPDGTAEFY/HEGNQERERNKGYSIRKRGSHIVPVC R*HDCLFRKPHHLSSKSHEAVKQLQQSLRIQNQWAKITSMPVHQ*QTNREPNHE*TPIHNPCYKENKIPRNPTYEGCEGPL/QGELQTTAQQNKRQKEMEKHSMLMDRKNHYHENGTAAHGNL*IQCHPHQATNDPLHRIGKNVNHFMEPKKSLHCQENPKQREQSWRHHAT*LQTILQGYSNQNMSVLVPKQIHRTMEEQRGLRNNTTHLQPSDL*QI*QKQEMGKQFP**MVLGKLASYM*KAETGSLPYTLYKN*FKMD*RLKC*T*NHKNPRRKPRQYHSGHRHGGQLHD*NTRSNGNKNQNQRQMGSN*TKELLHGKRNYHQSAQTTYRMGENFCNLPI*QRAANIQLNQRT*TNLQEKNKQPHQKVVGKGHEQTLLKRRHLC SQQTHEKMLIITGHQRQANQN

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8654	39022	A	8711	3	1805	P,I,S,T,I,D,R,S,S,R,Q,K,V,N,K,D,I,Q,D,V,I,S,A,L,H,E,A,G,L,I,D,I,Y,R,T,L,H,P,K,S,T,E,Y,T,F,F,S,A,P,H,I,T,Y,Y,K,I,D,H,I,V,G,S,K,A,L,L,S,K,C,K,R,T,E,I,T,N,C,L,S,D,D,R,A,I,K,L,E,L,R,I,K,K,I,T,O,N,Y,T,T,W,K,L,N,N,L,L,S,D,Y,W,V,N,N,E,M,K,A,E,I,K,M,F,F,E,T,N,E,N,K,D,T,M,Y,Q,N,L,W,D,T,F,K,A,V,C,R,G,K,P,I,A,V,N,A,Y,K,R,Q,E,R,S,K,I,H,T,L,T,Q,S,K,L,E,P,E,K,Q,E,Q,T,H,S,K,A,S,R,R,Q,E,I,T,K,I,A,E,L,K,E,I,D,T,Q,K,T,L,Q,K,I,S,V,S,R,W,F,S,E,R,I,N,K,I,D,R,L,I,A,R,L,M,K,K,K,R,E,K,N,Q,I,D,A,I,K,N,D,K,G,D,I,T,I,D,P,T,E,M,Q,T,T,I,R,E,Y,Y,K,N,L,Y,A,N,K,L,E,N,I,E,E,M,D,K,F,L,D,T,Y,I,I,P,R,L,N,Q,E,E,V,E,L,P,N,R,P,I,T,G,S,E,N,E,A,I,I,N,S,L,P/T,K,K,S,P,G,D,E,F,T,A,K,F,Y,Q,R,Y,K,E,E,L,I,Q,G,U,R,Q,E,K,E,R,D,T,Q,L,G,K,E,E,V,K,L,L,L,F,A,E,D,M,I,V,Y,L,E,N,P,I,V,S,A,Q,N,L,L,K,L,I,N,N,F,S,K,V,S,G,Y,K,I,N,V,Q,K,S,Q,A,F,L,H,T,N,N,R,Q,T,E,S,Q,I,M,S,C,P,L,T,I,A,S,K,R,I,K,Y,L,G,I,Q,L,T,R,D,V,K,D,L,F,K,E,N,Y,K,P,L,L,N,K,I,K,E,D,T,N,K,W,K,N,I,P,R,S,W,I,G,R,N,N,I,V,K,M,T,I,L,P,K,V,I,Y,R,F/N,T,L,N,F,I,W,N,Q,E,R,A,I,K,T,I,L,S,K,K,N,K,A,G,G,I,T,L,P,D,F,K,L,Y,Y,K,A,T,V,T,K,T,A,R,Y,W,K,Q,N,I,K,K,G,S,V,W,P,I,S,L,K,S,E,K,R,G,H,R,T,R,P,L,W,K,I,L,C,H,N,D,V,Q,G,E,L,L,K,T,I,Q,F,L,G,S,P,L,G,H,S,S,L,D,P,S,A
8655	39023	B	8712	1	1743	
8656	39024	B	8713	1	1260	

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8657	39025	A	8714	1	1842	VPPITTCGNYGSTIQDEIWMGTQ NQTISVSEEMMFQAEIASAQK MWNQHHITPSKVDHVGSKAL FSKCKRTEIJTNYLSDHSIAIKLK LRIKKLTQRNRSTTWKLNNLLN DYWVHNEMKAEIKIFFETNEN KDITTCQNL.WDTFKAMCRGKF1 TLNAHKRKQQRCKIDTTLTSQLK ELEKQEQTSHSKASRRQEQITKIRA ELKEIEAQKTLQKINESRSWIFE KINKTDRLARIKKKREMNQI DAIKNDKGIDTTNPTEIQTIRE YCKHILYANKLENLEEMDKFLN TYTLPLRNQEEIESLNRPITGSEI EAIIINSPLTKKSPGPDPGFTAEFY QRYKEEMIEKKAFDKSQOPFM LKTLNKLGIDGTFLKIRRAIYDK PTANIILNGQKLEAFLPKLTGTRQ GCPLSPLLFNIVLEVLAIREIRQG KEIKHQLGKEEVKFSLFADDVI AYLENPIVSAQNLLKLISNFSKV SGYKINVQKLQAFLYTNNRQTE SQIMSEPFITIASKRICKYLGQLT RDVKDLFKENYKPLNKIKEDT NKWKNIPCS WIGRINIMKMAIL HKVIDRFSAIIPFKL/PKD/FFTEL EKTLKFIWNQKRPRISKTLSK KNKAGGITLR

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8658	39026	A	8715	I	1593	MGKKQRKTGNSSKKQSTSPPP KERSSSPAMEQSWMENDFVEL REEGFRRSNYSSELQEDIQTKGK EVENFEKNLEECMTRITNTKEC LKELEMELTKARELHHECRSLR SRCDQLEERVSAMEDEMNEMK REGKFREKRIRNEQSLQEIW YVKRPNLHLMGVPESDGENGS KLENLTQDIQENFPNLARINKI DRPLARLIKKKRNQIDTIN DKGDITTPTEIQTTCIREYYKHL YANKLENLEEMDTFLDTYTLPR LNQEEVESLNRPITGAEVIAINS LPTKSPGPDSIAEFYQRYKE E/PADIKQLQQSLSIQNQCTKITSI LIHQQTNTREPNNHE*TPIHNCFK ENKIPRNPTYKGCEGLLPGELO TTAQGNKRGYKQTEEHSMML GRKNQYRENGHTAQGNF*QC HPHQATNAFLHRIGKNYFKVH MEPKKSPPHRQVNPKPKPQEWSR HHTT*LQTILQGYSNQNSMVLV PKQGYRSMEQNRLARNNAAYL QLSDL*QT*EKHAMGK/EPPI**
8659	39027	A	8716	I	1578	MGDFNTLTLERSARQKVNK DIQELNSGLHQADLIDTYKTVKP KSTEYTFSGPHRTYSKIDHIVG SKALLSKRKRTETIJTNCLSDHSA IKLELRKKLTLQRNSTTWKLNN LFLNDYWVHNKMKAIEKMF TNENKDTTYQTLWDTFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTTHSKVSRRQE TKIRAELEKEIETQKTLQKINESKI QTTCIREYYKHLYANKLENLEE MDKFLDTYTLPRLNQEEVESLN RPITGSEIEAIINSLPTKSPGP GFTAEFYQRYKE\RPISLMNIID/ AKILNKLANGIQHDIKKLHDD QVGFIPGMQGWPNIRKSINVQ HVNTRDKNHMIISIDAEEKAFD KIQQPFLMLKTLNKLGIIDGMYLK IIRAMYDKPTANIIJLNQORLEAF PLKTGTRQGCPLSPLLFNIVLEV LARAIGQKEIKEKGQLGKEEVK LSLSADDMVYLEKPIISAQNL KLISNFSKVS/GYKINVQKSQAF LYTNRNRQTESQIM
8660	39028	B	8717	I	2982	

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8661	39029	A	8718	617	1155	SIAYQPKSPGPDGFTAEFYQRH KEELLIISNFSK/VSGYKIDVQKS QAFLYTNNRQTESQILSEFPFTI ASKRVGYGLIQLTRDVKDLFKE NCKPLLNEIKKDTKKWKNIPCS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEK^TTLRFIWN QKRDHIAKSILSQKNKAGSITL ^P
8662	39030	A	8719	1	1827	MGKKQSRKTGNFKKQRHLSFS KGIAVLHQQWNKAGQLRTFDE LREGFRPSNSYKLQKEIQTKGK EVENFEKNSDECITRINTKKCL KELMELKAKARELREECRSRLS RCDQLEERVSGMEDIENAMEMKR EGKFGEKRIKRNEQSLQEIJWDY VKRPNLRLIGVPESDGENGTKL KNTLQDIIQENFPNLARQANIQI QEIQRTPQRYSSRRA^TPRHIIVR FTKVEGKNIKGSQRERA^EIQTTI REYYKHLYSNKLLENLEMDKF LDTYTLPSLNQEEVESLNRTITG SEIVAINSLPTKKSPGPDGFTAAE FYQRYKEEVVPFLLKLFQSIEKE VILPNSFYEARII^LIPKPGRDTTK KENFPISLMNIDAKILNKLAN RIQQHIKKLJHHQVGFIPGMAI RQEKERKG^IQLGKEEVKLSLFA DDVIVYLENPIVSAQNLLKLISN FSKVSGYKINVQKSQAFLYTNN RQRESQIMSELPTIASKRKWL GIQLTRDVKDLIKENYKPLLN ^E I KEDINKWKNIPCSWSVGRISIVK MAILPKVIYRFSAIPIKLPMTFFT ELEKTTFK^FLWNQKRAR^IAKS ILSQKNK/AGGITLPDFKLYKA

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8663	39031	A	8720	I	1551	MEKFLDTYTLPRLNQEEESLN RPITGEIEAIINSLPTKKS PGPD GFRAKFYQRQYNEELVPFLKKIF QSIEKEGILPNPSFYEA SII LIPKPG RDTIKKD NFRPISLM NIAV KILN KILANQI QKHHKKFIIHDQVGF PGM QGW FNIRKSIN V IQHIN RT DKD KSHM IIISIDE FKA DFKI HLPF MLK TL SKL GID GM YLK II RAIY DKPTA NIIL NGQ KLEA FPLK TGT RQR CLS PPLL CNIV LEV LAIR QE KEIK GIQL GKEE VKL SFLAD DMIV YLEN QPTV SAQ NLL K L ISN FSK VSG YK IN VQ K S QAFL YT NN RQ TES QIM SEL PFT IAS KRI KYL GIQL TR DV KEL FKEN YKPL LN K IK E DT NK WKN IP SSW MGR NIM KMAILPK /VTW MKL EIV L VLS KLP QE QKT KHR MF SLT G V FEG RAL QN K SET S QSR HPG A THS LPE YTI PGSSPSNFYWTFLGLK EEV TSG WKREKKKR KREGG KEGRK EKG RKE GRKEG KEGRK KGR KEV P
8664	39032	A	8721	I	1983	
8665	39033	A	8722	I	2436	
8666	39034	A	8723	I	3139	
8667	39035	B	8724	I	3558	
8668	39036	B	8725	I	2133	
8669	39037	A	8726	I	3051	MGDFNT ALSTLDRSMRQKV NK DIQELNSALHQADLTIDY GTL H PKSTECTTFSAPHH TYSKIV HIV GSK ALL SKW KR REII TNCL SDH SAIK LEL RI KKL NQNC STTW K L NNLLNNY WT NK KK REK NQI DA/I KND KG DIT I NPT E QT TIRE YYK HLY YANK LEN LEEM D KFL D TYTL PR LNQEEVESLN RP IT GSE IEAI I NSL PT KSPG PDG FTA EYF QR MN YIS FK STW KII KNA YSL A HS RE LR DGG Q
8670	39038	A	8727	I	2706	
8671	39039	A	8728	I	2573	
8672	39040	B	8729	70	2029	
8673	39041	A	8730	81	385	
8674	39042	A	8731	301	515	SSWQAPAPVLGSSWASKK*MK KKYAAQQIEKQKSP*CSIKCSP LRSASYAQLLSFSLSSCLCFSTC HSTLA WYCL*SSWQAPAPVLG SSWASKRSLLWKEPSRSLPSF SITARS*ACCC LCS STEP QLL KA QYLL SHSRTRSF RLQ

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8675	39043	A	8732	2	4207	DTHRLIKKGWRKIQYQANGKQK KAGVAILVSDKTEFKPTKIKRD KEGHYIMVKGSIQQEELTILNIY APNTIGAPRFTKQVLRDLQRDL DSNTIITGDFNTPLSTLDRSMRQ KVNKDIQELNSALHQAIDLIDY RTLHPKSTENTFFSAPHHTYSKI DHIVGSKALLSKCKRKLEIITNCL SDHSAIKLELRIKKLPQNCSTIW KLNLLLNDYWWVHENMKAIEIK MLFETNENKDTTYQNLWDTLK AVCRGKFIALNA
8676	39044	A	8733	1	2770	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTKGKE VQNFEKNLEECITRINTEKCLK ELMELKTKARELREECRSLSR CDQLEERVSAMDEMNEMKRE GKFREKRKIRNEQLSQEIWDYV KRPNLRLLIGVPESDVENGTKLE NTLQDIIQENFPNLRQANVQI QEIQRTPQRYSSRRATPRHIIVR FTKVEMLKEKMLRAAREKEIQT TIREYYKHLYANKL

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8677	39045	A	8734	3	2169	FKPTKIKREKEGHYIMVKGSIQQEELTILKIIYAPNTGAPRFTKQVLSDLQRQLDSHTLIMGDFNTPLSTLDTSTRQKVKKDTQELNSALHQADLIDLYRALHPKSTEYTFSSAPHIHTYSKIDHIVGSKALLSKCKRTEITNYLSDHSAIKLELRINKLTQNHS TTWKLNNLLNDYWVWHNEVKAEIKVFFETKENKDPTYQNLWDFAKAVCRGKFIALNAHKRKQERSKIDTLTSQLEKELKQEQTSHSKASRRQEITNIRALELKEIETQKTLQKINESR TEIQTIREY YKHLYANKLENLEMDKFLDTYTLPLRNQEEVESLNRPITGSEIVAIINSPLTKKIPGPDGFTAEFY QRYKEELVPFLLKLFQSIEKEGI LPNSFYEAISIILIPKPGRDITTKKE NFRPISLMNIADAKILNKILAKRJQQHIKKLIPHDPQVGFI PGMQGW FNIRKSINVIQHINRAKDNHMI ISIDAEKAFDKIQQPFPMLKTLNK LGIDGTYFKIIRAIYDKPTANIIINGQKLEAFPLKTGTRQGCPLSP LLFNIIVLEVALARAIRQEKEIKG IQLGKEEVKLSLFADDMIYLENPIVSAQNLKLISNFNSKVGSKYKINVVKWSQAFLYTNNRQTEQNMQIM SELPFPIASKRIKYLGQLTRDV KDLFKENYKPLLNEIK EDTNK WKNIPCSWVGRINIVKMAILPK LIGNCSKISGYKINVKQSQAFY
8678	39046	A	8735	1	5166	MGKKQNRKTGNSKTQSQASPPP KERSSPATEQSWMENDFDELREEGFRRSNYSSELWEDIQTKGKE VENFEKLNLEECITRITNTEKCLK ELMELKTKARELHEECRSLSR CDQLEERVSAMEDEMNEMKRE GKFRERKIRKNEQSLSQEIWVDYV KRPNLRLIGVPESDVENTGKLE NTLQDHQENFPNLARQANVQI QEIQRMPORYSSRRATPRHIIVR FTKVEMKEKMLRAARQKAPH HTYSKIDHIVGSKAL

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8679	39047	A	8736	1	4553	MGRKNRKLDQRQHSHYTSQPSQRS HEDPAAVLQALSSSGVVIYQSL VAVQSPLAAPGCDGSRCERVG LTVGSRYSWRLAGCRDNEMV NACQSGWCYQNLTVLRGWKV LLEMTPHHHTYSKIDHILGSKAL LSKCKRTEIIITNYLSDHSAMKR ELRIKNLTQRNSTTWKLNNLLL NDYWVHNEMKAEIKMFETNE NKDTTYQNLWDIFKAACRGKF ALNAHKRKQERSKTDLTSQL KELEK^EQTHSKASRQEI
8680	39048	A	8737	1	2673	MVKGSIQQEELTILNIYAPNTG APRFIKQVQLSDLQRDLDHSHTLI MGDFNTPPLSTLDRSTRQKVNK DTQEELNSALHQADLIDINRTLH PKSTEYTFSAAPHHTYSKIDHIV GSKALLSKCKRTEIIITNYLSDHS AIKLERIKNLTQSRSTPWKLN NLLNDYWVHNEMKAEIKMF ETNKNKDTTYQNLWDFAKAV CRGKFIALNAYKRKQERSKIDT LTSQLEKELEK^EQTHSKASRQQ EITKJRAELKEIETQTKTLQKINES RSWFEEERINKIDRPLARIKKR EKNQIDTIKNDKGDITTDPTIEQ TTIREYYKHLYANKLENLEEM DTFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLPTKKGSPGPDG FTAEFY/PESYL^QTHSQYHTEW AKTGSIPFENWHKTGMPSLTAP IQHSVGSSGGQNQAGEGNKGY SIRKRGSQIVPVCR*HDCLSRKP HRLSPKSP*ADKQLQQSRLIQN QCTKITSILIHQKQTNREPTHE* TPIHNCFKENKIPRNPTVKGCEG PLQGELQTTAQRNKRGRHKQME EHSMMLGRKNQYRENGHTSQ GNLQIQCHPHQAATNDFLHRIGK NYFKVHMEPKKSPhRQVNPKP KEQSWRHHTT*LQTILOQYGSNQ NSMVLVLPKQRYRSMEQNRAL RNNAAYLHYSDLI*QT*EKQA WGKGP^IYKM\AL\GKLAS\PM*
8681	39049	B	8738	1	2792	
8682	39050	B	8739	156	391	
8683	39051	B	8740	1	2824	

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8684	39052	A	8741	3	4167	PLSTLDRSTRQKVNKDIQELNS ALHQVLDIYRTLHPKSTEYTF FSVPFHNSYKIDHIVGSKALLS KCKRTEIITNCLSDYNAIKLELR TEKLTLQRNSTTWKLNNPLLN YWVHKEMKAIEKMFETENENK DTTYQNLWDAFKAVCRGKFIA LNAHKRKQERSKIDTLLSQLKE LEKQEQTHSKATRQRQEITKTRA ELKKIEIQTKLQKINESRSWFFE KTNKIDRLLATLIIKKREKNQI GARKNDEGAITT
8685	39053	A	8742	I	1107	MKVEIKTFFETNENKDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKIDTLLSQLKELEKQEQT HSKASSRRQIQTIGEYKKHYLT NKENLEEMDKFLDTYTLPLRN QEEGESLKRPMAGSEIEAIINS PTKNSPGPDRTAEIFYQRYKEE L/PDKQLQQSLRIQNQWEKITSI PIHQ*QTNRNPNE*TPIHNCFK ENKIPRNPTYKGCEGPLQGELQ TTAQRNKRGHKQMEEHSMLM DRKNQYCENGHTAQEETAFCT HSRRESSRLGLLVANFRACHQE RFRRERSVPAGVHAEAHPCWE NRGREERHWEQHPGPETVLLQ AGGHVCDQGLHHGQPQVGQV PRGSRGHSGHFQLPSPVQDRSWL
8686	39054	A	8743	1971	5654	RSPTAGRNTNYPSPRDYKKHY A/INKLEN\LEEMDKFLDTYTLPK T/IQEVEVESLNPITGISEIVAVI NSLPTKKSPGPDGFTAKFYQRY KEELHNIRTKDNHMISIDEAK AFDKIQPQPFMLKTL\NELGID GT/YFFKIIRAIYDKPT\ANIRLE WGQKLEAFPFEKLAQEQQGMP LLNPLPQSNIIVGKFIA'RAI'RQ EKEIKGIQVEKQEVKLSLFADD MIICLENPIVSAQNL\UKLISNVS

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8687	39055	A	8744	1	4901	MTGSNSHTILTNLNINGLNSAIK RHRRASWIKSQDPSVCCIQETH LTCRDTHRLKIKGWRKLYQAN GKQKKAGVAILVSVDKTDFKPT KIKRDKEGHYIMVKGSQQEEL TILNIYAPNTGAPRFIKQVQLSDL QRDLDSHTLIMGFNTPSLSTD RSTRQKVNKDTQELNSALHQA DLIDYRTLHPKSTEYTFFLAPH HTYSKIDHIUGSKALLSKCKRT EIITNYLSDHSAIKLERIKNLTO SRSTTWKLNLN
8688	39056	A	8745	2	1887	SASVVPASGLRPSSSTLTSRQP RFLGLLRSHPAALLVPGWD DLAVCCIVAPSHVCRMVFVMD RTLGISLPGLLKREEDACCWVEA NINGRVLAAQCNIDELKEMNM NFGDWHLFRSTVLEMRNAESH VVPEDPRLFSESSSGPAPHGEP RRASHINELPHTELSSQTPYTLN FSFEELNTLGLDEGAPRHSNLS WQSQTTRRTPSLSSLNSQDSSIEI SKLTDKVQAEYRDAYREYIAQ MSQLEGGPGSTTISGRSSPHSTY YMGQSSSGGSIHSNLEQEKGKD SEPKPDDGRKSFLMKRGDVIDY SSSGVSTNDASPLDPITEEDEKS DQSGSKLLPGKSSERSS\LFQA SLK\LKGRGLRISKL\PSEEDEC GAEEDNTPLLK\DDKDRKPEG KVERVPKSPEHSVPEIRTFIKAK EYLS\DALLDNKGNSSDSWSD PRES\SPNHVSQAQCKC\ADDLPD LKRHNHIE\LEDDSHSGKRGVIPH SLSGLQDP\IARMSICSEDKKSPS RIASLD*PSSP\EEENW\PACQKA YNLN\NRTPSTVTLNNSAPANR ANQNFDMEGIRETSQVILRPPSS SPNPTT\QNENLKSMTHKRSQR SSYTRLSKESPELHAASSSESTG

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met Ind	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, -=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8689	39057	A	8746	1	385	EGNEAQTCFSWNTRRQLASS DPSLSVSRMDPSWRSSHSWP QPMPDSGRAPVRPHLAKEED VWPCPQFHQTAKAASGPPFVTFQ PANCFPSVISFHLHCHTWSEQD RAYHPVYQMR*GSDVQLLEY EASAAGLIRSFSERFPEDGPELE EILTQLATADARFWKGPSAEAPS GQ/ALRK/SVWPCPQFHQTAKAA SGPPFVTFQ PANCFPSVISFICT AIRGVSKTGLTILSTR*GNGSSE KSLV
8690	39058	A	8747	2	2015	QDFLDQSQNL SAYNTRLFKEVD GEGKPY YEVRLASVLGESEPLSD SEVTSKLKS YEFRGSPF QVTRG DYAPILOQKVVEQLEKAKAYAA NISHHQGQML A QYIESFTQGSIE AHKRGRSRFWI QDKGPIVESYIG FIESYRD PFGSRGE FEGFVAVV NKAMSAKFERLVASAEQLLKE LPWPPTFEKDKFLTPDFTSLDV LTFAGSGIPAGINIPNYDDL RQTL EGFKVN VFA GGI VLGCGLT PTK REKL TLF EEDDKDLY ILWKGPS FDVQVGLH/ESLLGHGSGKL FV QDEKGAFNF DQE TRDPQPKRG EQIQSWNRTGETW\DSKFSTIAS SY\ECRAESVGLYLC LH P QV L EIPG FEGADA\EDVIY VNWL NM VRA GLLA LEFY TPEAFN W RQA HMQARF VIL RV LLEAGE GEL VT TPTTGS DGRPDARV RLDR SKIR SVGKP ALERFL RRL QVL KSTG DVTEGR ALYEGY\STV TDAPPE CFL TL R\DTV LLR KESR KL SV QP NTHLEG N/E VSDV QLLEY FAS R AGLIRSFSERFPEDGPELE EIFT Q \LATADAR FWKG P Q*GPHGSPS LRKIVVA LPPK F H QTAKA\SGPS HSV C VFRG WGGGGAGA WTL V L\PQLEG W\HNP LPI COHVSSL P NCFPSVIL SFI CTA\IRGVSKT GL TILSTKMR\NGSSEKSLV
8691	39059	A	8748	1	519	
8692	39060	A	8749	786	864	
8693	39061	A	8750	1	468	

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8694	39062	A	8751	128	605	MWWTGTVPLFHIFQMRRCCHWSC QGIMRGWGGLCSQTLNCLLSSK C*TCSRGGGQIWSRKFRFLVRVE *GV=GNFKTPELQQPGVPPGLPP PGSCFKCRKSGHWAKECPQPGI PPKPCPICAGPHWKLCDPTRLA ATPRSPGTLAQGSLTDSFPDIRG LAVED
8695	39063	B	8752	I	615	
8696	39064	A	8753	I533	1767	PSPTCPAISYSGKGWSQRHSQG ACYTCRKSGHWAKECPQPGI PPKPCPICAGPHWKLCDPTRLA ATPRSPGTLAQGSLTDSFPDIRG LAPAGT
8697	39065	C	8754	84	329	
8698	39066	A	8755	911	1497	SQRKARDQRRKRKNRASSIAK HKEPKRPILPSGKNSQEVATH TKPLAQQGVWLDP/NETNEIPN ANFRQQIRKLIKDGILRHRKPV TVHSRAQQGWKSTLARRKGRL GIESKKIDRHMYHSLYKLKGN VFHKHRILTEHSHKLKADKAR KKPLADQAFARGSKTEARKL REEHLQTKEEIKTLSQEEAK
8699	39067	A	8756	34	280	EVIAHAIKEKKGSY/NA**PWVE EQLTRQPLIHHQPAHSLSVY/RC RYHSLYLVKGNVFKNKRLM EHHIKLKADKARKKLLA
8700	39068	A	8757	I	692	AFLLQELCLKSSTGELFFFAAV AAALSMRLQKRKLASSVLCCG KKNIWLDPNETNEITNANSRQQ IRKLIKDGIIRKPVTVHSRLRC RKNTLAR)*KGRHMGIGKRKV PANA RMP EKVTWMRENEGF CRRLASEDTRES KKIDRPHVTT ALYL EVKGNGVFKNKRL MEHI HKLKA DARKKL AD QAEA RRSKTKEATKRREERLP/APRK REII*TLSKEEETKK
8701	39069	A	8758	46	131	
8702	39070	A	8759	5	447	PATELPGLPTRPGMLCIWRGAP DWPEGPPSSGELESIQPTQGLHN CFQPDGARPAAPGPV/PQLGL PWSCRPAEPTLFMESLVQWP GDGIRQ*CEDAAELREPVGQRH QGSPG*VRTLPPLRGPSQVPA/G SSSSASPRSIPGSRG

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8703	39071	A	8760	1	201	MPNIYTMEEYYAAVKKDEFMSF VGTWMKLETIILSKLSQQGKTK HRMFSLIGTRMKLETIILSKLLQ GQKNQTPYIILTHRISFEDVRNY MPLAVIHSDESPILPLHEQQDAS ENGWIKDTTERDADELIYIVSGIG SFRWVGLADFKSEAADPCGM KLTQTEAVSVTALKGGASRVVH SSWWVCVLTDFRSEAAVLSVT ALEGAGSRAVHSSRFVVSLTSG VKLQTFTVNATAHKGSADPKS EQHQDQLLQRACKHTFHSMKGE PRRVVAAGWGGAIKADSNNL ILLFOTIEKYPWPFPDKGSV DLL DWDRVGTTLQCLMRDGVLPI SVWTDWALIRVALLPFGQSGDTL QLPQVNADVEPLPLPRCIGGIGT PEGGDPPGPSPFHYLGVVYYFLT CRSTWEQRKSPVALR**KLPG GSPPSGPVMPMPMHRGKGSGSTS ALTCGS
8704	39072	C	8761	42	179	
8705	39073	A	8762	11	1713	PKTLKMGGGTAGLVGMGFSTT G\RTPSAPGRPHPCRGA/GSPG KAGLFQLRPRLGTGL*GSAPRG PG*MGC/P/GTGRGSNSRH*RGPP RRPQAS*AAPFQPGPLETWTPG *SQVPGAPSPCNFSYPHREVPW WGPVPPPAPHGSCGWALALPR RKRAAVFSSWAPQOAGQQLDA ASVGAAP*QDIPPCRGSSAPSPC SPHPPGPLESGPK\PGAAWSAGP QTPFSGRAQQLCQEAGPAGGN TSGRSA*AASAGTCDCPRSRRGG VRVTPGLP*CRWTPGSRSSAAS SIIHCRMPSPGGI\CTRLSMKRV GSAGGRQLQGRAPS*PARGT*Q RPRGGQSGLAAPPLESRH*DGE C*AFWRAETVRSSVQRREFATG LSGPSS*PRWSTCSVP/ASSPGG GDVAGPQEGRPSFHCLPSCL*V RPSHPGEDAAIP*GALHK*RMII EEEGRPGPCGGWGLV/GSWEPV QGCRRNLLARWGRAWNCLQFPE *PPGGPGLADSGFIQ\TARLNFQ GWASVFSIKRPGRAILRPCPTS EFLLPESFVSGNCSTERAMWP FWAPPRAVGAENFPCASVPC

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8706	39074	A	8763	I	409	LTHLTAQNVPNLFARNERVICLFDTEFGPMAQILVGATIVGSIETVWAGTTTPREGIIKRWTWPAGENDGSVALLKGQEMGRFKLGS TVINLFAPGKVNVLVEQLESLSVTKIGQPLAVSM*SKATQLGNPR
8707	39075	A	8764	I	1528	MTFVNAQAEDSQIFLYKRRYVP VEGYAPWLVSQGNASELERIHYE GMDDVILLDFLPKELGFDNMN HILSFAPGANHGYIEHTFKEHG GATQAFAKENNHHKAYKDYG VSHITRHDMQLQPKQQQEKYQ DTHDTPYCEPLPGETRLWGDT DVIGLFDAETDMNDVVAILENH PLLGAGFAHKIEQLLEDKDWERE WMDNFHPMRFGERLWICPSWR DVPDENAVNVMLDPGLAFTG TIQTLSPVPAMLDSSTHRRMRSTLNLYEITRMSTVSTSEHSMTY TLVQVDMKEAQKPDASRTF NEFFVRPLRDEVRPIDTDPNVL VMPADGVISQLGKIEEDKILQA KGHNYSLEALLAGNYLMADLF RNGTFVTTYLSPRDYHRVHMP CNGILREMIYVPGDLSFSVNHLT AQNVPNLFARNERVICLSDTEF GPMQILVGATNGSIEETPESE GATVDESFVVGGPVGDFELLCC QERSALSGRCV1*SFNSAKVRFI QQSRPVKSA
8708	39076	A	8765	2	420	QNFKEIFVRLRDE/VRPIDNP NVLVMPADGVISQLGKIEEDKIVSNLFARDERVICLFDTEFWPN AQ/ILVGATIVCSIETVWAG/TITPPREGIIKRWTW/QAIEEDSWQ NLGRVAG*NKLPTELCNFDW AQTLSRNRG

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8709	39077	A	8766	1	1130	MHFAKKEDVSEIEGTSDGEKPK ARAGCLIGNSERLFSVTFCVQF QATLPLSYTIMKHKDITGTSVP ESIDASLEASQQNPAFLKTLTRS CSPSWPCSRNWPHLIPLTCPA QAGATPQLPGLGPQGHLPQMNQ PASSFPPIRPNAASQILTSTFHKP PPGSSLACCCCPGPCDWQEDSQ *PTPACPSWPPWPTQLSPSAAGS PMHSPIQGFHSQLLS*RSPGTEE P*EANKLPPWTGHREPEPHPGL PGHPCAAG/MHRPLAPTTAIRPL ATLHGERQRHLHPGQRRRVPR APAESTEAPALWLHRIIPPEC SGHGPAALEQGAGMA*CRSCR HLCPFPGEAADAGSREGPHQE PRSKICQQPQAASFICLHSIF
8710	39078	A	8768	179	1908	KKQNKSRCGNVNWAMRRAKL MCIPYRNNGHSIFLVMVVKVERS RFALKLSVAEKNQMPRNATVIE NSAGYSYKGKMAFS*PRICTQIV GPRIISTTAVIS/SQPATHHRATR GAIIRTAFCGCPFGAGDTPINNG LSIRHTTRNFPNREGSKPANGQ MSAVALMDARSIAATAANGGY LTSASELDCWDNVPEYAFDVTP YKNRYYQGFVKGATQOPLIYG PNIKDWPELGALTNDIVLKVC KILDEVTTTDELIPSGETSSYRS NPIGLAETLSRRDPGVYVSRSK ATAELENQRLAGNVSELTVEFA RIKQIAQGEHIDPLHRYVRHCS RSGNCPSDVFDSDKDQVQDHDRP QKRVTLIWGYDIHPQIEIQTG NFFQFRAIANNFGFLRFYQIRHF GLSGQHGVQIFTADVERGVGL RLQRFPVVKAIVQRQVEVIAV AHIEVQADIFTRSFRAIEANGHK VEQHFDRHPANGVRGTGGAVA ELMHPFQAQLFRAGQVETAPCG GLGLIAQLFKVIRLQILRGESKK FSANLTALKLPLPMVYEGDKV LKHLRRPKFNLPPLVQPPKML
8711	39079	B	8769	1	1881	
8712	39080	A	8770	2093	2287	

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8713	39081	A	8771	1	1358	MKINLKLNTDSKVADGGFANI VVFLINWFYIHATTCEIDNGGV VADGFQASKAYS\DSIVDYN AHYKTSVDQDAWGFVPGGD PWKKYEPAKAWSASTVYVKG DRVVVDGQAYEALFWTQSNDP ALVANQNATGSNSRPWKPLGK AQSYSNELNNAPQFNPETLYA SDTLIRFNGVNYSQSKVQKVSP SDSNPWRVFWDWTGTKERVGT PKKAWPKHVVYAPYVDFTLNNH HRRRTDSFRSKATAELENQRLAG NVSELTEVFARIKQIAQGEHIDP LQTEIGSMVYAVKPGDGSARE QAASCQRVIGGLANIAEEYATK RYRSNVN\WGMLPLQMAEVPT FEVGDDIYIP\GIKAALDNPITT FKGYVIHEDAPVTEITLYMESL TAEEREIIKAGRIRHLLSDAMLA HLIRPTNRIESVGQIRHFRSIRHL LSDAMLAHLIRPTNRIE
8714	39082	B	8772	21	1623	
8715	39083	B	8773	32	1850	
8716	39084	A	8774	1	1193	MSEVEAAAGATAVPAATVPAT AAGVVAVVVVPAGEPKGGG AGGGGGAASGPAAGTPSAPGS RTPGNPATAVSGTAPPARSQA DKPVLATRVLPGVTAKRNFNVR GYGFTNRNDAKEDEVFHWT VKRNNPRKFRLSRVDRGETVEFD VVEGEKGQAQTNVTGPRAAGV PMKGSRYAPNRRRFRTFIRPPS VAPPPMVAEIPSAGTGPGSKGE RAEDSGQPRRWCPPPFFYRR FVRGPRPPNQQQPIELTGAFACS QGTDRVEPKETAPLEGHQQQG DERVPPPRFRPRYRRPFRPRPRQ QPTTEGGDGETKPSQGPADGSR PEPQPRRNRPYFQRRQQAPGP QQAPGPRQPAAPEEAPTEAIKP MIAHDGHAPPNPsPTCCLEPSY QLVDVN

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8717	39085	A	8775	3	933	RHQESLCAPLEILQKKGCPI.E EPLQRQPCPCQSSVTA**NISF RFASPGGN/SPWASH*APSVRG AAPAGPVGLEAAAGSEPHPGP/ PDAGGARPVPVGGAGSRRPRMVL/ SPRSAPHLGGGRSA/PAARTGN PCTHTQVVTISPNLNPPIP*GAKS HPI/VERPLS*KGTGPSAQPATE NIYP*QLHGKGKPLIRD*KIVPHD GAAGQSPILLPVRSQCRGQYLPSA K*FFDALIKFTLKFLHLRRFSC TLSLRGLLVSPLLLVPVRLLLAG WAHAWMHGCGGWEPERITQQR ASCQLPDRTKSkmRVKIPAAANS SWLCH
8718	39086	A	8776	3	925	RGSEQIPPSSIPGPAP*KMLFPSG/ SSEPEHL*TVPASSLGCRCRPGGPV ASRSRPPRPPARAALRGPPASSP IRFPVGASPRAPPTS*MRSGAGS KT/TPRPGPSASGDPRPAPCVRG PGCGSEPAAAASSPTGPAGIVPRA R*GPGHGQTSPHGWW*PSSMQQ RTRRCSPSVPGQFPLLP/LSCS QVSPWTW*GLPYSLIIPVSSLLP WPEDRVPSSFA/GPLPSFDNTS LPVEFGS*L/HPVCLLYYYQENS SKHIPYSCRGSRIFPFSSQRQVM AGQRKLCDHPGGLISKPLAWT RIPEAPVVAAMVEGGGL
8719	39087	A	8777	144	503	
8720	39088	A	8778	15	427	
8721	39089	A	8779	1	1055	
8722	39090	A	8780	280	1480	FQTRMIGISVATIPGTSCSWSMR ASEKEKDFTESTVQVSKLQDLI HRSKMARCRGRFVCVPLFKKG HICRSAATLAGWGELYGR QATT YFFSGGADDAWADVEDVTEED CALRSGDTHTLFKVVRGYDIKLL RYLSVKYICDLMVENKKVKFG MNVTsseKVDKAQRYADFTLL SIPYPGCEFFKEYKDRDYMAEG LIFNWKQDYVDAPLSIPDFLTH SLNIDWSQYQCWDLVQQTONY LKL.LLSL.VNSDGQTDKSLVAI RTSVGVALAQTSGNALAYGTK KAQEQQDGLIHTSLKPTEILYL TVAYDWFLFGHMLVDRLSKG EIFFFCFNFKHITSEEFSAKLTQ RRKSLPARDDGFTLEDIC/C*DE RTVAVPPDLVCDCLPGHGEFPR

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8723	39091	A	8781	2	588	HSFFFNPNEKCSTKR<RLSASRF PP*PWSRLPSG/QPAGGAGASAGSP SAPRGTRGRGAGSRPAHG/VQPP RAHPEACPACPRSVGGAR/RA PEPSSNLSGEAPASGDRDVPVPPPS PLAR*VPLGGREFGVWPWANAA LRPGKTP/RSDRVS\RSRWS\PAG FSPVSPASWPRRSTSGNRGPPSRPS RLSRTSGPLNRLGEPFDVQGPL
8724	39092	A	8782	1	198	
8725	39093	A	8783	1	275	MAGA PAPASLPPCSLISDCCAS NQRDSMGVGVPSEPGAGYNLVP V\EKRSIRVGVTGFSRCCPSPLSL TRKGNSLTPWASQVRQCLAIL QLAH
8726	39094	A	8784	349	478	KLSKFPYTEELSSGLYGIGSLCP HKYNCLVSSHRSRKNV\VTGY
8727	39095	A	8785	1	325	FSEGNSYLVGIMHPLKAMLPGL QQQTETFPFGYLM\PCRLQQQ SHLLTLRDCCASNQRDSVGVG SEPGAGYNLVVRRFLSLEKRSI WVRVTRFSSAI.NHELKVNNDH
8728	39096	A	8786	113	313	
8729	39097	A	8787	2	1991	
8730	39098	A	8788	512	1178	
8731	39099	A	8789	135	1562	DTLVPTSQGDISRGLEGNLNSC PT*Q**RAPFLWCQ/PKAEGWT WIFNPEAEESLEPRSLISDCCAN NQRDSGVGPSEPGAGYNLVV RSFLSPSEKRSVRVGVTLSRCR PSPLSLTQKGPNLTPCASQVRQ CLALLRLRHVYFYNFQGWKDYG VASLTTILDMVKVMTFALQEG KVAIHCHAGLGRTVLIACYLV FATRMTADQAIIFVRAKRPNSIQ TRGQLLCEAQQSAGAFSADVSGS HSPGEPVSPSFANVHKDPNPAH QQVSHCQCKTHGVPSPGSVSRQ NSRTPRSPLDCGSSPKAQFLVE HETOQSKDLSEAASHSALQSEL SAEARRILAAKALANLNESVEK EELKRKVEMWQKELNSRDGA WERICGERDPFILCSLMWSWVE QLKEPVITKEDVDMVLVDRRAD AAAELFLLEKGQHQHTILCVLHC IVNLQTIPIVDVEEFLA.HAIKAF TKSIIIFVNQNPEVTVLL
8732	39100	B	8790	563	2017	
8733	39101	A	8791	108	194	
8734	39102	A	8792	1	164	

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8735	39103	A	8793	1	1068	MEESRYWGTGRNRREGLKLQ WAQPAPLFNIRQQGPNEGDNQQ GSYWEALASIMQIHLVPSGLG MVTAFHCSWYLSTTATFPGVL NPALTEIKSGNYYVHGSFILQV ADYKEFQTLLMITKATFHQKTQ CWACEEGVQQSFHCPCRMQAA ASVERYTELLKEFLKEHTCDN QEPTISTLHYHSKLTVHIIHVYSS RCTLPCQPSQAQAEISOPAP ACEDFVFAALAPP/ESG/RCPTL RLLGQLCTPTNARRTRTHSTTA CWARAQWDSLGPLKLSHRIPR VCGGTRAPGRQGMNCRLGT SNSEARDPGGLRVKH/CEAIQ EPPNRSRRQGAPLHSPAY^MS SWRP^FSKSRHNL\$
8736	39104	C	8794	78	331	
8737	39105	A	8795	129	1734	QWMHRMLDIFKGSSQHPSPVPR VSSRPLLPGPQGYSLHHFGTQGI HSATPINTQGLQPAPMGTQQPQ PEGKTSAAVVLADGATIVANPIS NPFSAAPAATTVVQTHSQSAST NAPAQGSSPRPSILRKKPATDG MAVRKTLIPPQPHDVASPRVES SMRSTSGSPRPAGAKPKSE/STC LWPLRSLCPWRLYP1K1M1S1PL PSLKLPSSPHRPFQL*LQQPVPR HNQQLPFPQPFERSPLSHPSQPL HCTTSISHCGWQSFLRLGPRSR* N*SERRSRTNGYHEASFVSPPL ATNTVSPSLALLANNLSMPTSD LPPGASPRKKPRINNSMWISTEE GDMMETNSTDDEKSTAKSLLV KAEKRKSPPKKEYIDEEGVRYVP VRPRPITLLRHYNPWKAAYH HFQRYSDVRVKEEKKAMLQEI ANQKGVSCRAQGWVKVHLCAA QLLQLTNLEHDVYERLTNLQE GIIPKKKAATDDDLHRIELIQG NMQRCKLVMDQISEARDMSLK VLDHKDRVLLKLNKNGTVKKV SKLKREKEV
8738	39106	A	8796	1	169	RPTRPKSNKRQCLVFVTP/KEE EPVRNILEKFNTISGSKVRSLYL HAPLLPLER
8739	39107	B	8797	156	398	

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8740	39108	A	8798	20	723	VWGGEFLPRIWFMLPTSHQWM LFSVFLGWGSCQWCSCHLLSCL WRAAFSEFPLGPEPGEGIGPELC LCFQMEAIELSVDPKSNKRQCL VFVTPKEEEPVRNILEKFNTISG SK/CTEVQRGVIVYGHIR*R**SI PRGF*FYSK*GRPDSAGGHGPG GVLQGEKGHSACARQGGRFQE GAAFAQRETAGRKRVGQRWC DCFRITPVHRKSLSSPNFGGFGA GSEAVPCHLVLYLVW
8741	39109	A	8799	79	256	LRLTLLFFQNLLGGKSSMLWTA HPCPEGACSSSCTSLSGHLLSS FPVLR*PGPSGDH
8742	39110	A	8800	402	996	TFFKFPPDSGAQLASPRGSRIGA AGGAA ⁻ S ⁺ PEPSAALLSPWVVD GTGRPGAGGGARRGGSGCTGA HGGGGSSGM/VG/PAGPEPCPA GRQLRPGEKSSAAPLREPASAL AGPERGSHSAAAG*RAPQIGRQ SGSPRGGAESERGL*GLPSCC HLSPGSAAAVPRSVGSRWPC GA ⁻ PTLATPPTSASFFSAATPEGP PLAS
8743	39111	A	8801	7	602	TFFKFPPDSGAQLASPRGSRIGA AGGAA ⁻ S ⁺ PEPSAALLSPWVVD GTGRPGAGGGARRGGSGCTGA HGGGGSSGM/VG/PAGPEPCPA GRQLRPGEKSSAAPLREPASAL AGPERGSHSAAAG*RAPQIGRQ SGSPRGGAESERGL*GLPSCC HLSPGSAAAVPRSVGSRWPC GA ⁻ PTLATPPTSASFFSAATPEGP PLAS
8744	39112	A	8802	262	349	KEGEGGK\PD*PVRCMCPKPSG HWKHPGE
8745	39113	A	8803	2271	2863	GGASGVVRSSWWARGLAGFRS EAADLRLGLPVELRASPAPCVRT PQPLGGRIGIGRPGAEAGGSSLQGP GSGRTGAHGGAEAGGSSLQGP RKGLPQCSGG/PEGLLKCGQSG SPGRGRAQSERGL*GLPACCHL SH*PQGRQI*PRTCPTPFQSCKTS DQGGPSGPAVSGSERQV*LHHQ *PGCRDYLCPFCWEINPVG

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8746	39114	A	8804	3	561	NCPSLLVESCFQECGSSIPFALPS TQVEHALYASER*QRAGSPHPSP HSLSVPLPGLPLWRLHRSPS/G PPLH*PP*ASTLTGGPQ*RLGSA GINVSSEPVSSEPNV*SFPPFQY TVTLLVKGWRSRREPSPKSVLGS/ MVP*STKSEP*REPPP*SLTGKA GERGEKGREKAIGSGR*GVAKC SDHVR
8747	39115	B	8805	298	380	
8748	39116	B	8806	1	1292	
8749	39117	A	8807	1	1224	MKPRTLAWSVTALKVARLEFV PSDVRMCSEFLPSGGLVVSLAS GVKLQTFAVSVTARNSDPKN SGAQLASPGSSTRAASGAAC* SPSPPPCARTPQPLGGRIGTGC GAGGGTRRGGSGRTGAAHGAEE GVGSGLGQPRKGPTVQWWAE GLLKCRQSGSPGRGGAESKRGL *GLPASTLSPPPGIECAGKSENS HMNLNCSSGGLGPGTGAHLPL GPDSGQPAETLLWGPCCGPG TGTGSGQTISLGCGGGQPRRE VKPPVPQRVSLLVAVVNPPDS RCRVETDRPWRLCIQSCLCGTL KRDVLHSPSVFNTTRGGTAE WSREDKDALLPEYALHMPFAV GFKLEYKEGVVLGSNLAAGPEK ELCEAKRNQCPKSGVGSHTSRPL KPEWSDFVAEIDESKLPLDRS
8750	39118	A	8808	1	1298	ESLRAGSFQQEIQPTELAPLIIH FGTWPGWSFQATGFCVGVVRGS PGSGFRGCGAYRAP*SFRTQLW PWQPLQGLDPKPLKDARLPSPL GRRACEAHILCSADERPDLGFE GLQRWGGCRGSQGKPAVHQ WGRCEGETGGGHTGSPPPRLTP P/PGPSFRAQPGERRPAACGQ QRALGPMRPPPA/C/GPSPT*GCA LNPTSPPAPLV*GFIHIVAAFCSF VTPVSKSHSFQLGELRVAQSD VGRWGERENTQGSTLPPSSPAS SPGSPSPDPATPPGPATPGLIDIL LLLPMVASSSRKHDFVSGSGRDL PQGEFFQ*GPTGWQSVVWPLD PSYLGCGQGGCGQGPRTGRRG ASSHCCVPAAP/GLSMDCSRGS GGSPPRSPPWALLGDLPLSSLET VCLVMMPCPWIWMASEFAMEI QLLGPFWQIMLIGLCW

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
8751	39119	A	8809	2	662	RIPLLVTRLKINEKVLQLVLTNIF LFHDFSVQNFIFKGLQLSLEHFY SQPLSVLCCNLPEAKRINFLSN NQCENIRRLPSFRRYVEKQASE KQVALLTNERYLKEETQLLLEN LHVVYHMNYFLVLRCLHHKFSS LPKYPLGRQIRELYCTCLEKNI WDSEEVAYASVQLLRLMLAKDEL MTILEKCFKGFKSYCENHLGST A*RIEEFLGOFQSLDEPRGR
8752	39120	A	8810	326	1215	NPILHGDNFIFMLDHSLSKKNVQDQE E*TLM*/HYGPQVVTCMCQCSFIE RNKRIPVQQGIRRRGRGHVQWG RYVEKQASEKQVALTTSERCL KKETQLLLENLHVYHMNYFLV LRCVHKFTSSLPKYPLGRQIREL YRTCLEKNIRNSEEYASVLQLL KMLAKDELMTILEKCFEVFKSS CEKHLGSTAKRJQEFLAQFQSF DETKEANEALKREEGCIPNITPDI CIAYKLYLECRRLINLVDYSQA FATILTAAEKMDANSTSSEEMN EIYYAWCIRTVFELELLGFIFKPTK QKTDHVARLT
8753	39121	A	8811	70	613	SLLEMKELRRSKKQTKEVLR NVVNFIIDLVLREYLLPPEIQPL HEVVYFSAAHALREHHLNAAPRI ALHTALNNPPYYLKNEALKSE EGCIPNIAVPDICIAYKLHLECSR LINLVDVSEAFATVVTAAEKMD DANSASSEEMNEIIHARDIRAVS ELELLGFIFKPTKQKTDHVARLT WGCG
8754	39122	C	8812	598	762	
8755	39123	C	8813	138	296	
8756	39124	A	8814	1	395	

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8757	39125	A	8815	2	1289	DDLCALAFKVLHDKQRGPTGYAPFNSRPL*KPQLAHSIIILMETATERISRLLLPFADQHVEIPSLTAGNIALTVGLKHTATGDTIVSSKSSALLQLVEPNGREKRSTDKTMKAERLLLGSRGFQEPVFC TIGTPITV*GSQIWEHAFEMSFSVRIPVLIKVRLDPPDSGQTVLCLGMGELHIEIIJDRIKREYGELEYLGPLQVAYRETIILNSVRATDTLG*EL*GDKRHLVDLLGSGKARPIETSSVMPVIEFEYAESINEGLLKVSQEAIENGHSACLQGPILLGSPIQDVGNYLYIP*QIHPWAPSTTYDFCLCLKMPCKKALERKADKQVLEPLMNLEVTVARDYLPVLA DLAQRRGNIQEIJQTQRDQNKV VIGFVPLAEIMGYSTVRLTLTSGSATFALELSTYQAMNPQDQNT
8758	39126	A	8816	545	849	LAIHLSSLISRHDEATRTSSEGLEEGEVGETLIVESEDQAFS/VDLSDHQSGGISLNSDEGDVSWMEEQLSYFCDKCQKWIASKELLNSFDLSIPV

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8759	39127	A	8817	1	2395	MDSSIHLLSSLISRHDDEATRSTSEGLEEGEVEGETLIVESEDQASVDSLHSDQSGDSLNSDEGDVSWMEEQLSYFCDKCQKWIPIASQLREQLSYLKGDNFFRTCSDCSADGKEQYERLKLTVHQVVMLALYNLSLKGSGGRQGYFRWKEDICAFIEKH*TFLLRNRKKTSTCRSTGAGCLSVGSPMYFR*GA*EFGEPRWWKLVHNLPLTMKPEREKTAASTLNIfAASKPTLDPII7TVEGLRKRA8NPV8ESAMELKEKR SRTQEAKDIRRAQKEAAGFLDRSTSSTPVKFISRGRRPDVILEKG EVIDFSSLSSSDRTPLTSPSPSPSLDFSA8PTPASHSATPS8LSEADLIPDVMPQQALFHDDDEMEGDGVIDPGMEYVPPPAGSVASGPVVGGRKKVVRGPEQIKQVESEEEEKPDRMDIDSEDTDSNTSLQTRA REKRKPQLEKDTKPKEPRTYTPV SIYEKKLLKRLEACPGAVAMTPEARRLKR\KLIVRQA\KRDGLPLFDLDQ\VVNAALLLVLDGIYGAKEGGISRLPAGQATYRTTCQDFRILDYQTSLPSRKGFRIHQ\ITTKFLYRLVGSEDMAVDQSIVSPYT8RILKPYI8RSDPHWTP8EPDPLDYCYVRPNHIPTINSMCQEFFWPGIDU8ECLQYPDFSVVVLYKKVIIAGFMVPDVVKYNEAYISFLFVHPNWARRAGIATFMIYHL
8760	39128	A	8818	3	364	GDSVPTAEGGDQCVLSSVPQTVWEPMFNKRACG/P*SP*SLSA TSIYPRELKAGTQKDTCPVFR AVLFTTATQCPSTDAWMNKM WYSRTMECYSALKRKEIPPHTARHPMCLQFCRW
8761	39129	A	8819	292	508	ARPGDQATSGGQGTTFQHPLFC FELGGSQNPALQ*PFAAACPVG AD*TKFTFAFCCR8LK*KRTCCL SLGSRC
8762	39130	C	8820	253	369	
8763	39131	A	8821	295	393	IYFGCLLGEPVVA\EA8I\WDN DCVKKQLLHSW
8764	39132	B	8822	91	479	

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8765	39133	A	8823	I	544	ARHPDMKKRVEDASILPCNVSL EYEKTEVNSGFFSKSAEEREKL VKAERKFIEDRVKKIELKRKV CGDSDKGFVVINQKGIDPDFSLD ALSKEGIVALRRAKRRNMRFLT LACGGVALNSFDDLSPDFCLGH AGLVYEYTSPACPKQSGLCILSS TLGEEKFTFIEKCNNPRSVTLLI KGPNKHTLTQIKDAVRDGLRA VKNNAIDDGCVPGCWCRGKW AMAEALI*P*APVLKGRAQLGS PKHLLDAAFAHYFPKVLCFRNSG FLTFQGNIKLKFKAEHSRQVQL VGVDLNTGEPIMVASSRKAQAVW GHT*LW*KKTSLPSTPCTW*IA\TN ILLGLNNEIMRAGMSFS*KGF VVINQKGIDPDFSLDALSKEGIV LRRAKRRNMRFLTLAGGVAL NSFDDLSPDFCLGHAGLVLYEYTS PACPKQSGLCILSSTLGEEKFTF EKCNNPRSHI*DQRTK
8766	39134	C	8824	636	1025	
8767	39135	A	8825	33	1505	KCISASVKVDFSDLLLSSNNTS*S AFTPTRTQKSSSKLLRKESHYS GMMSIQEKSKENNSKVTKKSD DKNSETEIQDSQKNLAKKSGPK ETIKSQAKSSSESKINQPELETR MSTRSSKAASNDKATKSINKNT VTVRGYSQESTKKKLSQLQQKL HENPKANEQLNRRSQRLLQQLT EVSRSSRLRSREIQGQVQAVKQS LPPTKKEQCSTSQTQSKSNKTSQK HVKRKVLEVKSDSLGED/GKSSN **SNKFS/SKGKNAR*NIR/SACA CSSQCTQGSEKCPQKTTTRDET KPVPTSEVKRSKMATSVVPK KNEMKKSVHTQVNT/KHNTPK KSTAISA*TK***AGASRKEQTR *YSPAVEREIAGEIIESDNVEVK ESSQMESVKEEKPSIEKLEETSV ERQILHQKGTNQDVQCNRFFPS RKTPVKCILNGINSSAKKNSN WTKIKLSKFNSVQHNKLDSQVS PKLGLFTNQFFTTSFRNASSSDS KYIFRDKAT
8768	39136	A	8826	I	394	AISRALGRYVLFPCLIQDGIVFA HTAHAILTSLEDDSL*MFQPKTC WCLVAN*HDTLSVNMETPHPSF QEELSGLLLKMLRSPIEASKD KDKVKSNAVRALGNLHLHFQP SHIE*PTFAQINEEAIQALIS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met codon	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, -=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
8769	39137	A	8827	52	730	KSACDALSSILPPEAFRNLPNDR QMLCITVLLGLNDSKNRLVKA ATSRALGVYVLFPCRLQDVIFV ADAANAMVMSLEDKSLNVRA KAAWSLGNLTDTLIVNMETPD PSFQGRVLWSPALENQYDQAL EASKDKDKVKRHAVRALGNL LHFLQPSHI/GKTPHLQKF!*GSL SRALNPLL*QKLAMKVRWNA CYAMGNVFKNPALPLGTAPWT SQAYNALTSVVTS
8770	39138	B	8828	47	1576	
8771	39139	A	8829	2	2753	
8772	39140	A	8830	1	273	
8773	39141	B	8831	104	206	
8774	39142	A	8832	1	987	
8775	39143	A	8833	111	2187	DERRVGAADMFGGRSRSWVGG GHGKTSRNIHSLDHLYKLYHVLT KNTTVTEQRNRNLLVETIRSI TEIWIWGDNQDSSVFDFLEKNMF VFVFLNLRQKSGRYVCVQLLQT LNIFENISHETSLYYLLSNNYYV NSIIVHKFDPSDEEIMAYYISFL KTLSLKLNHHVTFFYNEHTN DFALYTEAIKFPNNHPESMVRIA VRTITLNVYKVVDNQAMLHYIR DKTAVPYFSNLWVFIGSHVIEL DDCVQTDEEHRNRGKLSLDLVA EHLDHLHYLNDLINCFLNDV LTDHLLNRLFLPLYVVSLENQD KVFLIIHHAPLVNSLAEVILNGD LSEMYAKTEQDIQRSSVLPTLSS LWQGS HLSLNQLQSGLHKCSS HLCGAQAAADSVTGEIPAIRSL EWLISAGSKARTFFFKLKMLIGF WEKVVDCEYQRQQVLSLRLQEA LPSNRLTDVAAVHSSCMLGFGS TAPRGWSWIGDPAAVHLPPLPGEL AEHLGSKGTTTVTKHQPKAQKPS IRCEFIKPTETLERSLEMNKHKGK RRVQKRPNYKNVGEEEDEEKGP TPTEDAQEDAEEKAKGTEGGSKGI KTSGESEEIIFMVIMERSKLSELA ASTSVQEONTTDEEKSAAATCS ESTQWSRPFLDMVYHALDSPD DDYHALFVLCLLYAMSHNK/G KSPEKEEGLSGTQSHPGKAGTF GKEGAERKRAQV

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8776	39144	A	8834	1	3050	RNLLVETIRTSITEILIWGDQNDS SVFDFLEKNMFVFFLNLRQKS GRYVCVQLLQLTNLNLFENISHT SLYLLSNNYVNSIIVHKFDFSDEE EIMAYYISFLKTLSLKLNNHT VHFFYNEHTNDFAKYTEAKFF NHPESMVRIVARTITLNVYKVSL LDNQAMLHYIRDKTAVPVFSNL LVWFIGSHVIELDDCVQTDEEH RNRGKLSOLVAEHL.DDHLHYLN DILIINCEFLNDVLTDHLLNRLF LPLYVVYSLEN
8777	39145	A	8835	111	270	
8778	39146	A	8836	240	406	
8779	39147	C	8837	86	286	
8780	39148	A	8839	172	243	DPS*EARSMLLLFLPDPDHSGLP H
8781	39149	A	8840	280	526	GRNAVVQSAHCRSQTPGPK* SL/LVPSSWTYRHMPHLAN* KKFFLHRDGGDLMLPRLVWNS WPQVILPPQPKALGLLL
8782	39150	A	8841	3	1785	VLDARNAGAGGLAGPAGVLRG RASCRDPGAAGVGAGQGGARVR PGRAAAPSPGPPGGA*CVPTDA GAGPGSAGARQPLPFAAGALS HSGHC*RGLRGPGSLASPAQAK AAWSGLLSPAAAAGRDRGRGH NPRDPPPRLREHGPGP PGFHGDR G*ELYQCHLGEGG GPDKPGS PCASCLGHDHWYRALLLETFRP QRCAQVLHDYGRKELVSCSS LRYLLPEYFRMPVVTYPICALYG LWDGGRGWRSRSQVGDLKTLIL GKAVNAKIEFYCSFEHVYYVSL YGEDGINLNRVFGVQSCCLAD RVLQSQATEEEEPETSQSOSPAE EVDEEISLPALRSIRLKMNAYD AQWKENGYYRAITVKLDDDKSV DVFLVDRGNSENVDWIINMLL RELTNQEQQEETISKVIAQAGY AKYQEFETKENILVNAHSPGHV SNHFTTESNKIPFAKTEGEQEKG AKRENKTTSVSKALSDTTVVTN GSTELVVQEKFVKRASVYFPPLM QNCLEIKPGSSKGGELEVGVSTVE VRVSYVENVPGYFWCQLTRNIQ GLKTLMSDIQYYCKNTAAPHQ RNTLACLAKRTVNRQWSRALIS

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8783	39151	A	8842	2090	2901	THLLVPGMQLTWQMPFSPFLS ISPTRSNLPSAATPVIAQW/A/HE QSGHGRDGGYTWAAQHGLA FTNTDLA/TVNAAKIGFAYPVCDA SAKTTIRGLLECLIRCDGPHSIA SDQARIHRSRNQEVEVEVAPLT ITPSDPLAKFLLSVPVTLRSAGL EVLVPGEGMLPPGNTRTIPLNW KLRLPGHFGLLTSLSEAKNG VTVALAGVIDLDYQDEISLLLHN GKGKEYARNTGDPLGRLLVLP CPVIKINGKLQQPNPGTTNGS DPSGMKV
8784	39152	A	8843	1	585	
8785	39153	A	8844	1	1697	MDKYFMIKTPKAMATNTTIDK WDLIKLKNFKCTAKETMIRVNR QPIECKKMFAIYPSDKVILLFKM APKRNAEGLSTVSTCKKAAMC LIEKGCGELVGPVGPQTHPVVT S PVSECIIGIDILSGWQNPHIGSLT GRVKAIMVAKDKLKPLPELPLPG KIVNQKQHCIPGWIVEASITKD LKDAVIGIPTLPPFNSPIWPVQK TNGSWRMTVDYHKLNNQVVTPI AAAVPDVVSWEQINTSPGTCL HWWPHGEFPRLVDREERTRTW FTDGSAQYAGTTQKWTPAALQ PLSRTSLKESECFIHHHGIHPSIA SDQGTHFMAKKVRQWAHAHEI HWSYHVPHYPEAAGLIEKWNG ILKPQLQCQLGDNTLQGWDKV LQKALYAALNQHSVYGTISPIAR IHRSRNNQEVVEVTPLIITPTD PLAKFLLPVPSTLHSLEVLVP EGGMLPPGHTAMIPLNWKLRL PPGHFGFLLLPLSQQAKGVIVL AGVIDLDYQNEISLLLHNGKE EYALNIDPGLGHLLVLPCPVIN VNGKLQQPNPGRITNGEDPSG MKVCVTPPGTTTTKKP
8786	39154	C	8845	1	720	
8787	39155	A	8846	57	261	WNF/CDPGGPMMKL\IFISFLKT ISSTFLSPTCLVL*RRPSRSASSL TVLCTTTRSSSPLLGALV*TWP
8788	39156	B	8847	1	1158	
8789	39157	B	8848	1	2523	
8790	39158	A	8849	3	375	
8791	39159	A	8850	3	169	DFQPFTRVTVHWGKGNQJFR GLLDTGSELTLIPGDPKHHYGP PVKVGAYGAQIL
8792	39160	A	8851	3	376	

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8793	39161	B	8852	1	592	
8794	39162	A	8853	1	319	
8795	39163	A	8854	1	1071	
8796	39164	C	8855	1	862	
8797	39165	A	8856	1	1488	MGRARRLTPVIALWETEADGS RALTVETTVTQLQHLNTVGII FRGRRGQVAAVNCQKRDQPF TRTVHWGKRNDQTFQALVDT GLELTLPGDPKHHCDPPVKVG AYGHQVINGVLAQIQTIVGPVG PWTHPVVIFTVPKCIIDIDLW QNSHTGSLTGRMKAIMVGRAK WKPLEPLPLRKTNVQPKYHTPV GTAEISATMKDLKDAGVVIPTT TLFNSPIWSVQKTGGSWRMTV DYCMILNQVVSAVEAIVLDVVS LLEQINTS/P/WP/SGCTAAFH QMEVVHT*SGSSRS*RHNICTN GLMGFSFL*SVDRGREDVGLVH RRFFTC*HHPKLDSCSTTVPF* DIEPGQL*REI/PPPPVSWRQGWR LCMGSATWTFTTHQG*PGYGH *VPNLPAETNTEPSIWIHSSG* SASYLVAG*LYGTSSIMERAEV CPHWNRHLF*IWVCLSLCTLCF C*DYHPWTLEMPPYPPSPYSTKL CCCPRLHYG*RSAAV
8798	39166	A	8857	1	1056	MSSVLLRLIYQLTQKTAASFEGG PEQKALQQIQAAVQAAALPLGPY DPANPMVLEVSVADRTVWSL WQVPIGESQRSLGFWSKVLPY SADNYFPFERQLLACYWALLETT DRLTVGHQVTLQPELPMNWV LSDPSSHKGVGHVHQHSIIKWK WYIRDQTRAGPEGTTTPVITQ/ WDAHEQSGLSGRDGKQGRFV LTGVDTYSGYWFAYPAHNASA KTSIYGFTTECLIHCHGIPHSIASD QGTLFTAKEVWQWAHAHGIH WSYHIPHHPIAAGLIEWWNGLL KSQLOCQLGDNTLQGWGKD QKAMYSLNQRLIYSTVSPISR GSRNRQVEVEVAPLTTLSPL AKFFFLLP
8799	39167	B	8858	603	1785	

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8800	39168	A	8859	3	467	RIHVRPEITLTANTARPY*IDP HDTLLSHSNFGSSDCPSSKMR QALELVRERAPELMIDGEMHG DAALVEAIRNDRMPDSSLKGSA NILVMPNMEAARISYNLLRVSS SEGVTVPVLMGVAKPVHVLPIASVRRIVNMVALAVVAAQTQPL
8801	39169	A	8860	1	1878	
8802	39170	A	8861	3	684	MPNYLRFVRGLIDSSDLPLNVS REILQDSTVTRYLRNALTKRVL QLLEKLAKDDAEKYQTFWQQF GLVLKEGPAEDFANQEIAKLL RFASTHTDSSAQTVSLEDYVSR MKEGQEKIYYITADSYAAAKSS PHLELLRKKGIEVLLSDRIDE WMMMYLTEFDGPPFQSQSVKVD ESLENLADEVDESAKDAEKALT PFIDRVKALLGERVKDVRTHA GSGLVGENV
8803	39171	A	8862	2	393	LEFGKKLGNAAADYFIANKIDQ PKIAVINCEAFEVCVQRKGFE EVLKSRRVPGAQIVANQEGTVLD KAISVGKEKLIISTPDLNAIMGES GGATLGAVKAVRNQNIRPEKLF LFSVRI*QPKLLRSWKTJRC
8804	39172	A	8863	414	805	TPSRVEGNQEYPSLVYI/PSQAPWNM*TRDHKHGLNLNVQRVFIMTDAEQFMPNLYRFFVGGGLIDSSDLPLNVSREILQDSTVTRNLNRN ALTKRVLQMLKEKLAKDDAEKYQTFWHQFGRGIIFTDSQFNRL
8805	39173	A	8864	3	684	MPNYLRFVRGLIDSSDLPLNVS REILQDSTVTRYLRNALTKRVL QLLEKLAKDDAEKYQTFWQQF GLVLKEGPAEDFANQEIAKLL RFASTHTDSSAQTVSLEDYVSR MKEGQEKIYYITADSYAAAKSS PHLELLRKKGIEVLLSDRIDE WMMMYLTEFDGPPFQSQSVKVD ESLENLADEVDESAKDAEKALT PFIDRVKALLGERVKDVRTHA GSGLVGENV

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8806	39174	A	8865	1	624	AKLIRFASTHTDSSAQTVSLED YVSRMKEGQEKIYVITADSYAA AKSSPHLELLRKKGIEVLLSD RIDEWMNMVLTTEFDGKPFQPG AKVDESLEKLADEVDESAKEA EKALTPFIDRVKALLGERVKDV RLTHRLTDTPAIVSTDAD*MTP RMAIKCFGAGQKVPEVKYIFE LNPDHVLVLRVADNEEEAKF CVWGKNCVLGP
8807	39175	A	8866	471	659	
8808	39176	A	8867	638	834	SSNTMMHFQIHMKQESTEQQT MTARR*Q*SEVDE*REDTTLAA RGRTEA*SARYQLT*QSVPSPH
8809	39177	B	8868	1	1383	
8810	39178	A	8869	4452	4896	SQHSEVFVCHMLSQPRAPGAG RYL/LQRKA/SEALEVEV/VDTW QADAVRDTRTLSGGESFLVSL ALALALSDLVSHKTTRIDSLFLD EGFGTLDSETLDTALDALDN ASGKTIGVISHVEAMKERIPVOI KVKKINGLGYSKLESTFAVK
8811	39179	A	8870	31	185	GHRRRPFKRGRKSR*RGGSQRR VNEDARRSAWMRKKQRLISK ISDRTARK
8812	39180	A	8871	1744	2670	

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8813	39181	A	8872	1	1680	MGFWVNEGIQYPVSEITIAVSS LVFSSASFAADLEDNMETLNDN LKVEKADNAAQVKDALTKM RAAALDAQKATPPKLEDKSPDS PEMKDFRHFIDLVGQIDDALK LANEDVFTRTLGADALYQFQNI RHVLRMQRRIAAGEGNTLAFDT SVIQIVNDLVFHCFGKWLTGYI PPCAFVIATGAFMNTPGDKQGA TSAGAVDDVDRISNEITIGPML TGYILLHVKGVRAKSSADHRR RPLASLATPPHKSWTCLLFFR LPNVVCYANRJQQLTPILETPQ SDELPHCEETVYLENWRQVHE QCLALHSQQQTLQQQDVLAAQ SLQKAQAFDFTALQASVFDQQ QAFLAALMDEQTLTQLEQLKQ NLLENRRQAQTLVTQTAETLA QHQQRHPDDGLALTVTVEIQI QELAQTHQKLRENTTSQGEIRQ QLKQDADNRQQQTLMQMIAQ MTQQVEDWGYLNLSIGSKEGD KFRKFAQGLTLDNLVHLANQQ LTRLHGRYLLQRKASEALEVD VVDTWQADAVRD/TRTSGGE/ SFLLRLR*VTRRHQLWLHPLRH
8814	39182	A	8873	3	823	
8815	39183	A	8874	287	426	YSGLSAVNPNVNDAYGVRFQLP SVNRIPVS***VKLAPPAAHQIKRI SGKCRFIPLC*YAPPGFSSASTM RATGILSTASQPPGKLCMEEST AERRVGLPPLAKW
8816	39184	C	8875	1	2058	
8817	39185	A	8876	1	1989	
8818	39186	B	8877	1	3132	
8819	39187	A	8878	194	789	LTKLPSLFTFTRLSSSDNDLRGG DKRGGANGARLAL*PQTRGD VTRRQPIRVCTVIEMFELLE/PIA DGFRNYRARLDVST/TESLLIDK AQQLTLTAP/EMTALVGGMRV LGANFD/GSKNGVFTDRVGVLS N/DFVNVLLDMRYEWKATD/ES KELFEGRDRRETGEVK/FTASRA DLVFGGSNSVLFVRILGGFFCEYS LTIRILH
8820	39188	A	8879	1120	1395	

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8821	39189	A	8880	I	629	THRPPKGPPCAKIKTRTHVTA KPLFPQTNPKQTVRRMKGELY LVDESGQEFVSLANYYRRRKTR NNATAYPIRLFYLSPRPRAGSK SSRTIWILLAD/AKITPYERRQL VARIEA/LSTEIPAPAQRVLQYQLW RDGQALQLQLAERQR/YTGG ADTKQDGATTTKDKQQR/*TKG TRSQPSTREVQQQSTQKHSTSR PPNHSAQPSNSALVTRQ
8822	39190	A	8881	3	307	
8823	39191	C	8882	161	337	
8824	39192	C	8883	34	168	
8825	39193	C	8884	172	456	
8826	39194	A	8885	174	516	VSGVRCWIHSSAFPPVPGFFLP VAFFDRPPARLYRMHTWSHME SQEPARLPSHYAD*GQGSQKR\ DSCSSGWAGLLFISPQFVLSWA EIEGSLNHTILGFRLSHGTTSD GMTF
8827	39195	A	8886	I	2964	
8828	39196	A	8887	I	2724	
8829	39197	A	8888	3708	7098	
8830	39198	A	8889	115	339	
8831	39199	A	8890	445	634	VINTFSLHTMGSTS*HQGNWR HLTLHPRNSKHPLEOPTGVLQ LRPTASLRQLLSNAGCSG
8832	39200	A	8891	1663	2234	GEGLRRGLFPGAEEAQGRAETA GCLRRGRGALALALPGSPGLSP WVEDAGGHRLVHGRAVLRCA RAPPVPQAGLAKVEPYSGVVSS LTAFPQAPILLSSGGQSRAGET TM*G*PEMEKL*SCIGEHQPC HRKSRPAACPSSMLFLTPR SSATLLSSSSKGAGGGWEPSAA PLGGSGQPFREMVVSQH
8833	39201	A	8892	202	542	
8834	39202	A	8893	564	1179	QHRLTYRTALWIHYRDPKPL MSFRPGHQLSVTSLLVCHGLL MVGTSLGVLVALPVPRLSSPSL PPVELI*HSCVCVSRGISCL*W RLWDQISDW\SRTEIQPPRPPSC CPVVASPGPKGPQCNQDPKW KSCEAASVKGTSPATGKSRPAA PCPPSAMLFITPRYSATLSSS SKAASGAREPSAAPLGGSGQPF REMVSQH
8835	39203	C	8894	321	539	

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8836	39204	A	8895	630	983	NLETNGKIPFENPWSKVPIRGFRQNLLRVCLTTGGQIPTGRWVTAATDSRGAGDYRCLHLR*PDGARLSAGSADCAANRDRVDGSGRGLPGRLSVQQPVRVRRGQPDVQPVWPSC
8837	39205	A	8896	31	144	
8838	39206	A	8897	I	1775	MEISFTRVALLAAALFFVVGCDQKPQPAKTHATEVTVLEGKTMGTFWRASIPGIDAKRSALKEKIQTQLDADDQQLSTYKKDSALMRFNDSQSLSPWPVSEAMADIVTSLRIGAKTDGAMDITVGPLVNLWGFGPEQQPVQIPSSEQIDAMKAKTGLQHHTLVINQSHQQYLQKDLPDLYVLDLSTVGEGYAADHARLMEEQEGISRYLVLVSGGAALNSRGMNGEGLPWRVAIQLPDTKENAVQAVIDINGHGISTGSSRGD*DGYGQQGLSRVIDPQTGRSIEHNLVSVTVIAPIATAEADAWDTGLMVLGPEKAKTCSPGGLRGTESLNTRLDRITQINGIDEVRMDDSWFARLAALTGLVGRVSAMIGVLMVAAVFLVIGNSVRLSIFA RRDSINVQKLIGATDGFILRPFLYGGALLGFSGALLSLISeILVLRLSSAAVEAQVFGTKFIDINGLSFDECLLPLLSSMVTFWCRNLF TSLLELWINHADKQDDDNCLSSASVYLIKAKMMKVMLPMQLSSGTGFYRDRRLENSRRGGRYESRRSLTRQFREEPTAPIPRECSQRIDFLLFETPSVSASSAAGFWLRFGSTA
8839	39207	A	8898	10	300	PTSIPRESSSGTWFQVASTTVFSAILAGLGSASAFCCLGPQIPQARPNNSAVNSKNNSRFGIPRPQAE*PEQGGVYHHTAGVLKKLIPPSARQHPDRC
8840	39208	A	8899	1657	2061	QMPGNNPFAFSALLVAFKHQFAIAGGIKIKEVTFIAKTSQQLWFGQPIFNNETTHQACFLSVEADDLKFAVLLIEEHRLDNLGIQFLRLHRFKILI*RQINHHIIALCCERLVQLVGDDISPEFDELELRFSEVH
8841	39209	B	8900	26	1540	
8842	39210	A	8901	I	3396	
8843	39211	A	8902	I	3522	

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8844	39212	A	8903	1	105	SPQPDRHYRHRQGPLVCIVIF YFCAKRWMAAIL*TQHRHRL TTDDGKFAVANGSFS*RGLHH/ ATGLLRRFPIC*GPLVCIVIIFY FCAKRWMAIL
8845	39213	B	8904	1	960	
8846	39214	B	8905	1	2618	
8847	39215	B	8906	1	490	
8848	39216	A	8907	2820	3332	ATEGYRQQCRQFHPAAAYDESP HRNRRKKWRPTYRKHPADPHR TACLRSAFYGNAPGCVQTGPV RRSGAAASAPPASFLSGTSPWS FARTIALVRGRS/LKIDTNSPWA YFSALLM/F/DLSSHVHEWGR YISPPRFAQTTGETLPCCRHHQGSR YSAYLSASRYPARRKWWYFSR
8849	39217	A	8908	3	716	EVDDTAKHRRRDSDFPQ*DP/LM NIRYAPS/P/HLPATV/ALTGA/IT VLYALAGKRLFCSW/VCPLNPIT DLANWLRRFDLNSATIPRHII RYVLLV/LVGSALTGT/LIW/EW INPVSLMGRSLVMGF/GSGALLI LAFLFLFDLLV/VEHGWC/GHICPV GALYVG/LGS/KGVITVAATDRQ KCNRCMDCFHV/CEPEPHV/RAP VLDEQSPVQVTSRDCMTCGRC VDVCS/EDV/FPITT/RWSSGAKS
8850	39218	A	8909	3	323	
8851	39219	B	8910	94	2205	
8852	39220	A	8911	504	694	FNQLGRDWRTYYRKSDPPR/Q WLRHS/PVR*/VLMV/PMAIRGL LWMLS/AQPAPAICSSRQTKMV
8853	39221	B	8912	1	2031	
8854	39222	A	8913	3	190	FIATPGYTGEAGYE/ALPNEKA ADFWRALVEAGVN/PC/PLGARD TLRLDGDES/YG/QEM/DETVP*
						AMK1.RCPMKRPISGVRWWK RVLTHVAWARVTRCVWTGMN LMARDGETVSP
8855	39223	A	8914	1	621	MWP/SVSHLTQMNIPS/RFSEPSG AIEVPPDKVHELRRLAQQGLP KGGAVG/FELLDQEKFGFQS/E QVN/YQR/AL/EGELSRTIETIGPV KGARVHLAMPKPSL/VREQKS PSASVTVNLLPGRALDEGGQISAI VHLVSSAVAGLPPGNVTLVDQ GGHLLTQSNTSGRDLNDAQLK YASDVEGRIQRRIE/ALSPIVGN G/T/ALQDFAS
8856	39224	A	8915	1	2274	
8857	39225	A	8916	957	1067	

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8858	39226	A	8917	1	1242	MDGINTDKGSSVFPHTPTDRLV CCPVDADEMRMTTPRRLWDHEP SKPLFFTNTYPSAQPFGVL/PGK RPQGGFRAGNL*TSSKTIGRDL NDAQLKYASDVEGRIRRIEAF LSPIVGSGNIPAQVRQAQLDFASK DQPEEQYRPNGDESHAAALRSR QLNESEQSQGSYYPGGVPGALSNN QPAAPANAPISTPPANQNRRQQ QASTPSNSGRPRSTQRNETSNNYE VDRTIRHTKMNVGDVNQYRKLGII GQGKNEKPLKQLERVEEKPGPN EGWEKKWQGEVWKEDGTI YLQKNKLRAPTDSTLWFAKNG RVAKIAKALVEPANNFNPGV EDDTTEKLLEVVPEELTNEKLDL EQKCIIHYDDKRKQTQPKTDV FLKRVTSQPQEPPGPGSSGIPEEG IVIGEDSSVQLAPEDLPVEKL
8859	39227	A	8918	256	1510	RRFVGFRGTVTKEDAIGKRGV DQFFRQSQYRVLGVTVAGMPE LTRLFVQRFTQFRMRMAQRVH RNATREVLDILFPLLIQPARTFAT YRYKGCRSVNRYHPFKVFTRN WREADLSLRV*TLNNDTGQYQ EVITYSFVDPKVQQMIHPGV LLLPSPISVEMSAMRLSLWTGL LATVYYNQNRRQNRVRFESGL RFVPDTQAPLGLIRQDMLLAGV CGNRVYEEHWNLAKETVDFYDL KGDLSEVLDDTGLKLNNEVEFRAE ANPALHPGQSAAIYLKGERIF VGVVHPELERKLDDLNGRTLVFE LEWNKLADRVVPQAREISRFPA NRRDIAVVAENVPAADILSEC KKGVNVQVVGVNLFDMYRGK GVAEGYKSLAISLILQDTSRTL EEEEIA\AT\VKCVEALKERSQ
8860	39228	B	8919	47	156	
8861	39229	B	8920	139	993	
8862	39230	A	8921	1	284	MRRKRLIRPTVQAQVCRPDKTR KRRIRQWC/YGCRMRKRRLIRPI KYANRQAETA*GLDAIHLSCSS HG*KGPT*SSGHGFRGCKPQAL EASMWC
8863	39231	A	8922	1	813	
8864	39232	A	8923	1	1176	

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8865	39233	A	8924	3	618	AGGPNLPIEMA*KSWDIEIVK LEKDPLKTQFLEVYPOGFSGE NITDAIAEFKTLITPDSPFDKW LRGDENALTAQQKKGYQLFKD NKCATCHGGILGGRSFPEPLGL KKDFNFGEITAADIGRMNVTKE ERDKLRQKVPGRLRNLVALTAPY FHRGDVPTLDGAEVLMRYQV GKELPQEDVDDIVAFLHSLNGV YTPYMRDKQ
8866	39234	A	8925	2	212	QYPGLDLHGAKGLGDLAGKR YRQLLVSCVRHVLYRHYPAGPT RK*RRSGIRWLHRLCGNEPRGK LLVDQ
8867	39235	A	8926	I	640	
8868	39236	A	8927	I	704	MSSFQFEQIGVIRSPYKEKFAVP RQPGLVKSANGELHLIAPYNQA DAVRGLEAFSHLWLFVFHQ MEGGWRPTVRPPRLGGNARM GVFATRSTFRPNPIGMSLVELK EVVCIIKDSVILKLGSLDLVDGT PVVDIKPYLPFAESLPASASYA QSAPAAEMAVSFTAEEVEKQLL TLEKRPQTLTFIREVLAQDPRP AYRKGEETGKTYAVWLHDFN VRWRV/SP*ACSTFQLEP
8869	39237	A	8928	3	313	AQRGGI*RGSLATAGLRSFGGL HPIRTSQFCLPVRGKPPQTQAS VMVDAPHISTKLKHRLRSIDCCT GSKNFKPVDSLSSLGSMGVGST LDHLPWLQAPFPGE
8870	39238	A	8929	13	453	
8871	39239	A	8930	380	966	LRHAVLLTEGF/SYKPHAFALG FVEAPRGEDVHWMSLGDQNQL FRWRCRAATYANWPVLYML RGNTVSDAPIIISLDPYCSTCD RVTLVDVRKRQSKTVPYKEIER YGDNRNRSPLNRSLSYPREVPSTT LQPLRTPRCPGKLNALALAVNVST GTNGQKPESCOPGRCRMKKG YKRTISGRTIIRVHARLLRTF

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8872	39240	A	8931	1415	2085	SQVPICQRSTSCRVKRLFSWKM AYRSALVTPWRVFRNPAVPR TSPVVFVGGDVFSRVMVRVKE T/FDSLAMLEFALDNMPDTPLL TEGFSYKPHAFALGFVEAPRGE DVHWSMLGDNQKLFRWRRCRA ATYANWPVLRYMLRGNTVSD APLIIGSLDPCYSCTDRVTLMPS QCIACGACACACPANALTIQTD DQQNSRTWQLYLGRCIYCPSST NNNGPVISFN
8873	39241	A	8932	1	1127	MKKRKTVKKRVTALVIVIAG LMTLWIRNAPVPTYQTLIVRP GDLQHSVLAPGKLARTSKNFA Q FIRVRYSAFSLAGEKKKR**P RVHGVNASSGRYRGTGCRLG SDSRKKLVIELATVNPMEQRT QGIGILDPPQIARDLRFDPHYAEY DNIPIKTLFTFTAADVFSRVMVVR VKETFDLAMLEFALDNMPDT PLLTEGFSYKPIIAFALGFVEAP RGEDVHWMSMLGDNQKLFRWR CRAATYANWPVLRYMLRGNT VSDAPIIIGSLDPCYSCTDRVTL VDVRKRQSRTVPYKEIERYGID RNRSPLNRRCTGEGWTRAWITL PLLIKPLTPLMIAASFNFNFNV LIQLLTNGGPDRLLGTTTPAGYT

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8874	39242	A	8933	1	2466	MLRGVNVLADAVKVTLGPKG RNVVLDKSGAPTTIKDGVSA REIELEDKFENMGAQMVKVEVA SKANDAAGDGTTTATVLAQAIH TEGLKAVAAGMNPMDLKRS RSRKGGYGPARIQELNQNKGISR EATEKAMRECDIDWCALARDQ ATRKYGEPLPTVSEKSRKLIA GVKRAFTHQAVNAGFCQPAV SVIAGDFDRHGFNTTRHIFTRLF DDFSFEITRFPQAQIHTLKHARP VLCFRTRARPLRNIEVAVGAVIF AREHTAELKLRQFFQGAPQKA VISIPVVPQVTGVVIEVTDKNT LIKKGEVLFRLDPTRYQARVDR LMADIVTAEHKQRALGAELE MAANTQQAKATRDKFAKEYQ RYARGSQAKVNPNFSERDIDVAR QNYLAQEASVKSSAAEQKQIQS QLDSLVLGEHSQIASKAQLAE AKYNLEQTIVRAPSDGQVTQVL IRPGTYAASLPLRPVMVFIRSET SLRTHCPGHADYVKNMITGAA QMDGAILVVAATDGPMPQTRE HILLGRQVGVPYIIVFLNKCDM VDDEELLELVEMEVRELLSQY DFPGDDTPIVRGSGALKALEGDA EWEAKILEL/RWLPGFLYSGTR ACD*QAVPAADRRA/SSSPVV VPLLPPV^NAVSSKLVKKLK^R WYPRDSEVYLYWR^NVPPTAG RRPCW^ERRCSAAWYQT^RNR

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8875	39243	A	8934	1475	2904	FWRAA APIPDCWRSGAVKKHQ VEVTQLDWTPPGRQYAGPIPACS RRGYCPLPRSGSVRWA/DL/FPP A/LD/LAGHPG/AKVNLPVKT FIDGVIDQTSSFLGTNGQSNRKA EHYFLNGKLAAVRMDEFKYHV LIQQPYAYTQSGYQGGFTGTV MQTAGSSVFNLVYTD/PQESDSIG VRHIPGMGVPLQTEMHAPGLPLA SSMKRWIRRATGFIFGK/EQ/FED VVVPVLGSKVNGVQFNELVAD SLGIQICRCIAFLTVVFPVLUH KQAFDLISLLLQQPGRNNGIDT AGHADDYFFCGFRHWITHDIEL QGGARQKDAADHYLAGDIESL PLATATFDLAWNSLNQWQCGN LSTALRELYRVVRPKGVVAFTT LVQGSPELHQAWQAVDERPH ANRFLPPDEIEQSLSNGVHYQHH IQPI TLWFDDALSAMRSLKIG ATHLHEGRDPRJLTSQQLRLQ LAWPQQQGRYPLTYHLFGVVI
8876	39244	A	8935	I	920	MARADTVSVPFMGLAAKPC WRDTEPNTRYGRPHVVRNIQLT HDRPLDYRSI/LIDINDIGQTFH RLHPDACLSNAILVHNKKGGP LADGIVITPSHNPPEDDGKYNP PNGGPADTNVTKVVEDRANAL LADGLKGVKRISLDESDGIRSK NDVIDTSDDDM**QCLSLRRSN GHGPAKVAANLVPKTTIDGV QTSSFLGTNGQSNRKAEHYFLN GKLAAVRMDEFKYHVLIQQPY AYTQSGYQGGFTGTVMQTAGS SVFNLVYTD/PQESDSIGVRIIPM GVPLQTEMHAYMEILKKYPPR
8877	39245	A	8936	471	668	
8878	39246	A	8937	I	1233	
8879	39247	C	8938	I	1548	
8880	39248	A	8939	I	1260	
8881	39249	A	8940	I	1468	
8882	39250	A	8941	261	596	RSESCCGHEPDGPETRQP*PQR LWTCAYSPTGESERYFPRSDRK SDA*M*HRLVRTGARSQDAKI WRTFANCLFRKIKKTYVRSQTG FYAPGGERRFLYAASKRKNRR F

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8883	39251	A	8942	2	1356	CLPGLKLVLRLYLRLLEERNARRT SAAVDAT*RAGAWLAQCGLTV EQLARQVDPDPMITRAHLYHC DHRGLPLALISEDGNIAWSAEY DEWGNQLNEENPHHVYQPYRL PGQQHDEESGLYNNRHRYYDP LQGRRYITQDPMGLKGGWNLYQ YPLNPLQQIDPMGLLQTWDAA RSGALTWYGWDGDRLLTIQND RSRIQTIIYQPGSFTPLIRVETATG ELAKTQRRLSLADALQNSGGED GGSVVFPPVLVQMLDRLESEIL ADRKRAATTWSHNHYANKKE GIKATGYRLAQLTGFKCEESSV FRVTRKSHSSFVWLDAVT PHP TSNVRAGCLMRRWRVLSGLHR CEVLHPIHTHPAYHAGCGVSL QRNIRHFFLNGLRFQLRFRRTIC CLRLVVVQPQHFAGVLQLAFC CRYITVQLASIRRNDRFQRLSP RAGNTIAKYFFQQIQLHNRGG
8884	39252	B	8943	1	1159	
8885	39253	A	8944	1	1304	MAETQQQFKKRMMAASGLETRF DEVGNLYGRLNGTEYPQEVV SGSHIDTVVNGGNLDGQFGAL AAWLAI DWLKTQYGA PLRTVE VVAMAEEEGSRFPYVFWGSKN IFGLANPDDVRNICDAKGNS/IC RCDFGLRIYSSSERPTNS/VVRL KPLLNCILNRA/DVLERITAWD KPDCHTLHHHDLSGHFPEEIG PLLFAFGSSAWQNNGPSAFSWQK HGSAQTSSIAVLHRTPRHAGCL AQCDFTTRAFFQIMLKKNYLRK RWKKIHFVNASKSS/RAIPEG YVTTYGDVAKLGGIAPGRAPG GR/VQRQALLAEGAGTAEDGFT *VGEVEDAARDGP*TDAERTG* TYADAGRQDPQSAEDRQRANL HGNADR***RFASGGFHRYHYP RAAACGFCDJRKPA CGNARRAG WPDRASKSSAYAFRYR YEHL HAGRSG

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8886	39254	A	8945	1	1695	MRSDPDTSVNEIETKLSALLGS ETTGEILFDLLCANGPEWNRVF TLEMKYGRIMLDTAKIIDEQDV PTHILSKLTFTLRNHPGEGVVMK NFEVLQPLQNSLQLPLWVSER ILQQINQLTHYEPVAGMKGKTGA GKSSLCNALFAGEVSPVSDVAA CTRDPPLRFLQIGEHFTMTIVDLP GVGESGVRDTEYAA LYREQLP RLDLIILWLKADDRALATDEHF YRQVIGEAYRHKMLFVISRSDK AEPTSGGNILSTEQKQNSRKIC LLHELFQPVHPVCAVSRLHPV VALLQFQRTDDERTHRYHYDS QHRLVDYTRTQYEELPVESRYL YDPLGRVRAKRVWRERDLTG WMSLSRKPQVTWYGWDGDRL TTIQNDRSRIQTYYQPGSFTPLIR VETATGELAKTQRRLSLADALQ QSGGEDGGSVFPPLVQMLD RLESEILADRVSSEESRRWLASC GLTVEQMQNQMDPVTEGTTAW Y/AEYDEWGNLNEENPHQLQ QLIRLPGQQYDEESGLYYNRHR YYDPLQGRVITQDPIGLKGW NFYQYPLNPISDIDPLGLSMWE
8887	39255	A	8946	605	1395	SMSLLKNIRLSSASKQCAACSG WPAAAIGRGVSGGQG!ARVSSS ANTATALSSRLLPGQNSVTPVPH A*RMNCVLRVTPL!SKNRGGKP APSGTEGKGLPEVQPQLRAH GLPSENLLEQDFYASGPNQK WAGDITYLRTDEGWLYLAVVI DLWSRAVIGWMSMSPRMTAQLA AGCPKPLWGTPSPFGPACGLAP SSAGVLPRGFVPAVVLDSEDPE EYVGSSDFLTKMQSMKKVVDLK KNRAATDADGQFSPRCCMPEK YAGSHN
8888	39256	A	8947	1	1914	
8889	39257	A	8948	1	4767	
8890	39258	B	8949	1	2294	

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8891	39259	A	8950	115	3551	NPALTRIVPAQONLYTNTLAA RIKQLRTEQFELMLRQAQIDFA GKAHSLTEAQANTTQQSAERD RLFKNYQRYLKGSQAAVNPFSE ERDIDDDARQNFLAQDALAQIQS QLDSLVLNGEQSQVSLKAQLAE AKYNELEQTIVRAPSNQYVTQVL IRPGTYAASLPLRPVMVFIPDQK RQIVAQFRQNSLLRLAPGDDAE VVFNALPGKVFSGKLAISPAV PGGAYQSTGTLQTLNTPGSDG VIATIELDEHTDL
8892	39260	A	8951	845	1213	DKGEIGGWAAQTHRGSHQEQA RRVPEDRDRARARRKNEEP/AAR PRTTNTRNGSRKGPERK/WADG RGHKAEAGRKRKRQ*KEEM RKIRQQESGGEKKRGLCGRPPG GGNNCMEGERRGRKR
8893	39261	A	8952	843	1061	NRPPPVCAHQRQVVLPPVPNR APAEKWQVPRVTLPGRQSTS FAAVVYRN*YQYCALTAQRGR RSPRQLPHR
8894	39262	A	8953	1	682	MIRIPGCEDDKLGADQQPAFVLY LEIDPHQVDVNVHPAKHEVR HQSLRVHDIFYQGVLSVLQQQL ETPLPLDDEPQPAPRSIPENRVA AGRNHFAEPAAREPVAPRYPTA PASGSSRPAAPWPNAQPGYQKQ QGEVYRQLLQTAPMPMQKLKAP EPQEPALAANSQSFGRVLTIVH SDCALLERDGNISSLSPJITGIW CS*H**PMI/PRLLIPASVRSSSM VESAK
8895	39263	A	8954	1	1887	
8896	39264	A	8955	189	552	LFRGEKGARNEVLATRYYYRQT VSGDFRHILHCLADQYALGGAY QF*AGLY*LHQAWEMNRGLQL LSDALGEQYAQHGHNWRFLRNN DRFVFQILRSFEHDNSEDKPGP GMPPHGWRTOFWGG

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8897	39265	A	8956	263	3549	TGGPSSPHWKTPVVIYWDGT ALRCVFVPVLGETGAQKRISAR RKGSLLTSCPQGALSEHCPTP APLPSQRNNHWMENISPFRSVG VSASRCSES*MRPWNSRMPRLG RSQGDSSAL/MSTGVAFRGRF LKGGI/PQAPAVAAATPWLCQTQ GVAGETTPAVNVKYNVRVRS EYISMHVHREVTAARNVYVTQT RRPMTTFPTLAWEYPHYHRRY GVSLSSAWVQVGPPRHYCRQT NALSNLPNFNLKGADTQ
8898	39266	A	8957	1	1799	MMRDRLINH\AIRPACE*QLGA DQQPAFVFVLYLEIDPHQVDVN HPAKHEVRFHQSRLVHDIFYQG VLSVLQQQLETPLPLDDEPQA PRSIPENRVAAGRHNHFAEPaar EPVAPRYTPAPASGSRPAAPWP NAQPGYQKQQGEVYRQOLLQTP APMQKLKAPEPQEPAIANSQ SFGRVLTIVHSDCALLERDGNI LLSLPVAERWLRQAQILTGPGEA VCAQPLIPLRLKVSAEKEKS KAQSAELGGMVNSTRFLSH HPDAERSPGQSGEQRQOQPAVD DYAIVDEYGRHYRRAVAGTLL HVSVDGTTQTVFMYTLSMA LIIALPAFIFARVPNDTHQNV RRKTESRNEVLATRYHRQTV GDFRHLHCLADQYALGAPIPPD GTRRPLVNGAEVGAVIASPVE RLTRNTDINFDKQQRQTSWL ALATLAAALATFLLARGLLAPV KRLVDGTHKLAAGDFITRVT TSEDELGKLAQDFNQRAS NQTPITSRGHPRIFLARHPAP TTLTSLALKIIRSPAFLPD AMAIIDCYILA ASTQAYKAASSL SLSVVLATSA RFKTSSTS IWVK SSTNSCE
8899	39267	A	8958	1348	2190	
8900	39268	B	8959	1	105	
8901	39269	A	8960	1	781	
8902	39270	B	8961	1	1716	
8903	39271	A	8962	754	807	
8904	39272	A	8963	821	875	FFSLFFFISLASGLSIL*W*VFVL WDRW*YPLYHFLLHLFDSSLFS SLLVLLVVYQFC

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8905	39273	A	8964		315	SGSVMPPALFFWLRIDLAMQALFWFHMNFKVVFNSNVKKVIGSLMGTALNL*ITLGSMAIFTILILPYP*AWNVLVPFCVLFYFLEQWFVVLLEEVLIHPCKLDS
8906	39274	A	8965	42	403	GLCSVPPLVVISVLVAVPKLFW*L*PCSIV*SQVA/SIPPA/LFFWLRI DLAMWALFWFHANFKEVFSNS VEKVIGSLMGMALNL*MTLGN MAVFTI/LILPTHEHGMFFHLFVSFISLSSGL
8907	39275	B	8966	179	1225	
8908	39276	A	8967	342	407	
8909	39277	B	8968	143	3122	
8910	39278	A	8969	692	1360	MCGIISEGSILFHCSITLFWYQS HAVLVTVAL*YFLKSGGLMPPLALFFWLRIDLGMLALLWFHMNLKVVFSNSLNKVIGSLMVMALNL*ITLGSMAIFTILILPIHEHGMFFHSFVSSFSLSQL*FSLKRTFTSLVSWIPGYFIFVVAIVNGSSLMIWLSVCLLLVYKNACDFCTLI LYPETILLKLICIRRFWAETMGRSRDTIMSSANRDNLNTSSFPN
8911	39279	A	8970	2116	2418	FFSLFFFISLASGLSIL*W*FVFLWDQW*YPLYHFLLLHFDSSLFS SLVLLVVY/PILLFSKIKNNKPAPGFIDFFEGGFVSLSPSVLL*S*LFLAFC*LLNVFALASLVLIVLGMQF*IFPAFSCGHLVL*ISLYT
8912	39280	A	8971		558	LYKNSVKYFHN*PVGNIMSNIPIVGALFLSGPAFGIGILAAVGLIAIMIIPYIAAVMRDVFEQTPVMMKESAYGIGCTTWEVIWIRIVLPFTKNGVIGGIMLGLGRALGETM AVTFIIGNTYQLDASLYMPGN SITSALANEFAEAESGLHVAALMELGLILFVITFIVLAASKFMIMRLAKNEGAR
8913	39281	A	8972	1879	3735	
8914	39282	A	8973	16	452	VGQLFWKGYPLAGFPDPCAQS WKVAHVLLRLGHIKSVSANGKEVTSKFRKENLARGLHSRPRRGQRVRGGVAQHCEPR*TPPPACRVRLPGCPVDPASPGRRRTSAGTPEPALRHPTPRGPVAAARTLPAEPGPARPSGLPP

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8915	39283	A	8974	158	531	CSLRRGPPDP/PGAYCKRRATG AASTRSLSGAVAGSPAHRCESR PLQAMGAAGGLPHPEGRGGSG GRKRTDGPVCGCGERAPREYP DPSRSWRGPQRKPAPSQHPCLP RLSRGPGRHPEGPHQVR
8916	39284	B	8975	22	387	
8917	39285	A	8976	241	389	VASQAPGVRALQVGPAAHSC*G RGHVSWPWPPWGPCCPLCL LNGLPNI
8918	39286	A	8977	1620	1936	TLFFFESESHSVTQDRVQWYDL ^NSLQQPPPGLK*FSCSLPSSWD YRRPPPCPANFFFVLEFHHV GQDGIELLLTSGDPPALASQSAR ITGMSHCAQQNKHIL
8919	39287	A	8978	3	105	
8920	39288	A	8979	1	1821	MLKNFKKGFGNDYGVMTMPG KLRTLCEIDWPTELEVGPSEGS LDRSLVSKVWHKVTKSGHSQ QFPYIDTWLPQWVRGQAAAVL VAKGQIVKEGSRSTHRKSTPE VLFDPTSDDPLQEMAKVIPVVP SPYQGERLPTFESTVLVPPQDK HIPRPPRVDKRGGEASGETPPL AARLRPKTGQMLREQRYTGI DEDGHMAERRVFCVCPFTSAD LLNWKNNTPSCTEKPQALIDL QTIIQTHNPTWADCHQLLMLF NTDERRRVLQAATKWLGEHAP ADYQNPQEYGEESPAQFYER LCEAYHMYTPFDPSDENQRM NMALVQSQAEDIRRKLQKQAG FAGMNTSQLLEIANQVFVNRD AVSHTGAEHSSVTGPVAPLSK KTIDIIGAMGVSAKQAFCLPRT CTPGTKDYRLVQDQLRLVNQAT VTLHPTVNPYILLGLLPAEDS WFTCLDLKDAFFSIRLAPERQK LFAFQWEDPESGVTTQYTWTW LPQGFKNSPTIIGEALARDLQK FPTRDLCVLLQYVDDLLLGHIP TAVGCAKRTDALLRHLEDGY KVSKKK^AQICQQQVRYLGFTI RRGVRLGSERKQVICNLPEPKT
8921	39289	B	8980	209	2272	
8922	39290	B	8981	1	228	
8923	39291	C	8982	375	472	
8924	39292	C	8983	266	408	
8925	39293	A	8984	1	1105	

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8926	39294	A	8985	108	708	LTNQKKSRTTRIHSRILPEVQGG AAADRHCPIDRRLGSQLQDHRRS RLLSQWSP*KSTHD*HGFSVQS AEDIRRKLQQQAEGAMNTSEL LQIANQAFVNRAVSRKENHR DNERQAGRNTDLAAAIRGVPP KRQGKGPPGKETQPGCQSLQR NQCAYCKEIGHWKNKCPQLKR KPGDSEQEAPDKDEGALLNA EGLLD
8927	39295	A	8986	125	444	DCLAVKRASWVQPTGYSCPKL L/QGVLTYQRRQAAFPPLRER LASSSRDKPKCAGKHTSSLVRA GDMQGTIVTGTEVLRLDMEPK FEDDQLRPVLLEHKVPRREMA
8928	39296	C	8987	80	325	
8929	39297	A	8988	566	1857	
8930	39298	A	8989	1	1037	MEEGWIRLPDGRVAAPQQLGA AVVLAQETTHRGQESLEKLL GRYFYISPLSALAKTVRQRDFA DFGTTIKQDFRLLGQTSVDRLL QLSQGQAVKGQNQLPVSLTSQ CQVYKCVWNWWVVLGLTDFFKN EAKELRLLYKQEKEKAKRWKE TEKGFGNDYGVMTMPGKWR YFEIDWSKLEVGPSEGNLERS LVSKVWHKVTKSGHISDQFPY IATWLQLVLDPPQWLRGAAA VLVAKGQKPRKDPTPPAEGNQ LLK/SLFPTSEDPLQEME/PSDP SGALPLPGKDAPH*AHPCAS TRQTYP*ATRSRQERR*SLERNP YIGSSFTQNWDTNAPERAVV
8931	39299	B	8990	1	2082	
8932	39300	A	8991	6	367	ENLNKAPHAVVTLMITTGP WISNAILTKDFCLLCENTHISRW GCNTLNATTLLLVSSESPVKHNC LEVLDSSVYSSRPNLRDH*TSV DWELYVDGSGFANPCVKTLKK ETSPAPVTPRS

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8933	39301	A	8992	1	2991	MLKNFKKGFGNGDYGVMTMPG KLRTLCEIDWPITLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTFLWPQWVRGQAAAVL VAKGQIVKEGSRSRTHRGKSTPE VLFDPTSDDPLQEMAKVIPVVP SPYQGERLPTFESTVLVPPQDK HIPRPPRVDKRGGEASGETPPL AARLRPKTGIQMSLREQRYTGI DEDGHMAERRVFVCOPFTSAD LLNWKNNTPSCTEKPKALIDL QTIIQTHNPTWADCHQLL
8934	39302	A	8993	1	444	SSASTPETRAKFT*DNLCCASW QR LASANFRVLD CILS DTFED LRLQCDAVNLAFGRCEELED ARYKLHHHLHKAVE*GGGAEH VPHVRLREKLLAEAOQLSRNLEDI HMSLEKDIAAMTNSLFI DRQKC MAHRTTRYPTIQLAGYQ
8935	39303	A	8994	1	1576	MVQTDVLLPEPAPQTVSPCELP CKEYDVARNMGPGRHQLEVW FQNCYARYHQAFADCNQSERE LQGRESQQLAAETQALAQPTQ QDSTCRVGERLQDTHSWKSEL QHEVEVLAATDLLAQKQRL ERALDAMEVPFSIATDNMQCS QRHQHANLVRDYVETELLKAY PPAPSQCLKNCCSRKPSACNK GACEVMETLTQEEAPNGTEG CRTLALAHKEEAEPIRNIQELLK RAIVQAVSQIQLNREHTEICEM DWLDKVEAYNLDETCGRHHSQ STERP/WTKFTQDNLCRAQRKR LISSANLWVLVDCILRDTSEDL GLQCDAVNLA FGRCEELED RHKLQHJHLHKMLREITDQEHN VVALKEAIKDKKEPLHIAQTRL YLPSPHRPNMQLCREAAQFRAA FPG*ESFQWRLPRTSLPAPNWE FWVPFHPSRCILLPSPAPAHTPP TPPSW*VRWRSLYKSITALREK LLQAESLRLNLDI H MSLEKD TAMTNSVFI DRQKCMAHRTCY PTIQLAGYQ
8936	39304	C	8995	99	442	

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8937	39305	A	8996	177	622	TESSASEKTTGEDGTRVFVSSL RSLLSLLPSAPLRRHPPSA*LSL CSCVS*AVALIPOSAAHHFPNIS *PFPLHCFAHAKPPWIFHSH/S LWLP*AF LAPMTSFTDQVAVD DFLSIVYLFTTPFLAFCGEPEST ALATREQVWVVESAS
8938	39306	A	8997	I	329	AAARPGRGSETGDWVLLCYPG WSAVV*S*LTAA/SELLGSRG*G SLLSLPSSWDYRLSAPCLANSK KP SER*GLSMLP*LVSNSWPQVI LLLGP KALGLQAPGTMGLRP
8939	39307	A	8998	I	814	
8940	39308	A	8999	57	274	TASSSLT VYGHRLCWLGPSHP *PSLWL P
8941	39309	A	9000	I	1236	
8942	39310	A	9001	I	1095	
8943	39311	A	9002	I	2313	
8944	39312	A	9003	166	494	FSQQLCGENHPHLRTENTQAQR AGVPLGVRI LSRPGFP LSTHSC FSCPLV*PPSQGQP GPLS LWTLC SAIQAPAEI ESCRSSCDRDGRSH WPRVSGGLWLSQVPRPR
8945	39313	A	9004	3	974	MGESPAV*GYFVLAGMNSAGL SFGGAGAKYLAEWVMHGYPSE NVWELDLKRGALQSRTFLR HRVMEVMPMLYDRLDAQE AR KTVSQLRTSLLYDRLDAQE AR WMEKHGPERPKYFVPDPDKLL ALEQSKTFYKPDWF DIVESEV KCCKIEAVCVIDMSSFTKFEITS TGDIQALEV LQYLF SINDLDPV GHIV\HTGMLNEGGGYENDCSI ARLNKRSFFMISPTDQQVH\CW AWLK KHMPKDSNLL LEDVTW KYTGTVRALYGDV EHEWSLS CVRHAHHPDPI CIAHTYLHLRS FSQADGREWRKVLDKH KIFLF ARS LC
8946	39314	A	9005	I	1872	
8947	39315	A	9006	I	2250	
8948	39316	A	9007	I	1257	
8949	39317	A	9008	I	1596	
8950	39318	A	9009	I	1584	
8951	39319	A	9010	I	1461	

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8952	39320	A	9011	110	993	TSTELSTPSQQNIHSSQHHIALV PKLTT*LERIKYLGQLTRDVKD LFKQNYKPLL/NKIKEDTNKWK NIPCSWTGRINIVKMAILPKVIY RSSAIPKLPMTVFTELEKSTLK FIWNQKRAHIAKTILSQKNKTG GIMLLDFKLYYKATVTKTAWY WYQNRDIDQVNRTTEPSEIIPHIC NHHLIFDKPDKNRKWGDQLSLFN KWCRENWLAIKRKLLKLDPLTP YTKINSRWIKDLNVRSKTIKTIE ENLGNNTIQDIVMGKDPMAKTP KTMATEAKIDKWDLIKLRASA QQKKLPSE
8953	39321	A	9012	1	1185	
8954	39322	A	9013	1	185	
8955	39323	A	9014	2	1321	
8956	39324	A	9015	2	1757	
8957	39325	A	9016	1	1008	
8958	39326	A	9017	1	1311	
8959	39327	A	9018	1	1152	
8960	39328	A	9019	1	526	MPSLTTPIQHSVGSSGRAIRQEKG EIKGIQLGREEVKLSFADDMIV YLENPPIISAQNLLKLISNFSKVSR YKINVQKSQAFLYTNNRQTESQ IMSELPTIAKRKYLGIQLTRD VKDLFKENYKPLLNNKIKEDTNK WKNIPCSWVGRINIVKMATLPK MTWIANWLRNSLQAO
8961	39329	B	9020	1	1626	
8962	39330	A	9021	1	2361	
8963	39331	A	9022	1	1140	
8964	39332	A	9023	1	2112	
8965	39333	B	9024	1	1065	
8966	39334	A	9025	1	1416	

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8967	39335	A	9026	1	1690	MPMVEELYGNYGINADITTERV GQHKDAYQVILDGVKGGTKEK RLAAQFILKFFKHTELAADSAIN AHLQTIVSGRQQQLVKLVAEQAD LEQTFNPSDPECVGRLLQCTQQ AVPFSSKTVHSTRSVITYFCEQV LPNLGILTAVEGLDIQLEVLKL LVEMESSFCGDMEKLETNLGKL FDKLLEYMLPPLPEEAENGNA GDEEPKQLFSYVECLLYSFHQL GQKLPDFLTAKLNAEKLKDFFKI RLQVFARGLQVYIRQLHLALQ VKQCFAQYMEKENGDIAKILN KILANRIQQHIIKKLIIHHIDQVGF1 PGMQGWFNIRKSINVQHINRA KDKNHMIISIDAEEKAFDKIQQQF MLKTLNKLGIIDGTYFKIRAIYD KPTANIILNGQKLEAFFPLKTGTR QGCPLSPLLFNIVLEVLAIRQ EKEIKIGQLGKEEVKLSLFADD MIVYLENPVSAQNLLKLSNSFS KVSGYKINVQKSQAFLYTNNR QTESQIMGKLPTIA/S/KRIKYL GIQLTRDVVKDLFKENYKPLLKE IKEDTNKWKNIPCSWVGRINIV KMAILPKNWKKLL
8968	39336	A	9027	1	1575	
8969	39337	A	9028	1	2682	
8970	39338	B	9029	1	2088	
8971	39339	A	9030	1	2406	
8972	39340	A	9031	1049	1500	
8973	39341	A	9032	1	4341	
8974	39342	A	9033	103	366	NHPQLKVAGLKNGCCVCVMCV CVC CVCVRVW WVCVCVC VCVCV CVCV CVCV CVCV C WVCVCVCLCLSLPKCWDRH PQRPA
8975	39343	A	9034	232	735	YLSGNNGGEKGFCHALPDHRLR VLHQHPPHACVETDTVDLGITS ISLADVRVCVCMCVCVC CVCV RVWIWVVCVCV CVCV CVCV C CVCV CVCV CVCV CVCV C CVCV CVCV CVCV CVCV C CVCV CVCV CVCV CVCV C VLCIHSFLTARNAHQPIGH
8976	39344	A	9035	163	795	

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8977	39345	A	9036	34	758	RVPHRHGMKVRQRHGMKRV PHRHEMKRVPHRHGMKRVPHR HGRKRVPHRHGRKRVPHRHGR KRVPQVQDDEEGHCQKPGRCV CMCVCVCVCVRVWIWVCVC VCVCVCVCVCAVCVCVC VCI*VVVCVCVC CVCVCVCIC CVCVCVCVC/CICVCI*VCVC VYVCVCVCLCLFYLVLQCFCIS/ CIISGGQRWC RKTMCSCPFAH SHHSFPGHFFLIFQSRSFQVSHP
8978	39346	B	9037	34	156	
8979	39347	A	9038	3	419	GGENVKAINQQTGAFFEISQL/PPN/GDPNFKLFIRGSPE\QIDH AKQIIEEKIEVGWGLLWFGL TARIPAHLPWLLSFLLG\PLCTV G\PGPGPPGPAGPMPGFNPNGPF NQGPPGAPPQ*VSSASWVLRP/E GLLSWQEE*QTTPFPFP*KCRAG ALIQAHFCGYHQALSCL/PGR ACAFQHPSVHVQVSRLLSCPQA DAARPSSCFLSRPFPGAPLSLV WVSGASPLKNIPTPGPAA PPP HHCSSIPFFSPAVPGGPLLTSTH PRAGAIPTPSGS/QPAPHDPSK* WALQPGATRGSPTVSILCLLG EAGLSSWQEE
8980	39348	A	9039	1	445	ATADPNAAWADDYSHYYQQP PG PVPCPAPAPAAPPAAQGEPPQ PPP GQSDYTEWAWEYVKKI GQQPQPGAPPQDYTAKAWE EYYKKQAQVA TGGGIPGAPPG SQPDYSAAWAEYYRQQAAAYY GQTPGP GGPQPPPTQQ GQQQA

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8981	39349	A	9040	38	1297	TCVSALSVLASDDGTGPEKIAHIMGPPDRCEHAARIINDLLQLSRVGGPGC*RGWQGLQGSARPDRLPGFIILLLLSCRVVPPQQGPVPGGPGMPPGRRPKEEGQGN\WGSPWAGKMTFSIPTHKCGVLIGRGGENVKAINQ\QRGAFAVEICRQLPPNGTANFKLFII\RGSP\QQIDHAKQLNE\EKMKGPLCPVGPGPVPGPAGPMGPFPNPQ\PFN\QGPVPGAPPHAKK\PPPQHYPQPGCGNTYPQWQQHAPHDPSISAGKAAA\AAADPNAAW/AAYYSHYYQQP\PGVP/GPA\PA\PA\APP\A\PA\Q\QQPQ\Q\QPGAP\QQD\YTKAWEY/YK\KQAQV/ATG/GGP\GAP\PGSQPDYS/AAWAEYRQQAA\YYG/T\PGPGPQ\PPPTQQGQQQWVA\PETPSPRGVPLMPA\AGAVWPE\VPGV\THRQGSIRWVQR
8982	39350	A	9041	1	1777	MPVLPVTATEIRQYLRGHGIPFQDGHSCLRALSPFAESSQLKGQTGVTTSFLFIDKTTGH\HFLCMTS\LAEGSWEDFQASVEGRGDGAR\EGFLSKA\PEFEDSEEVRIWNRAIPLWELPDQEEVQLADTMGLTKVTDTLKRF\SVRYLRPARSLVFPWFSPGGSGLRLKLLEAKCQGDGVSYEETTIPRPSAYHNL\FGPLISRRDAEVVLT\TSRELD\SLALNQSTGLPTL\TLPRTGTTCLPPALLPYLEQFR\JVFWLGGDLRSWEAAKL\FA\RK\LNPKRCFLVRPGD\Q\PRPLE\LN\GG\FNLSRLRTA\LP\AWHKSIVSFRQLREEV\LGELSNVEQAAGL\RW\SRFP\DLNRILK\GHRKGELTVFTGPTGSGKTTFISEYALDLC\SGVNTL\WGSFEISNVRLARVMLTQFAEGRLEDQ\LDKYDHWADR\RFED\PLYFMTFHGQQNIRT\VGTM\NHAVVYDIC\HVII\DNLQFMMGHEQLSTDRIA\AQDYIIGVFRKFATDNCHVTI\VIHPRKEDDD\KELQ\TA\SF\GSA\KGGEWSAP\HSTSSRPSA\QPKSD\STVAEAA\PLASDFTAYWIWFLT\WGRGRASRDREFGYLAALN

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8983	39351	A	9042	3	679	SPLIVSARMHAGRDI.PLYFMT FHGQQSIRTVIDTMQHA\YVG\Y DICHVIIIDLNLQFMGMGHEQLSTD RIAAQDYIIGVFRKFATDNNCH VTLVIHPRKEDDDKELQTASIF GLSQRQARIEADNVLDPAVTGK LGNRQGKRYFAGVPKEPF*W EM*GVFPLEFNKNNSLTSIPPKN KARLKKIKDDTGPVAKKPSSGK KGATTQNSEICSGQAPTPQDP TSKRSK
8984	39352	A	9043	90	317	GTLRKRYRAFHCRITIFKALTEV CKNFSALHCEFSWGFFFFCSFFF LASS*G^*NCLPSQPQPCWFQLQP CPWQIL
8985	39353	A	9044	2	2136	PRLSVLSEFIFTIHYFLLSETTY NYEWNLISLYVVDPSSLRAC*TV QLFFMLQLSVGGLYVFNVGNDIC LHKGMSVTVLFFVTARRVNLPV VAVIKLMSSSSCISFLSLFLNLV ESTDDTEIVSYHWEINGPFIIE KTYLCFFTFLFCFVFFVFAIT*G VQTPYHLSAMQEVDYTFTQLT GLQT*CKEIIILFHTVSVIPENNRP PVAVAGPDKEIIPVVESETCLS YSKPHAPSLMLTTSMFYRGPSA VEMENIDKAIAVTGLQVGTY HFRFYSITGVLNQSCLCHFAIFD LENNSPPRARAGGRHVLLVLPN NSITLDGSRSKSKPRNWDPRIDSC PVIIRVLSQDVIDGSDHSVALQL TNLVEGVYTFHFLMLV*SLCKCP SANPVSSLSPDRPKSGLVELTLO VGVGQLTEQRKDVTLRQLAVG VSW*SPSDHVAVLSHCLLHSTV IVFYYVQSRPPFKVLKAAEVARN LHIS*ISRDSLFCMLPSALHTS/S AGCLLKCSGHGHCDPLTKRCI* K*SWSTNSL*LCPLWFSCVSEW SIFYVTVLKS*LSVTFLKI*VELF IVPPRQKRTKIRKKTLMY*VH LKYFTH*ILILPIAVRGMCNDYP HD*QLEVNHGVPPQMLLCFSLG IKHRSTEHNSSLMVSESVRSFD RDCLQSLNYLLSGLLQKEKNLQ KAGLTSPASLWEDKCSRTEH AQSARLPLKEDTEKTLMQF
8986	39354	A	9045	47	157	FDKICIFKRQVTKSEVILNLTN* VL*YLEYHIRNIN
8987	39355	A	9046	1	393	
8988	39356	C	9047	274	357	

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8989	39357	A	9048	727	1089	
8990	39358	A	9049	175	608	CGWEYGN*AIITMDEQYCKVC QAYKAPRSHIHCCKCNCTVMIK MDHHCPWINNCCGYQNHSFT LILLALPLGCIHAIFIVFVMTMYT QLYSFGMENNFRKQNFYLISS WDWKEEGLKDOPDFSIQLGWK SFVFHMDMGEVDFGEETF
8991	39359	B	9050	780	1166	
8992	39360	A	9051	3	681	HIRGPRYSGHHSAGFCGPYSDMN LKKEATLHDRLREQTQANLES DSSHISKSKSCLSLNFNGKHEKV NSQPRVLVQQAKCLIKKGKEDID LDNLRFREYSVEQAQQVLHQSV SMSTVS AHPFRDLPLGR EQHCK LLPGVADIRASQVARWTVDEV AEFVQSLLGCEEHHAKCFKKKEQI DGKAFLLTQTDIVKVMKIKLG PALKIYN SILMFRHSQELPEEDI ASGQEVRG
8993	39361	A	9052	30	981	TQDPWP SLPVLSRASSDPAAG HRAEH*TYWPWKLEGTDIWI VLYMLPVQPDNFKKHSHLPTV CLFKEDVKFPFRTCRLTYCWL YTEEITYLHTKKVSVGQSAVRE EFAAA C TWSIRIGEKLAILLSLY LCRQQA L NMRMSVPIHESGV AQRSPVMDKLAQYSVEQAQQV LHQSVSMSTVS AHPFRDLPLGR EQHCKLLPGVADIRARQVARW TVDENLHGLQTQKQTPHLDES KGESP ALVVT ELRMCM TATEP LVPTKNPYQERGHIGDSFLHYT DQE P QP WDQS V HPTP API YS SSGFRVTRGS DI
8994	39362	A	9053	1	864	MVSALPEVGRAQIILRLIA YIRSP APPVG VVERAARRPAQAFGLV ALPSTDATV FANQPL RACIGA ARHREPDAPGQSA WVGEECLK DALRSPETPKLGSLSPPCQDTRP GRASND FSLEMGYSSL AARLK IHQQV FQC CCGP GPLRTL IHW TQ S*T YLN LIA LET*GAQ NQP*EW QAVD*GAPGLFSHTLGVFPR/RL PQHPKQII CFQ NYEVS VEQA QQ VLHQSVSMSTVS AHPFRDLPLG REQHCKLLPGVADIRASQVAR WTVDEPYSSA PRGPEL SAGANS SRGA

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8995	39363	A	9054	1	1737	MKEKPAVEVRLDKWLWAARF YKTRALAREMIEGGKVHYNGQ RSKPSKIVELNATLTLRQGNDE RTVIVKAITEQRRPASEAALLYE ETAESVEKREKMALAQQMIMPQ HDQLHRYLFENFAVRGELVTV SETLQQILENDHYPQPVKNVLA ELLVATSSLTATLKFDDGDTVQ LQGDGPMNLAVINEINERAQNP LLCAFRCVNNTYGSYECKCPVG YVLREDRRMCKAVFPYCQNES SDVLWQFDSTSQIFLKGTPTKTT VRRGGHEHNLKNPDECEDNPNC DGGQCAGIPGRNRCLCYDGF ASEDMKTCVDIDECSLPNICVF GTCHNLPGLFCECIEIGYELDR SGGNCTEDPPDHSKSRSGRSQND WGRRKT/S*KRSAVYR*RQLY IRRQPYAERPSLR*RQRP*PCIR SQHGNRKMRMRRRFISTKRTT AAARTSSVKKARSFSRALKNA MLS*RTAPSVS*S*IMITH*KK** SR*SLQTR*LMKSSARVFSK*T ANGTWSL/HSRGSKVTIIDGINSND IYMLGYVNSLTGPYRVPDKTG LGLEMLDPNDVTLTYSHFRVP EAEAAMWVSHAT

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8996	39364	A	9055	1	1743	MTTSTMTHMMTMHFFIIVCAD SRDDVDVTNDVNDHDDSAKR KSHKERPIAAKRTETK'KRRRRA RPKR/RTKARS*SAK*QTAQHT RTTAAIIIMRDTQARRV*RPTKH AAEQRQNTTGKQRR*TKRVKA AKKEGE*RRRKMARTRTPQTR R*TRAKRRIINRPR/HGAKKRA*N /RRLKSAPKRHRVNRDRENART TTRHKRRNRRVKAERSGAE RTPYKQRHQQTREKRTCKRRQ TK/RTKAK*T*RDHENGDTRA YNKTPKKAAKRTRNNLRIHNA TKGGDNRGQTRRA*TKPRKYR PDENRYNTSSPERTPRKRRGKS E/RRDKTAQRQAQ*ADRYNSRKT QQRL*KGHTHTER*RQARMH RHAQNLDTOHSTRLCNA*ST/C HDRRSSSTMCHRYDQLYSRSH ALTMIVNKPLRQCIRMLSFHD RHSLAIDGDSASTGPSAFRCV NTYGSYECKCPVGYVLREDRR MCKDTCTEKAFPAGGCEVDKT HTVPQERAYIHTRTRLGRARTKK RDLYRRAHNDRRROQSAAYYE STSVRAHKYNNSGKSDTQNGS HHRQKLROQYDGAKSHYLOQ NIHFMYPLFNT
8997	39365	A	9056	3	451	FFEMKSHSVAQAGVQCSGVILA HCNLHLLESSDSPASAFRVAGII DARPHAWLIFVFVLTETGFHHVG QAGLELLS*VJHPPWPPKVRL QHETPCPAVSLYLNQSPENNLE EDSLAMSNNRRSKGPQIWQNP GFEILALSTFLVESDLK
8998	39366	A	9057	53	343	
8999	39367	A	9058	14	234	CLFIRIFNVICYSKTCNSICIGV IEIVIDGCMCGGEDGGGGGSV TAGGAPSPIETGSHGPPQPAVYF WRF

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9000	39368	A	9059	3	865	INF SVC VLARFFLGVV VLC VSC CW FRC VCA VC ALA PFC SCC VV VLP CGC RIC LFA V/CCCL/ CV CAL FCG FLL RFL FC LCL CV/CPC S/CS AR C RC/V CL ALG AVV CFPP CS VVA SC GCD WW WLCCGA V VAL VGLI CC VL VCA WS FR CG/C V/CLC/VC VVV VL VRCC/VCW CG S C VV D CAG VV I VCC LLV V MMS L/CG CR VY SW Y GVC W CS VV CR VIDL/CP C CL CW/ CVT* RG CWS VWC M/CT CCG/CV CG LA V M/C W C RC VV RL V CL CA V* FRC AC VCF ECA VGG FVG GCF LG SCL
9001	39369	A	9060	1606	1849	QGV S A SL CRE AG LTK IS PG APL WL PC SP G VT AE CS GERT VRH N VT DR VCG VL GA VT SP GRN* RG HV TH KF CIL CT DTV RD C
9002	39370	A	9061	2	682	A LEA VFG KY QV QI VE VH LM KDC ET NK S RGF AF IT FER PA DA KDA ARD MN GKS LDG KA IK VEQ AT K PS FES GR RG PPP PPS RS RG PP RVL RGG RG GS GT TREP PS RG GH MD D/S GRD S YRG PP RRS LPS CR/D AP PTR G/PPS YGG SS RY DD YSS SRD GY GG SR DS YSS SRS DL YSS GRD QV GR QER GL PPS MER GY P PP RD SY SSS SR GT PR GG RR GGS RS DR GG RS RY
9003	39371	A	9062	90	443	N VV YI QF IV LP YV LTID PAG NSR S AP TR GP PPS YGG SS RY DD YSS SRD GY G* SRD S YSS SRS DL YSS DRIV STL FFV S LN NW DF GP K FCL F L VS A SA SP SIR SASS RA ST SW CS AA
9004	39372	B	9063	12	1373	
9005	39373	A	9064	2	206	

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9006	39374	A	9065	2	1423	IHFREMASKSWLNFLTLCGSAI GFLLCSQLFSILLGEKVWDTQPNVL LHNDPHARHSDDNGQNHLLEGQ MNFNAADSSOHKDENTDIAEKUL EEKVRLCWVMTGPQVNLEKKA KHVKATWAQRCKNKVLFMSSEE NKDFPAVGLKTKEGRDQLYWK TIKAFQVYHEHYL^DADWFKLK ADDDTYVILDNLRWLLSKYDP EEPIYFGRRFKPYVKQGYMSGG AGYVLSQLKRFVDAFKTDK CTHSSIEDLALGRCMEIMNVE AGDSRDTIGKGNNFFHPFVPE^H HFNLKGYLPRFTWYWNWNYP PVEGGELRFLFSTVTRHSKALS LGVAQCSWLLKQQVISDDKTK RPDPDRSRIMKERVQIVLYES GQAPVESSPLPLPGYCSALFATCF QVTGNFSQDPTQAILYTQADKF IEGWMRASGERVAEQQSGQTA MDGGKKEAEWKTRKAKYRD DVCSDKHHPPYPTPVPPSLED
9007	39375	A	9066	1	311	
9008	39376	A	9067	1	493	ITRQHMRKAVPFQVPRKEIKL LKGRVVVGHALHNDFQALK(*S TLGARPGDTTYVPNLFSEPGLH TRARVSLKDLALQLHHKKIQVG QHGHSSSVEDATTAMELYRLVE VQWEQQEARSLWTCPEDREPD SSTDMEQYMEDQYWPDDLAH GSRGGAAREAQDRRN
9009	39377	A	9068	45	365	NQAAASRPHCARTMAGEEEQA ACVHEDRTQCRGDKAAPQAAH LCGPPRGSGSVSTAPRAR*CPV CSSCPGPGAPEDTPPEEVDVGA SAHRSPRLCCSHLTHRWPKH

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9010	39378	A	9069	3	1687	ICVPKSVPNFLWAGRGPVHCLLP CGSSSP*SGGLARA*GVFQGRA GVARAPSHLSFHNSPCVWSLST CCRAGSQDGPGCPHAAGQQGPWK QTSSGTGASSSPWTSCL*KSLPK VCS^GLETTTIGRGRVVKPIKVTD TAQ*CAASVTAPI.LSS*LQDGG STAKVTRCT/TAGGRAVYGTAE GKAFPEAPELTCRS/ALAALGT WPLPPLQVSCGRLRNPSQPDPLPSV VGSRASV*TKSGSSPAKVWPLA EWFKGSGA PVTGQEAWLLWA SDSSSELSLCPRKHAAPPHSAEH RQISQGLASSCWGAGGDKVVS ASMVGSAPGQCPMSALMTGSA SGQCPCGHPCWSGNTADS*GRDP HRASRLLALPTASYEQ*PQPHW GSWTAHGQNGLGIFFQRVSWF V*GQTMVSRPRISGLGQPVCLS AASFQAAPLGSHDPTPAGR*GL EPGGRQPSSS*IYVWEAPPGLW VPPGPFLSH*SWRFGRTKAAMPL KEPRPGGRCPGDRPSPRAEAGL PQTRKPALPAIGR/PKKACSLR PRVILEQSSQHLAAALSSWMQP ALLETGGKAVFFTPGGL

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9011	39379	A	9070	66	1956	PLLAIPAHSTFPARKPEEPPRPD* LCPHIHCAAV*GEIRTPV/SKTV RGVATRTRPRSSASSLTTGRLR VSSVRVQLSIKPGCSRNVENNS NSPCSSSQPGTSVLPCTVCRE AGP/AGP*PPG*ALSLPAAGFTT ATEWKQSQLSSGG*THSGEDM GRATAAATEKAQEQCMLREKL GTRQKAESGRGA\AGLQHFCS APRTAWQPRASRA/AGRAVRAW PCADPM*PPSHSPSFPKPFIPAA/ PGAQLTLGAAGVEHAGSARIPC CRTGLE/PHPHSRRTLERQARI SGAGRSSSPNA/TGARPRAAG SPVSARRAPRRRPA*SSPCSGPW TAVSAPRSPGPGRGGRPPSPGR RRPCCSVFSGGASPSSARVSSPS GSCSASPPAAPA/PGASGAVV GPVVGSPREHGG*LRRPLPRLG VPGLLAARTSGAEVIHQAAAQ GTAADTPGAGPLLAPAAAGA V/TRPGPPGASGCPRPAPRPTP ASRSGRP/VPGGGRGRGGRRGA GGEALQGAVVGGQVGGS GAL A/ATARGSPAAGVSRWATPCR HRRSDASASGTPARFPGAGRKG RTLWQ*SWRSAPPGLSELL*G LPRPLPESGRSKAPLPSGSTPLPS GRTPLPSGRSPSTRRSPS
9012	39380	A	9071	95	1423	GLENKRAKGTEAHTRACP*GK STEQDTWTNTGRNEQQGPRP KGEQTQRKTERKPGRERQVQV LSSPPGRWC*DVGPLGGLPSRA KAEAAALTAQKAQGRRGSPGS LPKSSPLPSAPGKR/TPPRGHLL VPLPSPYYPALLSQHPQPGPPCG ASAPPSSALLQRAPPGTRTLIQR PPGPRVTGTTP/MAAKAKQS NAPRGSLKKNSNFYNIPLKQV SCLITISKHSRNEVSVYQTSRPR AAATDVPRTPSLSVGCSWSCT RGHWPSSCPTAPRGQGL*EHS QGPGRSRSKLPWPTGPCCGGLTPS CWSLAGSAGERVDLNQAAASR PHCAARTMAGKTLSGGCCVD VGAASAHRSRPLRCITSPIDGP INTERGSRKTGWTPGPPGFWP RPPTSNTTPLGLMDSARPKA PAPFTDFRTPSGLLLPGWAVRA RREEDGCG

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9013	39381	A	9072	42	380	LGAPCTPPRSAVRTGRPEY*A RG*PVGDLCRGP*EA*AVVSTQVLL PRGLQ**NFAVLLLQM*SCATPPP NCALKGCV*VPLEQS*PFFHQAV ACREWKRKGKGMVCGGNASPQ RTEA
9014	39382	B	9073	116	341	
9015	39383	B	9074	52	190	
9016	39384	B	9075	70	310	
9017	39385	A	9076	1349	2456	HCSVPGAEWPRKPPAQICPQLT SRPHLSSPRSLSPCGHSPGP* SPQPVPM*LHEGPPRGPCQV/PSP VANPQPKPWLLRSV*DLPVWH LPTVDRTTSL/APSLQS*SDV/PAPS GAL**PSGRACSGV/*PID**APEA ALSAAPRPSLGSQQN*ASGLPA ASLPQDSSQPHKTVPSPARSVP PLGAQARAAPPRLWC*PHALVS G**EASPEAVSVAAGPPVGPTPS TSGSTASHSRRGC**SPR**TPAPP RRDHGRSAAFEVLA*AAA*AQP CASQGGPRPTGAGRTPSPLGLP FSRGPPAASARPFCRHP*SL**FW **SSPSGLSLSDTPHSPRPLGPV CGLRAPCPPQIPACRVPAAHSQ RWPGSSSRSCRCQCC
9018	39386	A	9077	462	739	ACEPMVLFC*LLQLQLDFLFLGS YPRVLA*AFDIQVF*FLGTSDRM** NTGILEYFMLNSWLWLLNRL**S WGELCHFIPILHSPVKRGLNFYL QE*FFI
9019	39387	A	9078	1	678	GTRVNMI*LMKMGFSGIVVHQE SVCATYGSGLSS*TCIVDVGDQK TSVC*VEDGVSHRNTRLCLAY GGSDVSRCFY*WLMQRAGFPYR ECQLTNKMDWLLQHL/KRN*F LSFRSRTSLGFRTMSFRFRHPDS PALLYFQLRGDEKLQAPMALF YPATFWICWTGK**RPLHTDRA ILKILTMNITCWPHKAHENSLQ KLLLTESLHPNULDLKGIFVASP LIFQKD*SIPR

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9020	39388	A	9079	227	1980	GERLRYGVTENGKEKGGEEK EQRGVKRPIVPALVPESLQEIQ SNFIIVIHPGSTTLRIGRATDTP ASIPHVIARRHKQQGQPLYKDR WLLREGLNKPESNEQRQLNGLIM VDQAIWSNKMMSNGTRRRNPVSP EQARSYNKQMMPAILEDHCSGN KWTNTSHHPEYLVGEALYVN PLDCYNIHWPIRRQLNHPGP GGSLTAVLADIEVIWSHAIKY LEIPLKDLKYYRWILVIPDIYNK QHVKELVNMILMKMGSFIVV HQESVCATYGSGLSSTCIVDVG DQKTSVCCVEDGVSHRNTRIFS WRSGHLW\VDQDHEFQIRHPDSP ALLYQFRLEDEKLQAPMALKFYP ATFGIVGQKM TTLQHRLRAILR ILT MNT CWPFRANKNSLQKLL L TESLHPNLFEFERGFLWASPLI FQKDSIPR*IWGLHREMA*WP ATIPRRPLTALMSRKTAISL FEG KALGLG*SPSSIAIDCCSSDDTK KKMYSSILVVGGGFDVFIKASR IFCSTEFSTKC PPSLQADYLKM WM*SQGLKDMDPRIIAWKGG AVLACLDTTQELWIYQREWQR FGVRLMRERA FVW
9021	39389	A	9080	1	756	MRRIVALVETGEQPFGAATVGS RFGCLEDLGTDQRERHDHEMA AAHTYFIGDGD TLTEDED EDT WGMAGKH HAINIEGFKLARVE DEM QFQEREP EKVKIRGRT RGY TFIMLA ALAAAEEAEDMQV GEE LIC*KVSLKASQLQCMALMLQS VT VQIGMVYGLPACGAQVN LQ DDKGSMVL/MCA SKHGHMEIIK LLL AQLGCNVHLQDN DGSTML SIA LEV GHKG ITVLL YAH SFAK AQSPGT PRLGMK PQSF I
9022	39390	B	9081	5	5440	

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9023	39391	A	9082	1	4294	WAVFDGNYYYLPLWAHTKPV VTLTSYWEDESHRLDAVNALLA MAERLQLTNEALKSGIQKGKIPA NQLAELWLKLIDEVIEDTRYTL PLTEGKANVTVLDTQIRKLRSR SLSQIHEAAAVRMRSEATDVKST LAEIEDWLDKI.MQL.TEEPQNS MPDIWWMIRGEKRLAYARIAPAH QVLYSTSGENASGKYCGKTQTI FLKYPQEKNNGPKVPVELRVNI WLGLSAVEKKFNSFAEGTFTVF AEMYENQALMFGKWG
9024	39392	B	9083	1	339	
9025	39393	A	9084	2	1767	KLYRKSDENEQPSVVGKFKG FRIYPLPDDPSVPAPPQFREL DSVPQECTVRIYIVRGLELQPQ DNNGLCDPYIKITLGKVKVIEDR DHYIPNTLNQVFGRMYELSCYL PQEKDLSKISVYDYDFTTRDEKV GETIDLENRFLSRFGSHCGIPEE YCVSGVNTWRDSLRTQQLLQ NVARFKGFPQPILEDGSRIRYGC GRDYSLDEFEANKILHQHHLGAP EERLALHILRTQGLVPE\HV\ET RTLHSTFQPNISQGKTLQMWG GMFFPKSLG\PPGPPP\NITPRKA KKYYLRVIIWNTKDVILDEKSIT GEEMSDIYVKGW\WIPGNEENKQ KTDVHYRSLDGEGNFNWRVF PFDYLPAAEQLCIVAKKEHFWSI DQTERFIPRPLIIQIW\DNDKFS LDDYLGFPRTLTCRHTHFLQK SPGGNCRVWT*FPGPSKAMNPL KAKTASLFEQKSMKGWWPCY AEKGARVMAGKVEMTLEILN EKFADERPAGKGRDEPMNP LDLPNRPETSFLWFTNPICKTM K\IVWRRFKWVIIIGILFLILL LFVGRAPLTLNPYFVQWKIVK PNVLTKGKGFIISRVVIQQ
9026	39394	A	9085	2	407	

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9027	39395	A	9086	15	759	SARPSHDYSHYYG蒂EYLCKYI LGDIIENSRIVLQINNACLAADD F*TKYEREQT/LA/RTDLEMOTÉ GLKEELAYLKKNHGEINALRG QVGGQISVEVDSALGADATNL SDMGSQYENRKDAERWFTSCT EELNWEVVGHMEQLQMNRSQ VTDLRCNLQGLE ELQWQLSM KAALEARFGPQLAQIQLASSIE AQLGDVRADSERQNQEYQLLM DIKLWLEQELATYSLLEGQEE HYNLSLSTKIL
9028	39396	A	9087	3	2026	AGPWDRMGAMGSLVGGDGL VWGCAEGFGAFGIPFSPCALTC EGNQGTRAKWVQTSTRILKGQ VKQARGAQVTPYSPLWHGKLG RAAPPTNAQGRWLLPPLLPPPL L*ITCLLGKRTLQEALSLKLQE LRKVCLQEAVERAWP*GYQAGR LGGGEELGPLGRPTTARAYPPP HPNQAHHSLCPAEV/MQMGVE SKRVGRGDYRGRVARRMALA PDLSTEQRRRRRQVQADALRRL HELEEQLQRDVRAVLGLPVLP QPLPLSTGSVTTQGVCLGMRL AQLSQGEHPLVRVGEWTLANG RGRAGMGDSYPNLPPTPTSL* PIPFIHPVSGGSPEERTPKWPPPS DLYGDLKSRRNSVASPTR*E*A PPPLRSRSEWDSPKGIAEGPAS DRASLFWARTRSNSSEALLVD RAAGGGAGGSPAPLASASGPP VCKSSLEVYERPQPTPAFFSRTA GPPDPRAARPSSAAPASRGAP RLPPVCGDFLDYSLDRGLPRS GGGTGWGELPPAAEVPGPLSR RDGLLTMI.PGPPPVYAADSNP LLRTKDPHTRATRTKPCGLPPE AAEGPEVHPNPLLWMPPTTRIP SAGERSGHKNLALEGRLDWYI RNSGLAAGPQRRPVLPVGPGPH PPFLHARCYEVQALYGAPSQ APLPHSRSTAPPVSGRYGGCF
9029	39397	A	9088	1	136	
9030	39398	A	9089	14	310	TFLFIYFFFETEWSHS\VPRECS GVI\$AHCNLHLLGSNNATSAS *VA\$VITGACHHAWLIFVFLV GFCHVG/RRLVSN\$*PQVIRLPW PPKVVLGLQAA
9031	39399	A	9090	1	436	
9032	39400	C	9091	75	410	

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9033	39401	A	9092	I	6691	MVNNTYREVKEGPVILEDVLIEVFRTLYSCKAELDLQTEPPFSKDHAQLSSKLRENKKTAELIKTANLLFNSFEPYVMWDYVARWFECCRRTLHVRLQIGPGDSNDSELQLTNFCLLVDFLLDIVSLETYIEIQTEHLPQPLLRLMISALTSHLQTHLSELTDSLRLCSKILSKVQPPLLSASTGGVLQFPGSQNNNSVKEWEDKKVSSVSHENPTEVFE DGENPPSSRSSESFGTFEIQYQA DRTDDIDRELS
9034	39402	A	9093	293	687	PTAKVYIFSIFLTYHIVCCINTSSLGFLQKNPEEDNSGRRTLGIWE PGHLLLTICTVRSMEQLLPFFN VLSQVFN SKVTSRCGHHGSPILYSNAFPN KDMKLENHNPCKSS KARQKIEEMVEKDFLEGMIKT
9035	39403	A	9094	3	4173	IPMVVSDFDLPDQQIEILQSSDS GCSQSSAGDNLSYEVDPETVNA QEDSQMPKESSPDDDVQVQVF DLICKVVSGLEVESASVTSQI.EI EAMPPKCSDIDPDEETIKIEDDSI QQSQNALLSNESSEQFLSVAEG GHECVANGISRNSSSPCISGTTT TLHDSSVASIETKSRQRSHSSIQ FSFKEKLSEKVSEKETIVKESGK QPGAKPKVKLARKKDDDKKKSSNEKLKQTSVFFSDGLDLENW YSCGEGGDIS
9036	39404	A	9095	5	1055	FDLERVRNLTYMVTRREKIKRSCVKVQEQQIFNLYTKLLEQERVS GVPSSC SSSLENMLLFNNSPSVG PDAPKIEDLKWPFCISSENKWV LPWVSG*KRPIKSRI LLQN*PW K*RONPAEAARPVW*KGGDGG PRELFGFRRKDLCRSTSHISTTEK WCGDARPWEKKRQSFSL*SH*R RLKGRI*TESQAS/PGPQMCPR GIWTTQELPPPWEWSQH LGTR KEIVPKCNGSLIKVNYNQTAVK VPPTPASPVKNWGGFRIPKGERRQ/PGRGPRWGLPPLRLPIFG LRPSSVTKERAKSCLKSDNNDGYVPDVEMSDSEASEAKKCIIHTSSTISRRTDIIRRSILAS

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9037	39405	A	9096	3	1136	FDIPFPKIGKLKISNVPVELRGHPLSITLVLRLMLLASKGDDPEDAKAKVLSVLKHSSL SFKQPRVM DMLKLFLFLSFLQFLGGKRAI*IQ EG*SYGVCDWLVTFTGIYWPWNL SNLVFVSVFLVNGLFHDLCPQTR KGSKHFSQDVMEKLVVLVLAHL FGRRYFPPKFQDAHFEFYQSKV FLDDLPEDFS DALDEY NMKIME DFTTFLRIVSKLADMNQEYQLP LSKIKFTGKECEDS QLVSHLMS CKEGRVAISPFCVCLSGNFDDDL LRLETPNHVTLGTIGVNRSQAP VLLSQKFDNQRGRKMSLNAYAL DFYKHGSILGLVQDNRMNEGD AYYLLKDFALT KTSISVSL/HVT YCENEDDNVVLA FQLSTTFW
9038	39406	A	9097	2	522	
9039	39407	A	9098	3	1080	FLLPFHQSKKKENSDQLMLTFLT SFNSLHSAMESFFQATGNSTNL ADDGKRTVVTPTVILTKIDGVN VDTHHIPVNVTLRRIAHGADAV AARWDFDILNGQGGWKS DGC HILYSDENITTIQCY SLSNYAVL MDLTGSELYTQAASLLHPVVY TTAIILVLCLLA VIVSYIYHHSLI RISLKSWHMLVNLCFHIFLTCV VFVGGITQTRNASICQAVGII LH YSTLATVLWVGVTARNIYKQG H*KS*KMPRI PDEP/RTFNQDQW LRFYPDLVGGYPPSLVLR A*AA NIKE L RQSAKPHPY/WLGW HGNPPWEAFYGPASFSTFVNC MYFLSIFIQLKRHPERKYELKEP TGQQQLACQ
9040	39408	A	9099	1	307	
9041	39409	A	9100	2	286	

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9042	39410	A	9101	35	1211	EKDLLWEEKFPDRRTVTELPQT SHVSFSEPDIPSSKSTELPVDWSI KTRLLFTSSQPTFWADHLKAQE EAQGLVQHCRATEVTLPKS1QD PKLSSCLRCTFQQSLIYWLHPAL SWLPLPRIGADRKMAGKTSP WSNDATLQHVLMSDWAVSFTS LYNLLK1KNFSPPYFVCTYQFT VLFRAAGLAGSDLITALISPTTR GLREAMRNEGIEFLSPLIKESGH KKETASGTSLGYGEYVIK1T/S SSDLWTHIEIDLHRNSL*NRDS NCSNF/LREQAISDEEESFSW LEEMOVQDKIKKPDLISLKLKE KHEVQMDHRPESVVLVKGINT FTLLNFIINSKSLVATSGPQAGL PPTLSPVAFRGATMQLKARS VNVKTQALSG1QRPI
9043	39411	C	9102	48	464	
9044	39412	A	9103	1	140	MNRLKKEWMLEHIVENNSGM ESQDIKGHIFHAADKDLLEMGY LQKRLGLGTVLHGWWGLTIM AEG*KRSGLSTLWK1PAWNL KTLKAIFMLLIKTYLKWA1YKR
9045	39413	B	9104	1289	2767	
9046	39414	A	9105	3	1278	INNTNTFRVLPHPSPFVYTAKFHP AVRELVVTGCGYDSMIRJWKVE MREDSAILVRQFDVHKSFINSL CFDTEGHMHYSQDCTGVIVVV NTYVKINDLEHSVHHWTINKEI KETEFKGIPISYLEIHPNGKRLLI HTKDOSTLRIMDLRILVARKFVG AANYPGEDS*YDF/VH/GGTFLF AGSEDGIVVWNPETGEQVAM YSDLPFKSPIRDISYHPPENMVA FCAFGQNEPILLIYIDFHVAQQ EAEMFKRYNGTFPLPGIHQSQD ALCTCPKLPHQGSFQIDEFVHT ESSSTKMQLVNQRLETVTEVIR SCAAKVNKNL5FTWPVAVSSQ QSKLKQSMLTAQEILHQFGFT QTGIISIERKPCNHQVDTAPTVV ALYDYTANRSDELTIHRGDIIRV FFKDNEWDWWYQHRRERGQEG

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9047	39415	A	9106	1	1249	MAVIJFLGCLLGGIAIGLPIAWA LLLGAALMFWLDMFDVQIMA QTLVNGADSFSLLAIPFFVLAGE IMNAGGLSKRIVDLPMKLVGH KPGGLGYVGVLAMIMASLSG SAVADTAAVAALLVPMMRSA NYPVNRAAGLIASGGIIAPIPPSI PFUFGVSSGLSISKLPMAGIAPG MMMGATLTLGKRARTFEDDR ERDAISVINHORNAVLIRQRVK LQQLFVIRVLAMRIFVYGSLRH KQGNSHWMTNAQLLGDFSIDN YQLYSLGHYPGAVPNGTVHG EVYRIDNATLAEGLARTRGGE YARQLIQTPYGSAWMYYVYQRP VDGLKLIESGWDWRVLRWLRVH SIDVPDPFIFGLTVTGDRTDRAG KTSPAQAGCKLFTNPLGIGVL TTAEKKSSLKPEHQGLATEVM CRMNIAGASFANIEGVKAMTD VTGFGLLGHILSEMCQGAGVQA RVDYEAIKPKLPGVEEYIKLGAV PGGTERNFASYGHLWLR*LAL AP/LEVVEANGSL*CSGERGCL YGQTTIQLNFRPAFCPEHAIAG QKVAILRLNMQIDIKRVSSRTH GNHFTNFKFTVQHYRSCLT

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9048	39416	A	9107	162	2106	KMSKLKIAVSDSCPDCFTTQRE CIYINESRNIDVAALVLSNDVT CGKLDEIDATGTYGIPVFIAHENQ ERVPAAEYLPRISGVFENCESSRRE FYGRQLETAASHYETQLRPPFF RALVDYVNQGNSAFCDCPGHQG GEFFRRHPAGNNQFVEVFGAVPC RLVIPALKQRKLSPLETAIVV VDRFSGEVRAMVGGSPEQFAG YNRAMQMARRSIGSLAKPATYLT ALSQPKIYRLNTWIADAPIALR QPNGQESVRVMLVDALTRSM NVPTVNLGMALGLPAVTETWI KLGVPKDQLHPVPMALLGALN LTPIEVAQAFQTIASGGNRAIPL SALR*TIAEHGKELYQSFPQAER AVPAQAAYLTLWTMQLQVVQR GTGRKLGAKYPNLHLAGKTGT TNNNVDTWFAGIDGSTVTITW VGRDNQQPTKLYGASGAMSIY QRYLANQTPTPLNLVPPDEDAD MGVDYDGDNFVCSSGMRLPV WTSDPQSLCQQSEMQQQPSGN PFDQSSQPQQQPQQPAQQEQ KDSDGVAGWITDMFGSNEHLS GYELDSYPLSSARRRARFTEDD TRERDAISVINHQRNAVLIRQR VKLQQLFVSNHIACWIRRPGDA NHPGFFANMQMLKIDVVFKLA FRQQFNIRTRRDKQIFFQSGVT
9049	39417	A	9108	1	66	
9050	39418	C	9109	79	150	
9051	39419	A	9110	2	475	GRGRWGAPRLRGAL*DP*GHF LQQQRPQLHSPAPDR\PAAPT DAEGL/PPAAAAAAAGATARVP GSRGG*GQAAEELHEAGEAQ CRGGTEDEEHG**HLCHGRAS* CPGVSGSTGSPHPSPSMAPDDT SGLLEFVGVPLQTLFAWVSPA AAEQRL
9052	39420	A	9111	171	462	PTSMGHLYSFPGN*SHAHYHPI KT*SPLPHSTPSNPSA\PLKGLK PVITRLLQHGQLLKPINSPYHSPIL PVLKPDKAYKLVQNLRLLINQIV LPIHSM
9053	39421	A	9112	1	573	
9054	39422	C	9113	100	297	
9055	39423	A	9114	1	1401	

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9056	39424	A	9115	24	482	VGSGDLPWEGNPLSSCSLLHEK DPPTTSGPQT/GP/GPRNISPILNR AAPRQAGLGPNSSSASAPPYNN PFITSPHHTWSALQFRIVTSPPPP AQQLTLKKVAGAKGTVKHEHFC HDLPASSMQSNEYPVHDGHLT TGPSLFKPTLNIEYSTGHAP
9057	39425	A	9116	1	489	
9058	39426	A	9117	1	642	
9059	39427	A	9118	237	748	ETNPLSSCSLLRDKDPPPTSSPQ THQPKKHIPPISNPAA PHQAEELG PNPSSASAPPYNNLFITSPHHTW SGLPFRSVTSPPPPAQQFTLKKV AGAKGTVKTTIDIELQVLTVE ARLRGEINSHVAHTKPVWWS LHTDTCDIWCRRPGBTGGLQET SPLSSPSLCEEIHL
9060	39428	A	9119	63	255	WVSGSPVQVKVERGWDEGCKGI VKKACLTYTNRIMHCVGRY*A *ESIWWHHGVNRQNNLVDKA
9061	39429	A	9120	24	389	SDVKANLSTGGPVGC GGDTL/P VAEKPSDAVEAPGV*APSAGG AGPA PSPGLEPSGAPPPIP/ALPP RAVLDSGLAPGRPLPLASSNP/P PAGRLLLCTSPGRRGGAAGSG PRCPESKSIPRLCL
9062	39430	A	9121	704	867	CVKECLDVRLHRPFAVFTTRII* ILQDGKIQSAIF/CVIWNHYCRVC GVKRHSRK
9063	39431	A	9122	1	7068	
9064	39432	A	9123	2	165	LLKRELNFDFYKISTTKERHLQ QS*PKDS VPSLLASQTPNAPFL APQRRLCLA
9065	39433	A	9124	1	148	IRHSVNLLAG/RIFVFEPPIGLK ANTQRTFESGMKHVRRIYMMEF HVFM

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9066	39434	A	9125	1	2340	QFGIWLDSSSPEQTVPYLWSEE TPATPIGQAIHRLILLIQAFRPRDR LLAMAHMFVSTNLGESUFMSIM EQPLDLTHIVGTEVKPNTPVLM CSVPGYDASGHVEDIAAEQNT QITSIAIGSAEGFNQADKAINTA VKSGRWVVMLKNVHLAPGWLML OLEKKLHSLQPHACFRLFLTME INPK\VPV\NLLRAGRIFVFEP\PP G\VKANMLRTFSSIPVSICKSP NERARLYFLLAWFHAIHQERLR YAPLGWSKKYEFGESDLRSAC DTVDTWLDDTAKASGRQNISP DKIPWSALKTLMAQSIIYGGRV DNEFDQRLLNTFLERLFTTRSF DSEFKLACKVDGHKDIQMPDG RREEFVQWVELLPDTQTPSWL GLPNNAERVVLLTTQGVDMISK MLKMQMQLDEDDEDDLAYAETEK KTRTDSTDGRPAWMRTLHTT ASNWLHLIPQTLSHLKRTVENI KDPLFRFFEREVKMGAKLLQD VRQDLADVVQVCCEGKKKQTN YLRTLNELVKGILP\RSWSHYT VPAGUMTVIQWGPISARRJKQ LQNISLAAASGGAKELKNIHV LGGLFVPEAYITATRQYVAQAN SWSLEELCLEVNVTTSQQGATLD ACSFVGVTGLKLQGAATCENNKL SLSNAISTALSLTQLRVVKQTN TEKKASVVTLPVYLNFRADLI FTVDFEIAKTEDPRSFYERGGG
9067	39435	A	9126	3	6375	HKVAAPDVVPTLDTVRHEAL LYTWLAEHKPLVLCGPPGSK TMFLFSALRALPDMEVVGLNF SATTPELLKTFDHYCEYRRTP NGVVLAPVQLGKWLVLCFDEI NLPMMDKYGTQRFVISFIRQME HGGFYRTSDQTWVKLERIQFV GACNPPTDPGRKPLSHRFRLRH PVVYDYPGPASLTQIYGTFNR AMLRLIPSRLTYAEPLTAAMVE FYTMSQERFTQDTQPHYIYSPR EMTRWVRGIFEALRPLE

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9068	39436	A	9127	3	617	SWFQPPSGPPWPGA PPPPLAR VNPGVPSLTTSLMDVED*AQV ELPSHPRVPSPAPGPAD*VLEPP RSLLTSVVGPGQGPSWAGGMA VRQALEAAACRDPCIAISSWAG GDRPLWLDGLLRRVYPDSC PPCPSRIPAIFGASLQGSINPILQ MRKLFPHMDLL*QQDPFCSR RPESWNRDVGWLALGVFCLVP FSLVGSLN
9069	39437	A	9128	1	702	
9070	39438	A	9129	1	1317	
9071	39439	A	9130	1	2641	MGLKARRAAGAAGGGGGGG GGGAANPAGGDAAAAAGDEE RKVGLAPGDVEQVTLALGAGA DKDGTLLLEGGRDRDEGQRRTP QGIGLLAKTPLSRPVKRNNAKY RRIQTLIYDALERPRGWALLYH ALVFLIVLGICLILAVALTTFKEY ETVSGDWLLLLETFAIFIFGAEF ALRIWAAGCCCRYKGWRGRLK FARKPLCMLDIFVLIASVPVVA VGNQGNVLATSLRSRLFLQILR MLRDGPGEGGTWKLLGSAICA HSKELITA WYI GFTL LSSFLV YLVEKD VPEVDAQGEEMKEEF ETYADALWWGLITLATIGYGD KTPKTWEGRLLIAATFSLIGVSFF ALPAGILGSGLALKVQEQRHQK HFEKRRKPAAELIQAARWYYA TNPNRIDLVATWRFYEVSVSFP FFRKEQLEAASSQKLGLLDRVR LSNPRGSNTKGLKFTPLNVDAI EESPSSKEPKPVGLNNKERRTA FRMKAYAFWQSSEDAAGT GDP MAEDRGYGNDFPIEDMPTLKA AIRAVRILQFRLYKKKFKETLRP YDVKDVIEQYSAGHLDMLSRIK YLQTRIDMIFTPG PPSTPKHKE VFRKGQHFTFPSQQSSRGLNHM *ARPSTISE EDQRH*WGKFVK LKGQV QGLGRKLDFLVDMHM QHMERLQVQVTEYYPTKG TSS PAAEKKEDNRYSDLKTIICNY
9072	39440	A	9131	353	477	QNEILPQISKSNNEL*SRSPII*ITR NLNNNSNKMAHKMKFAN
9073	39441	C	9132	170	310	

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9074	39442	A	9133	1	859	MSCGRRPPDVGMITLK\VNLDNL TYRTSPDSLRRVFEKYGRRGVGDV YIPREPHTKAPRGFAFVFRFHDE RDAQDAEAVAMDGAE*EGRAL R1QVARYGRDLPLRSRQG/PTP RGRSRGGYGRRSRSYGRRSRS PRRR/HNRNFFCPSCSRERRGR YRGSRYSRSPYSPRSYSPRSYSR SPYSRSRYRESRYGGHYSSSC YSNSRSYRSHSSRSHSKPGSSTS SRSASTSKSSSSRNSRSKFSVS\RS RSRISRSSSMTRSPVGVSKRKSK SR\RSRKRPPKSPPEEEGQMSS
9075	39443	A	9134	161	332	SCLNQLN/YLEMWKLFRKAQE DHHTGRDIDSYYAEVRPGEAGGR AHTGDSLLTMNPSFL
9076	39444	A	9135	1123	1489	LQTILQGHSNQNMSMVLVPKQR YRSMEQNRLARNNVYTQLQSD L*QA*EKQAMGKGFPIS*MVLG KLASHM^KAESGSLPYTLYKN* FKMD*RLKH*T*NHKNPRRKPR HYHSGHRHGQQGLHV
9077	39445	A	9136	277	367	
9078	39446	B	9137	1	1136	
9079	39447	A	9138	3	1168	
9080	39448	A	9139	1	1460	ERGLETNCSSEELSSPGRGGG GGGRLLLQPPGPPELPVPPVPLQD LVPLGLRSRGEQQQQQQQQQPPP PPPPPPGLPRLPLAGPSRKGSFKIRL SRLFRTKSCNGGSGGGDTGK RPSGELAASAASLTDMGGSAG RELD\GRKPKLTRTQSASFSPVS FSPLFTGETVSLVVDVDISQRLT SPHPPTPPPPRRLSLLDDDISGT LPTSVLVA PMGSSLQSFPLPPPP PPHADAFPRIAPIRAAESELHSQ PPQHLQCPLYRPDSSSAASLRE LEKCGWYWGPMNWEDAEMK LKGKPDGSFLVRDSSDPYIYL SFRSGQGITHHTRMEHYRGTFL WCHPKFEDRCOSVVEFIKRAIM HSKNGKFLYFLRSRVPELPPNS CQ\LIYPMRSFSIYESFQHIAKF RIRQLVRIDHIPDPLPKPLISYI RKFYYDYPQEEVYLSKREAQS VSKQKQVEPST*RGAPCWSPP RAFGCQAPALKNQIKLP

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9081	39449	A	9140	2	418	KSPSKYLCYTFIISTAALVLLIM LPHESMPVYLGMACTLGFGAIV FTQRAVIFFAPIGEAKIAENKTG AAMALGSFIGYAPAMFCFSLYG YILDINPGIIGYKIVFGIMACFA FSGAVVSVMLVKRISRKKEM IAAEA
9082	39450	A	9141	26	180	KPAHQCCQVFFCPVVAHQGEV LPYKGSGVTIESFVTIICKVIRR* LLSFLA
9083	39451	A	9142	299	921	FGTAALVL*IVLPPEISPSH*GM ACTLGLGAIVLTQRAV/FAPIG EAKIAENKTGAAMALGSFIGYA PAMFCFSLYGYIQLDNPGIIGYK IVFGIMACFAFSGAVVSVMLVK RISQRRIIRRLRRIRQFHRRNTSS RYGSFARGGRKATRGISQEL GQGLSGEEQDGASGGVTAGDI ATGDYFLTPHLQICTGAKGGL GCVVEGR
9084	39452	A	9143	1	752	MSELPAIASKRKEYVGQLPR YTIQKLEENLNVVLFDRSGHRT KFTNVGRMILLERGRVLLQAAD KLTTDAEALARGWETHLTVITE ALVPTPAFFPLIDKLAANKANTQ LAIIT*VLAGAWERLEQGRADI VIAPDMHFRRSSSEINSRKLYTL MNVYVAAPDHPIHQEEPEPLSEV TRVKYRGIAVADTARERPVLTV QIILDKQPLRTVSTIEDKQALL AGLVGVATMPYPMVEKDIAEGR LRVVSPESTS
9085	39453	A	9144	389	760	SWRIDVHPV*YTTRLFPFVLPY MQKGTSIRTSSRQLDKQPLRT V/STIEDKRQALLAGLGLVA/TMP YPMVEKDIAEGRLR/VVSPESTS EIDIIMAWRVTKRTPKN*WTM MPENIGEYTKTTHILG

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9086	39454	A	9145	1	941	MTAMERSRILRRAVDILRERND ELAKLETLDTGKAYSETSTVDI VTGADVLEYAGLIPIALEGSQI PLRETSFVYTRREPLGVVAGIG AWNYPIQIALWKSAPALAAGN AMIFKPSEVTPLTALKLAEIYSE AGLPDGVFNVLPGVGAETGQY LTEHPGIKVSFTGGVASGKVV MANSAASSLKEVTMELGGKSP LIVFFDADLDAADIAMMANF FSSGQAQR/NGARVLCGGDGVR ARDRPNLRRENLRGKYHS*QR HRRPDAC*YRPRL*RCGGRYAD D*VQAGAGSDGL*ATGHGGR EC*PYVTGEAG
9087	39455	A	9146	3	504	DQQQNQRQLIDCFPHAQWAKE VDVSDKEARCGVRCATRDHLP MVCNVPDYEATLVEYASSAEA KDDAVSAPVFDDLFILESGRGLC SGPLCAEILAT*ISDEPMMPMDA SMLVAALIPNRLWVRKLLKGKA VKAGAVHFRRSIIYFHPPQQANA LDFPSTHIKYCTMLL
9088	39456	A	9147	197	353	YGFRWP*D*AHPAIN*ASAASIF LRWLIRLRTSITETTAPLNAKQAI MPNTIL
9089	39457	C	9148	1	1263	
9090	39458	A	9149	3	726	GAKNAREAIYHIEGDPDHPIEN RLRYPEYRAPGSDKWQRISWEE AFSRIAKLMKADRDNFIEKNE QGVTVNRWLSTVNKKKISLRT VGAALVLQVVIIGGIMLWLPPG RWVAEKVAFGVHKVMAYSDA GSAFIFGSLVGPKMDTLFDGAG FIFGFRLPAIIIFTALVSILYYI GVMGILIRILGGIFQKALNISKIE SFVAVTTIIFLGQNEIPAIVKPFID RLRNRELFTAICSGMASIDG
9091	39459	B	9150	1	1662	
9092	39460	B	9151	1	2658	
9093	39461	C	9152	1	2526	
9094	39462	A	9153	422	585	PYRLKQNIAGA*PIKLPNAIAAP VLFSAIFASTIGAKILLAVLRLSR PHPSVHA
9095	39463	A	9154	1275	1485	
9096	39464	A	9155	1	439	

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9097	39465	A	9156	1049	2195	NMPKASSCRFSTATTYLDRSRC K*PWAGS*KKNSWR*CCRRTTS SHTRLNATWGVSVKRTKAR CSMVACASRG/SNARGLELVKE GRAQACVSAGNTGALMGLAK LLLKPYLEQHNHRMLLRWEAKL AALVRLQENTAQPVPFAPNNA RPLTLEDDRLSCTVRGYNFAITF SKMSGKPTSWQLVASALATKI AHEVNPNQNQVGCMLAGGNFYP YSCKPEDVWAALEKDRENFFI DVQARGTYPAYSARVFREKGV TINKAPGDDEILKNTVDVFSFSY YASRCASAEMNANNSSAANNV KSLRNPyLQVSDWGWGIDPLG LRITMNMMYDRYQKPLFLVEN GLGAKDEFAANGEINDDYRISY LREHIRCNGRSDCRQAFR
9098	39466	B	9157	482	542	
9099	39467	A	9158	115	1662	TPYPDIAITTHDIVDTYPVQGGA VRVLVFSAWSLRVVSSVLSFLV WGFVSCRRFVPCRVCVLLCLL FWCFVFGVWLPRRHMSNHAAI GVGEQQCQRGNINGA/PETFAS MANTGT*QW/QRISWEAEFSRI AKLMKA/DRDANFIEKNEQGVT VNRWLSTASLAPTFGRGAMTN HWVDIKNANVVMVMGGNAE AHPVGFRWAMEAKNNNDATLI VVDPRTTRTASVADIVAPIRSGT DITFLSGVLYLIENNPKINA/EYV KHYTNASLLVRDDFAFEDGLFS GYDAEKRQYDKSSWWNYQLDE NGYAKRDETLTHPRCVWNLLK EHVSRYTPDVV ENICGTPKADF LKAPDRTTTFLYALGWTQHT VGAQNIRT MAMIQLLLGNMG AGGGVNLARGHNSNIQGLTDLG LLSTSPLPGYLTLPSEKQVDLQS YLEANTPKATLADQVNYWSNY PKFFVSLMKSFYGDAAQKENN WGYDWLPKWDQTYDVIVKYFN MMDEGKVTVGYFCQGFNPVASF PDKNKVVSCSLKLKYMMVVIDP LVTETSTFWQNHEAVSGGKR PGRKRLNLLPMARLTIIASAT YANISAQWAKRLQTAFR
9100	39468	A	9159	1	2235	
9101	39469	A	9160	1	1821	

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9102	39470	A	9161	14	1785	FDQVEERVSVIEDQMNEKRE EKFRERKRVIRNEQSLQEIWDYV KRLNLHLLIGVPESDWENGTKLE NTLQDIIQENFPNLARQANIQIQ EIQRMPQRYSSRR\TPRHILNA HKRK*ERYKIDTLTSQLKELEK QEQTYSKASRRREITKIRAEELKE IETQKTLQKINESRSRSCFEKINKID RLLARLIKKREKNQTDVKND KGDDITTDPTEJQTTRREYYKHLY TNKLENLEEMDKFLDTYTLPLR NQEEVESLNRPITGSEIEAIINSL PTKKSTGPDRFTAEIFYQRYKEE LVPFLLKLFQSIEKEGILLNSFYE ASTILIPKAGRDTTKKENFRPISL MNIDAKILNKILANRJQQHHIKKL IHYNQVSFIPGIQGWPNICKSIN VIQHINRTKDKNHTIISIDAEKA FDKIQQQPFMLKTLNKLGDGTY LKIMTAIYDKPTASTILNGQKLE AFPLKTGTRQGGPLSPLLFNIVL EVLARAIRQEKEIKGIGQLGKEEV KLSLFADDMIVYLENPIVSAQT LLKLISNFSKISGYKINVQKSQV FPYTNNRQTESQIMSELLFTIAS KRIKYVGIGQLTRDVKDLFKEN
9103	39471	B	9162	1	2025	
9104	39472	B	9163	67	3156	

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9105	39473	A	9164	I	2019	MDTIKNDKGDIITDPTEIQTTIR EYYKHLYANKLENLEEMDKFL DTYTLPLRNQEEEVESLNRPVRG SEIEAIIINSPLT/KKSPGPDEFTAE FYQRK\AFDKIQQ\AFTLKTLNK LVIDGTYRKIIRAICDKPTANIL NGQKLEAFPLKTGTTRQGCPLSP LLFNIVLEVLDRAIRQEKEITC Q LGKEEVKLISLFADDMIVYLENP IISAQNLKLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKKIKYLG QLTRDVKD LFKENYKPLLNEIKEDTNKWEN IPCSWVGRINIMKMAILPKVIYR FNAIPKLPVAFFTELEKTTLKFI WDQKRAYIAKSILSQKNKAGVI MLPPDFKLYYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMLHIY NYLIFDKPDKDEQWGKDSLNFN KWCWENWLIDIWRLKLKLDPLT PYTKNSRWIKDLNVRPKTIKTL EENLGNTILDIGMGKDFMSKTP KAMATKAKIDNWDLIKLKSFCT TAKETTIRVNRQPTKWEKIFTT YSSDKGLISRIYKELKQIYKKKT NNPMNKWAKDMNRHFSKEDI YAAKRHMKKCSSSLAIREMQIK TTMRYHLTPTVRMVIIKKSGNRR PPLSKEQPPPIFRLSIILATTRDGN PAAVENVLHIKATLSPQQTHKA FYFQPS
9106	39474	A	9165	I	3477	

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9107	39475	A	9166	1	2460	MGDFNIPLSTSRSRTRQKVNDKTQELNSALHQADLIDIVRTLHPKSTEYTFPSAPHHTYSKIDHIVGSKALLSKCRRTIEITNCLSDHSAIKLEIRKKLTQNCSTTWKLNNLLLNNDWVWNEMKAEKIMFFENEDKDITTYQNRWDTFKAVCRGKFIALNAHKRKQFRSKIDTSQLKELEKQEQTFSKASRRQEITEIRAELEKEIETOKTLQKMNESRSWFPEKINNIDRLLRAKIKKREKNQIDAICNHKGDDITNPTEIQTITIREYDKHLYANKLENLEETDKFLDTYILPRLNQEQVESLNRPITGAIEIAINSLRTKKSPGVPGGFTAEFYQRYKEE/HVLEVLRARIRQEKEIKGIQLGKEEVKLSLFADDMTVYLENPTVSAQNLKLISNFSKVSGYKINVQNPOQAFLYTNNRQTESQIMSELPTIASKRKYLGQLTRDMKELFKENYKPLLSEIKEDEINKWKNIPCSWGRINIVKMAILPKVIYRFNAIPKLPMTFTTELEKTTFKFIWNQKRARIAKSILSQKNKAGGITLADFKLYYKATVTKTAWYWYQDRHDQWNRTESSEIMPHIYNYLIFDKPDKNKKWGKDSLNFNWCVWENWLAIKRKLKDPFLPTYTKINSRWIKDLNVRPKTIKTLLEENLGITIQTDMGKDFMSETPKAMATKDIDKWDLIKLKSFCTAKETTIRVNR
9108	39476	A	9167	1	1389	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, -=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
9109	39477	A	9168	I	1659	MGDFNTPILSTLDRSTRQVKNDTQELNSALHQADLIDIVRSILHAKSTEYTFPSAPHHTYSKIDHILGSKALLSKCKRTEIITNYLSDHSAIKLELRKNLQTQRNSTTWKLNNLLNDYWIHDEMKAIEKMFFETNEKDFTTYQNLWDAFKATA SKTNKEKEKNQIDTIKNDKGDI TTDPTEQTTIREYYKHLHYANKLENLEEMDKFLDTYTLPLRNQE EVESLNRPITGAEVIAVINSLPTK KSPGPDGFTAEFYQRYKEELHNRAKDKNHMIIISDAKAFFDKIQQPFMLKTLNKLIGIDGTYFIKIRAIYDKPTANIIILNGQKLFAPPLKTGTRQGCPLSPLLNFNILEVLR AIRQEKEIKGIQLGKEEVKLSSLF ADDMTVYLENPVSAQNLKKLISNFSKVSGYKINVQKSQAFLYTNNRQTESQIMSELPTIASRKIYLGSQLTRDVKDLFKENYKPLLKEIKEDTNWKWNIPCSWVGRINIMKMAILPKVIIYRFNAIPKLPMTFFTELEKTTLKFIIWNQKRARIAKAIALSQKNEAGGITLP
9110	39478	B	9169	I	1716	
9111	39479	B	9170	I	3171	
9112	39480	A	9171	I	2952	MLLNQGRKLPRVFAEETLKFGTSNKPQTLEQISTSIIAQKEATVMVPGSNQEIPSGAYAIRALGFKHKTGRLFEQTLNLYLQEFLFTPQWHLECQQERTVHSPGKAAEA REPSVIDRHLIQESSNWHLVGAALGQSFCRKEQAIAFAVLQPLLVIPRQTGSGVDLQKTPSDLQRGLIVRKTNKQKGIVINSTREQNWTENEFDKLTEGGFKRWVITNSSELKEHVLTLQCKEDKNLEKSAIKLELRKNLIQN
9113	39481	B	9172	I	2406	
9114	39482	A	9173	I	2307	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met codon in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, -=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)	
9115	39483	A	9174	3	2776	QRDLDSHTLIMGDFNTPLSILDR STROKVNKD^TQELNSALHQAD LIDIVRTLHPKSTEYTFPSAPHH TYSKIDHILGSKALLSKCKRTEII TNCLSDHSIAKLELRIKTLTQSH STTWKLNNNNNDYWWHNEM KAEIKMFFETNENKDTTYQNL WDAFKAVCRGKFIALNAHKRQ QERSKIDTLSQLKELEKQEQT HSKASSRQEITKIRAKELKEIETQ KTLQKINESRSWFERINKIDRP LARLIKKREK
9116	39484	B	9175	133	3213	
9117	39485	A	9176	284	1689	QNFGNFKDLL^RSLW^REKSWI CML^ARNTASRQQRNKAGQR MTLMS^EKKASDDQTSPS^R/Q EVRTHRKEAKNLVKRLDKWLNR RITSVEKSLNDLMEALKTM/RTR TTT^*MHKLQ^PI^SFGRKEIQT IREVKHLHYANKLENLEEMDKFL ETYTLPLRNQE^EVESLNRPITGS EIEAIINSLPTKNSPGPDRFTAKF YQMYKEELVPFFLKLFQSIEQE GILPNSFYEAISIILIPKPGRDPKT KENFRPISLMNIDAKIFNKILAN QIQQHIKKLJHHQDMGFIPGMQ DWFNIRKSVINVQHINRTKDKN HTIISIDAEKAFDKIQQQCFMLKT LNKLGIDGTVKIIRAIYDKPTA NIILDGOKLEAFPLKTSTI^QGCP LSPLLFIIVLEVLAARAVRQEKEI KGIQSGKEEVKLSSLFADDMTV YLENPPIASAQNLLKLKSNFSKVS GYKINVQKSQ^FLYTNREPN
9118	39486	A	9177	1	1515	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met codon	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, -=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
9119	39487	A	9178	3	1601	ESRS*FFEKINKI/D/RLALARLIK KREKNQIDAIIKNDKGDDTTDPT EIQTIREYYKHLYTNKLENLEE MDKFLNTYTLPLRNQEVEVESLN RLITGSEIEAIINSL!TKKSPGLD TFTAEFYQRYKEELVPFLKKLF QSIEKEGILPNSFYEAIILIQKPG RDTTKKENFRPISLMSNAKILN KILANRIQQHIIKKLHHHDQVGSI PGMKGWFNICKSINVMQHNRNT KYKNHMIISIDEEKAFOQKIQKRF MLKTLNKLKSIDGTYLKIIIRAIYD KPTANIIILNGQKLEAFPLKINGT RQGCPLSPVLFNIVLEVЛАRAI/ RLISCFSKVSGYKINVQKSQAFL YTNNRQTESQIMSELPTIASKR IKVLGQLTRDVKDLFKENYKP LFNEIKEDTNKWKSiPCSRVGRI NIVKTAILPKVIYRFNAIPKLPM TFFTELEKTTLKFIWNQKRACIV KTILSKKNKAGGITLPDFKRYY KATVTKTA/WSFHELGTKLAT RTTVSTFQQIPGI*VQLRFDPSR DITLLSLLCR
9120	39488	B	9179	1	2034	
9121	39489	B	9180	1	2088	
9122	39490	A	9181	1	1870	MKAEIKMFFETNENKDITYQN LWDTFKAVCRGKFIALNAHKR KQERSKIDTTLSPKLELKQEQT HSKASSRRQEITKIRAELEJETQ KTLQKINESRSWIFESINKIDRPL ARLIKKKREKNQIDAIIKNDKGD IITDPTEIQTIREYYKHLYANK LENLEEMDKFLDTYTLPLRNKE EVESLNRPITGAEIVAINSLPTK KSPGPDGFTAEGYQRYKEELVP FII.KLFQSIEKDGI.PNSFYEASI ILIPKP
9123	39491	A	9182	1	1410	
9124	39492	A	9183	1	3996	

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9125	39493	A	9184	281	3030	KPRLENMKNAEASRADAINW KKGY/LVMEDKMNEMKREGKF REKRIRKNKQSLQEIWDYVKRP NLRLISVPESDRENGTKLENTL QDIIQENFPNLARQANIQIQEIQ RTPORYSSRRATPRHIVRFSKV EMKEKMLRAAREKFIQTNIREY YKHRYANKLENLEEMDKFLNI YTLRLLNQEEVESLNRPGRSEI VAIINSLPTKKSPGPDGFTAEYY QRYKEELVPFLLKLFSIEKEGI LPNSFYEASII
9126	39494	A	9185	1	2250	
9127	39495	A	9186	248	2385	RQWAGVVGRCSHLASWVSSNT SETGAIRSSTEVDAPDDSMILLST CDIDLTAARRAWLGCLPTKKSP GPDGFIAEFYQRCKEELVPFLL KLFQSI/EKEGILPNLFDEAHSIL PKRGRDTTAKENFRPISLMNID AKILNKILANRNQQHIKKLIHH DQVGFIPGMQGWFNICKSINV QHINRTKDKNHNMIISDAEKAF DKIQPPFMKLTNLKLGIDGTYL KIIIRAIYDKPTAIIILNGQKLEAF PLKTGTROGCPPLSPLLFNVLEV LARAIRQEKEIKGJQLGKEEVKL SLFADDMIVYLENPIVSQAQNLL KLISNFSKV SAYKINVQKSQAF LYTNNRQTESQIMSVPFTIASK RIKYLGJQLARNAKDLFKENYK PLLENEIKEDETTKWKNIPCSWSVG RINIIVKMAILPKVIVYRFNAPIKL PMTFFTELEKTTLKFIWNQKRA RIAKSILSQKNKAGGITLPDFKL HYKITVTKTAIWYQYQRNDIDQ WNRTEPEITPHIYNYLIFDKPE KNKQWGKDSDLNFNCWCWENWL AICRKLLKLDPLTPYTKIHPRWI KDLNVRPKTIKTLEENLGNTIQ DIGMGKDFMSKTPKAMAAKA KIDKWDLIQLQKSFCTAKETTIRV NRQPTKWEKIFATYSSDKGLIS RIYKELKQIYKKKVNPNPIKKW AKDMNRHFSKEDIYAANKHM KKCSPSLAIREMQIKTTMRYHL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, -=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
9128	39496	A	9187	I	2229	MGKKQNRKTGNNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSSELREDIQTKGKE VQNFENLLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSAMEDEMEMKRE GKFREKRIKRNEQLSQEIQDYYV KRPNLRLLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRTPQRYSRRATPRHIIVR FTKVEMKELRAAREKEIQT TIREYVYKHYANKLENLEEMD TFLDTYTLPLRNQEEVESLNRP TGSEIVAIINSLPTKKSPPGDPFT AEFYQRYKEELVPFLLKLFQSIE KEGILPNSFYEAISIILIPKPGRDT TKKENFRPISLMNIDAKILNKIL ANRIQQHKKLIHHHDQVGFIPIG MQGWFNIRKSINVIQHINRAKD KNHMISIDAEEKAFDKIQQPML KTLNKLIGDGTYFKIIRAYIDKP TANIIINGQKLEAFLPLKTGTRQ GCPLSPPLLNIIVLEVLAIRARQE KEIKGIGLGKEEVKLSLFAADDM IVYLENPVSAQNLLKLISNSFK VSGYKINVQKSQAFLYTNNRQ TESQIMGELPFTIASKRIKYLGQ LIRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWSVGRINIVKM AILPKVIGKTTLKFIWNKKSRIAK SILSQKN/KAGGITLL TQLYYKA TVTKTAWYWYQNRDIDQWNR
9129	39497	A	9188	I	2667	
9130	39498	A	9189	I	3033	MADMLTWESCLEESLQEESPL VTHCGPSCCISGQSPPSSARPSS VSSAISVLMLPQNRLKPPAWTS PGIFPTDLVVYSMSLPHALARY NCDVCKSMSLPPRLYAPEEKAR TSPLCGTWYSPSLPLCGAWCKK NEKKRERERERKRQREDILSGA SSYKDTHIQLRPPTYDVLQQIQ TTIREYVYKHYANKLENLEEMD KLLDTYTLPLRNQEEVESLNRLI TGSEIVAIINSLPTKKSPPRDPFT AEFYQRYKEE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met and	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, -=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
9131	39499	A	9190	1	950	MQAJCTGQARALICMGGNFAMPDREASAVPLTQLDLAVHVATKLNRSHLLTARHSVILPVLGRSEIDMQKNGAQAVTVEDSMSMIHASRGVLKPAGVMLKSECAVVAGIAQAALPQSVVVAWEYLVEDYDRIRNDIEAVLPEFADYNQRIRHPGGFHLLNAAERRWMTPSEIQTIREYYKHLYTNNKL\ENLEEMDKFLDTYSPLPRNLQEEVESLIRPITGSEIEAVVNSPPTKNSPGPDRFTAKFYQRV/K/EELVPFFKLFLAAVPAPSSHGPCCSRKA LRGSKTGSAYPSSALLRRVTSEVVCLFAEAQLF
9132	39500	A	9191	1	3470	MASVSSATFSGHGHARSLLQFLRLVGQLKRVPRTGWVYRNVQRPESVSDHMYRMAVMAMVIKDDRLNKDRCVRLALVHDMAECIVGDIAPADNIPKEEKHRREEGNKCHKQKAMGKHLLKEPHVLGQETKGLESTDVLLPLPAAGQDILGREKKIREEAMKQITQLLPEDLRKELYELWEDLEFESPSCLDSSLSCCSLKQSESSSPVLPPEGCTLIQRLCAVGTGVTAAALATRLCRASGLPAPHQWASELQRSRKE
9133	39501	A	9192	1	3907	MAAWNLLLKSAYWGGLRKEDFHCLDRKTLRTVSFLAALLSYESIGGKGKLTRKDIIYTNPSVHHHHQRPKVDKTTKMGKKQN RKTGNSKMQSASPPPKERSSSPATEQSWMENDFEELREEGFRRS NYSELREDIQTKGKEVENFEKNLEECITRITNTEKCLKELMELKT KARELREECRSLRSRCDDQLEERSAMEDEMNEMKREGKFRDK RIKRNQLSQEIWDYVKRPNLR LIGVPESDVENGTKLENT
9134	39502	A	9193	3	3197	

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9135	39503	A	9194	I	3158	MVKGSIQQEELTILNIYAPNTG APRFIKQLLSDLQRDLDLHSHTLIM GDFNTPPLSTLDRSTRQKVNKDT QELNSALHQADLIDIVRTLHPK STEYTLFSAPHHTYSKIDHILGS KALLSKCKRTEITNYLSDHSAI KLELRIKNLTQSRSRTTWKLNNL LLNDYWRKQERSSTDTLTSQL KELEKQEQTQSKASRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRPLARLIKKEKNQID TIKNDKGD
9136	39504	A	9195	I	3285	
9137	39505	B	9196	I	1366	
9138	39506	A	9197	735	3541	RSFPRSRSPFILLSSRYLRIHMVF SVLPFGLQNPKYLLSGSLQEK FRTPGINSHKTLDPNRVIKVR RLEKEKALRAYVGKSEVRNMH LERCKL**KREKNQDITIKND KGDIITDATEIQTIREYYKHLY ANKLENLEEMDKFLDTYLPLRL NQEEVESLNRPITGESEIAINSL PTKRSPGPDGFTAEPYQTYKEE LVPPFLKLFQSTEKEGILPNSFY EASILIPKPGDRDTKKENFRPIS
9139	39507	A	9198	I	5356	MGKKQNRKTGNNSKMQSASPPP KERSSPATDQSQWMENDFDEL REEGFRRSNYSSELREDIQTKGK EVENFEKNLEECITRITNTEKCL KELMELKTARELRECRLSRS RCDQLEERSAMADEMNEMK QEGKIKRDKEGHYIMVKGSIQQ EELTILNIYAPNTGAPRFIKQVL SDLQRDLDLHSHTLIMGDFNTSLL TLDRSMRQKVNKDTQELNSSL HQADLIDIVRTLHPKSIEYTFFS APHIHTYSKIDHIVGS

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
9140	39508	A	9199	1	2491	MGDFNTPLSTLDRSTRQEVNK DTQELNSALHQVQLIDIYRTLH PKSTEYTFPSAPHYTYSKIDHV GSKALLSKCKRTEIITNCLSDHS AIKLELRKKLTQNHNSTTWKLN NLLNDYWVNNEVKAIEKMF ETNEKDTTYQNLWDTFKAIN KIDRPLARLIKKREKNQDAIK NDKWIDTTDPTEIQTTCIREYYK HYANKLENLEEMDKFLDTYT LPRLNQEEVESLNPRTGEJEIA TNSLTTKSPGPDGFTAKFYQR YKEELVPFLLKLFLQLEIKEGILP NSFYEAISIILPKPGRDTTQKQK NFRPISLMNIDAKILNKILANRJ QQHIIKKLIIHHDQVGFIPGMQG LFNICKSINVHHINRTDKDKNYM IIS/I*DAEKAFDKIQQPFLKTL NKLIGIDGTYLKJURAIYDKPTAD IIINGQKLEAFSLKTGTQRGGPL SPLLNFIVLEVLRALARVQRKEIK GIRLGKEEVKLSI.IADDMIVYL ENPIVSAPNLKLISNSFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPTIASKRKRYLGIQLTRD MKDLKENYKPPLLNEIKEDTNK WKNIPCSWGRINIMKMAILPK VIYRFNAIPIKLPMTTFTELEKTT LKFIFWNQKRARIAKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWWYQRNIDQWNRTEPESEIT PHIYNYLIFDKPEKMSIIDTGGW
9141	39509	A	9200	1	3083	MGKKQNRKTGNSKTQSASPPP KERSSPATEQSWMENDFDEL EEGFRRSNYSLELDIQTKGKE VENFEKNLEECITRITNEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLLQEIWWDYV KRPNLRLLIGVPESDVENTKLE NTLQDIHQENFPNLARQANVQI QEIQRTPQRYSRRAATPRHIIVR FTKVEMKEKMLRAAREKEIQT TIREYYKHLYANKL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hnd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, -=Stop codon, /=possible nucleotide deletion, <=possible nucleotide insertion)
9142	39510	A	9201	1	4201	MRKKQSRKTGNSKKQSTS PPPK ERSSSPAMEQS WTENDDFDLRE EGFRSNYSKLQEEIETKGQEV ENLEKNL DCKCITRITNIKEKCLKE LMELKAKARELHEECRSLSRSC DQLEERVSVMEDEMNMEMKQE GKFREKRIKRNEQSLQEIW DYV KRPNLPPIDVPESDRN TKG NTLQDV IQENFPN LARQANIQI QEIQRMPQRYSSRRATPRHIVR FTKVEMKEKMLRA&REKAFKQ ASRREDDIAKVTSG
9143	39511	A	9202	715	6193	GQIIHPDTKAWQRJINKKKENF RPISLMNIADAKILKNKMLANQIQ QHIKKL IYHDQVGIFPGMQGW NICKS INVIHHHNRTKDKNHMII SIDAAKAFDKIQQPFMLKTLNK LGIDGTYLKII RAIYDKPTAII NGQKLEAFTLKTGT RQGCPLSP LLFNIVLEV LARAIRQ EKEIKGI QLGKEEVKL SLFADD MIVYLEN PIISAQNLLK LIGNFSK VSGYTIN VQKSQAFLYTNNR QTESQIMSE LPFTIASKR
9144	39512	A	9203	1	3682	KEGHYIMVKGSIQQEELTILNY APNTGAPRFIKQVLSLDLQRDLE SHTLIMGDFNTPLSTLDRSTRQ KVN KDTQELNSALHQADLIDY RTLHPKSTEYTFFSAPHHHTYSK IDHILGSKALLSKCKRTEIUTNCL SDHSAIKLELRIRKLITQNIRSAT WKVN NLLPPGM TYWV HNGNE GQKLKMFFETQWE/HKDTAYQ NLWD TFKAGCRGKFI ALNAHK RKAGKDPKL TPLTSQ LKK L EK QEQTIVISKAS
9145	39513	A	9204	1187	1680	DSPCTIASTRSYSFICNRLPSVDI QLRCSCRNVRRLSTYCLYL RQ LRIEGGNFVFTTKADNGPQHQIIT *TNSFPVGNNQA QTVKVR RHIL FFINLFGK EIGGP DHFN NGFTQP LPSGGTQPHLSCVTIDG GNVT M RIHRNQPFINRTKQ RL L TDH AC DLLW H
9146	39514	A	9205	3	293	ERSWSQ LFL FSTEQFWQQL PGTG SGRARQN ISRK TP REHAGGY RR DNGNNWAVPHIQC NL VPR ** K RPPV RAHRAPE TL CASKA L QE RYWVFELL R
9147	39515	A	9206	1	4509	
9148	39516	A	9207	1	507	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
9149	39517	B	9208	I	3448	
9150	39518	A	9209	I	2652	
9151	39519	A	9210	75	784	
9152	39520	B	9211	I	1968	
9153	39521	A	9212	I	298	LQGHVLGVGVSVSCLPFGVIMGH GNWPLWVLTACLVLLLC*WSL RRQ*IQQ*APSDQKRDFLVPHG A/VFDR*ISATCWSSINWPANCS RPSIAGWPQAS
9154	39522	B	9213	167	362	
9155	39523	A	9214	959	1267	YHWHQLLSMVRQLMVLWSKK ISSWFMPGPPIRKSLAENSI*KN LV*VILKLTEGISTLK*MAPQN TQY*MTVIKLFKWVARQTRLR SIMVCYSSTTLLT
9156	39524	A	9215	370	555	
9157	39525	A	9216	I	1016	MSHQLTFADSEFSSKRRQTRKE IFLSRMEQILPWQNMVEVIEPFY PKAGNGRRPYPLETMRLRHCM QHWYNNLSDGAMEDALYEIASM RIFARLSDLSDALPDRTTINMFR HLLEQHQLARQLFKTINRWLAE AGVMMTQGTLDATIEAPSST KNKEQQRDPEMHQTKKGQNW HFGMKAHIGVDAKSGLTHSLV TTAANEHDLNQLVNELETAE RFRRQQEDTQSCKLLSIMLYIKN LSGPDVSELISPLSEGFLNCSSV VVAVIAAVLRRAPJHMPSGW RSWNAESGAYNVTRSGDSYI/H G*LLYRSRKLPDPADEGALQK WWSVLPFFKRRLLWF
9158	39526	A	9217	408	643	PGCGSGHSWHRHQCQGPSCQSA TDCLSWSDASPDRVAAALCSWS SWVPQ*WWHR/HKVP*VIMTP ASASQRLLMVNNWRAS
9159	39527	A	9218	626	760	
9160	39528	A	9219	I	2469	
9161	39529	A	9220	I	756	
9162	39530	A	9221	1738	1913	PTAWSPPRPTSMTSISWVICFME RSNLSQMPATKERJSARSWPR WMWTG*SPSPVPR
9163	39531	A	9222	2403	2760	FRGDGILVSCPVLVFSSAFSWRA ADGGKRNVRNHPSV/VR*AGAL RPRTQSRIQ/SQRLNKVEKGGV KQFEHNQSCRQQVGVIIKKVVK QLADILPHGHFQFYAEVIGKLF RQRSARDAIRGSS
9164	39532	B	9223	I	3663	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met ind	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
9165	39533	A	9224	1	1584	MELIEKHVSFGGWQNMYRHYS QSLKCEMNVGVYLPKKAANEK LPVLYWLSGLTCNEQNFITKSG MQRYAAEHNIVVAPDTPRGS HVADADRYDLGQGAGFYLNA TQAPWNEHYKMDYIRNELPD LVMHHFPATAKKISGHSMGG LGAJVLAJRNPDVEYVSAFSP IVSPSQVPWGQAFAYLAEN KDAWLIDYDPVSLISQGRVAEI MVDQGLSDDFYAEQLRTPNDE KICQEMNIKTLIRYQRGAICSDA AATRGAKRESCRSGCGLLIAER PAKVEPGTASRQDNTAINIEYM KASIRARVEHPFRIIKRQFGFVK ARYKGLLKN^ETNWRCYSRP/ HLFRADQMIRNPHDLYAPEVV HQKAKVTTSGYRFLPCCGFAN TFWGKTTADGTLEHFGRRCQG WFEDDDGHREQCDFRFRFKNC PQCNAAENDIAARRCRECDTVL DPDDMLKAALRLKDALVLRC GMSLQHGHDEKGEWLKITYYD EDGADVSRFLRQTPAQRTAFE QLFIRPHTRTPGI
9166	39534	C	9225	1	2127	
9167	39535	B	9226	1	1917	
9168	39536	A	9227	1671	2198	RAGAWASDPRQRGVVRNAALL PPDRDSGRDAKTQSHRDG/VI SY/RAFDETILASGIVPTPPIDG/ DHPKNEADDMLRMGFIEDVETI /IGADPGRSSDRSVLCHNAGSDS SHYPPLYERAAGSAHSVQRDYP SGHOPELDCLGYARTRSTDTG TPERWSSGHPCDCRRCPWPGR
9169	39537	A	9228	642	746	
9170	39538	A	9229	1	2031	
9171	39539	A	9230	909	1058	
9172	39540	A	9231	2	268	WRCLLRQLKFIKTVTSWICTG KLMLSTTSPLMMQQMMVILLMP VLASKVKPKSTIN*LVSVGNM NSKATALNLKVPPKIKPVPLPSL
9173	39541	A	9232	63	463	FPATCWSSINWPANCSPSIAG WPK/PGVMMTQGTLVDATIIEA PSSTKNEQQRDPEMHQTKKG NQWHFGMAHIGVDAKSA*P TAWSPPRPTSMTSISWVICCM RSNLSQLQMPATKGRHSARSWP RWMWTG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=-Stop codon, /=-possible nucleotide deletion, ~=-possible nucleotide insertion)
9174	39542	A	9233	74	247	RNVMIKRRVLSSSTSAS*LPPASA FCRLFSTPARWRSTACFTSGNR YRFLTVRLSGYW
9175	39543	A	9234	3	271	ASYWNRSFSPWGTYNRHPR*N RQCASRHCRGLHKQYQWPRI S/WLNCTPAPHARDVLLWRPSS LPAGNADGPIWRPCCVFTACS IGTT
9176	39544	A	9235	1	1048	MCSFRSQTFCSSRTFARVSVI HSANIRVRVLDNSTIMTRRGQD PTLPEMRRVRLLEMADAMDMF CQGLRYGPLPAPVRQQAAIIIPC HRVVVRGDGTLSGYRWGVSRKA QLVRREAENEERPINRGWPQOP SDDPKHFVMPHTIEAPSSTKNKE QQRDEMHQTKKGQNQWHFGM KAHIGVDAKSGLTHSLVTAA NEHDLNQLGNLLHGEKQFVSA DAGYQGAPQREELAEVDVDW LIAERPGKVKTLCQNPBKNTA INIEYMKASIRARVEHPRIJKR QFGFVKARYKGLLKNAETNWR CYSPWPTCFGWTK*YPSIPTCLL TTRTASLLKPPGVRTSVCWQQL

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9177	39545	A	9236	I	2493	MTQIFTGTLVEADPFHAVTLVA NHDTQLPLQALEAPVEPWFVKPL AYALILLRENGVPSVYFPDLYG AHYEDVGGAGQTYPIDMPPIEQ LDELILARQRFAHGVQLTFFDH PNClAFSRSGTDEFPGCCVVMS NGDDGEKTIHLGENYGNKTWR DFLGNRQERVTVTDENGEATFFC NGGSVSVVWIEEAANNRQDY GAGHKIPVINYTDVHLRIERSCR FRADPRQQHELQLSSKLAVHD VLTNIYNRRYFFNSVESLLSRPV VKDFCVMVLVDINQFKRINAQW GHRVGDVKVLVSIVDIQQSIRPD DILARLEGEVFGLLFTELNSAQ AKIIAERMRKNVELLTGFSNRY DVPEQMISIGTVFSTGDTRNIS LVMTEADKALREAKSEGGNKH WYNLSDGAMEDALYEJASMRL FARLSLDSALPDRTIMNFRHL LEQHQLARQLFKTINRWLAEA GVMMTQGTLVDATIIEAPSSTK NKEQQRDPEMHQTKKGQNQWH FGMKAHIGVDAKSGLTHSLVT TAANEHDLNQLGNL LHGEEQF VSADAGYQGAPQREELAEVDV DWLIAERPGBKVRTLKQHPRKN KTAINIEYMKASIRARVEHPFRII KRQFCGVKARYKGLLKVNEN WRCYSRWP/HLFRADQMILCPV FVHHIPRFFGTFFGATDTQTFIL TESVIHQPLVLTNFIAIDGNFA
9178	39546	B	9237	I	3148	
9179	39547	B	9238	I	1680	
9180	39548	A	9239	I91	470	

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9181	39549	A	9240	1	1675	MFARVSTTPVTRYEMYRKTRS TRLEDNNALSQSCKPLPFSEVT GSKGKADKEKVGDYVFCLKAQ GRYNGEPLTGTGKIGGMALIR GEGETPFPVQADFRSGNTRVAFD GVVNNDPMKMGGVDLRLKFSG DSLGDLYELTGVLPLDTPPFET DGRLVAKIDTEKSSVFDYRGFN GRIGDSDIHGSLSVTTGKPRPK LEGDVESRQLRLADLGLPIGVD SGKGAEKSKRSEQQKGEKSQV PAGKVLPMYDRFETDKWVMD ADVRFKGRRIEHGSSLPLISDLST HIILNADRLQLPQKFGMAGGS IAANIHLEGDKKPMQGRADIQA RRLLKLKELMPDVELMQKTLGE MNGDAELRGSGNSVAALLGNS NGNLKLLMNNDGLVSRNLMEIV GLNVGNYIVGAIFGDDDEVRN CAAANLIANGVARPQIFAFDT ENALINVTGTASFASEQQLDTID PESKGIRIITLRSPLYVRGTFKNP QSG*WS/GTLLLSTKAKTIVAI TTLKVTVMASVSLPMLNTKDS VSVOQLMRNLIVPTLKLQMKGKF LKYLLPVKMQKFGPV
9182	39550	A	9241	72	506	GHVAHLQPRAGGRQPARLHHP QGTDRVLHGQRGQQPGP/LLPS LSAWRPSTSTLKPASCGLRGPT SKRMSM\QDGGGLPHHRAQAQP PVHPGQEAVG*C/EYWASSRP VTQPGALMWRLWS\AGRPRPY LLSHSQHDPHSGQGGGEHP
9183	39551	A	9242	1	447	
9184	39552	A	9243	70	490	CGCDAETIILRINALAFIWKCGT EWICCCFCRRLALRELQQAVHAG LPQQAKILFDGGSEIGKIH*LRC AHCPLSS\GKPVVPAAALMNRPT RGERRFAYWAPGWFFFSPVRR ATADCPSPGPVERVAASGPRWF APAGENPV

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9185	39553	A	9244	1097	1841	ANDGDLRSCVTLSCMHSHASE AADPPATTAAFTDEHMSVKLRR TVGVACSVCPGWVTSGHPVNP AAS/GAKVLPGDTDIALPGPLPF ILSRVQLRNDNTLILSDNNGGIRILY FELLFPGEDGYRRCESLWLVRG GVAKLDQGHRLAALWQALSEE LRLTPHRYLATNSPQGPWWLL GWCCERVPEADEVLPAPlPPYRV LIGLVDRIWRSEDVSAASGLHH DNRNAPSLSDQTRTDPPIRAHA SRYQRQKPDG
9186	39554	A	9245	456	928	EAATEPKHLHQLRHAALAQHR QAPRPQGRPLARPHQGDQPD RLHHLRGGGRHGARGHLHQA GAGESAAPKG/VTCPASPLGD VTGKPTSAWNTEKGRWAQHR GYPSPGPAAPLVLSWPPIPLFRP PPLLPLSSPAWILPSPLCHSLKA QSLVQATI
9187	39555	A	9246	1	1572	

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9188	39556	A	9247	1	2505	MAWRNSVNWQCKQEPGLFLRHGRRLTNGTTRRSILQNKEEDFYTSQPGFPALGCGCLRVNLLLGHHRGISAGSSYRPITSTPCHLCKLGQEVFAKPLNLQDQCQQNLVMQVQLKLVLNCLNCLDFIGSSADESADDLCTVQIPTTWRTMGLVGCDGVCCRTRWCQCCLATAVVSGVGPPWLLPACSSGPMISKRKKFVHKWAQDLVPRHGLENVWDLPRAMAGSYLMYKQRWKIMEFGKWALQHCKMTVKDIERLQLYNKVKEQPVQVEGSGRASTIFWVLKTFGGKSPCGAPGECAWTQCRILGWVQIHFKEHPADRVVGLIKMPGLDFYFAADVCYAEKVAQEKGFYRLRTSRYRHYAAFERATFEQGKSTKLMLMTDKQIADFQKHYQTEPERFOIPLPGIYPDRKYSEQIPNSREIYRQKNGIKEQQNLLLQVGSDGFRKGVDRSIEALASLPESLRHNTLLFVGQDPRKFEALAEKLGSERASMEFKRYEYNAAGDLTAITPDGNRSETQYDAWIKAVSTTQGLTRSMYEYDAAGRVISLTNENGSHSVFSYDALDRLEDEGLVILWYYDESDRITHRTVNGEPAEQCQYDGHWLTDISHLSEGHRVAVHDGYDDKGRLTGECQTVNPETGELLWQHETKHAYNEQGLANRVTDSLPPVEWLTYGSGYL
9189	39557	A	9248	481	857	PLAYLYRDPHVRRCVTASGPAPVYGFQPGFSAPTGIRKSVHGDHSYCKYAHSCSRQYRAPEPRLSRTSQCLFSHRSARCPLLDLMGRRYRRPECRLSPLLPAAPVPGLPPWTIYPRLYRNSP
9190	39558	A	9249	777	1229	GAGYSSARCQKHHARTGGAGRNILWRQLRRRGCRSTVDRSHHNQPGTWHRHOPGPRGPAKPARPWRAGTHLPTGTASVRHPCLGQPLRAEPRPAVPDAPRNQNLPFPAPQTDSALIGAVRG+RAR*YH*SRTTTPPDEHDHSWARACSP
9191	39559	B	9250	1	2681	

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9192	39560	A	9251	933	1828	VSRIHVLVWQPRMPAPPAVDW LTY/GSGIL/SGNKLVGTP/LVEY TRDLSH/RETLRSFASMGNSA AY/*LSTDTPAAGQLQSQH/LNS LVYDRDYGWSDNGD/LVRISGP RQTREYGYS/A/TGRLESVRTLA PDLDI/RIPYATDPAGNRLPDPE/ LHPDMRADGGATGQK/VEPEYT PARKAHLYHWTTGDCRWRLSA KTAIRVERGI**MGQPAY*GEPH HVYQPR*TWHWRWRQKGKRKS ASGRRYLRLPINPNNVGRENQRP TSPDGTHMAPISLMAWQPIQLR YRGHVRQRLLAVGGERIYRYLPP
9193	39561	A	9252	I	1409	MECDASALLRYDSRQFIPLAID GLAKDVLGRRFALEGHPRLEAI ARAGDVVRFPADSELPPDYPDG LIPGQESLKVKHACVGLPLFAQGQ NLIGAL'TLDGMQPQDFDVFSDE ELRLIAA\LAAGALSNALLIEQL ESQNMLPGDATPFEAVKQTQM IGLSPGMTQLKEIEIVAASDLN VLISGETGTGKEIVAKAIHEASP RAVNPLVYLNCAALPESVRKSE LFGHVKGAFITGAISNRSGKFEM ADNGTLFLDEIGELSLVHQAKL LRVGQQYGDIIQRVGGDRCLRVD VRVLAATNRDLREEVLAGRFR ADLFHRLSVFPLSVPPLERGD DVILLAGYFCEQCRRLRQQLSRV VLSAGARNLLQHYSFPGNVREL EHAIHRAVVLLARATRSGDEVIL EAQHFCAFPEVTLPPTPEVAAPV VKQSLREAT*AFQRETIRQALA QNRRKWTACARMLETSVANV HRLGKRLVLIK
9194	39562	A	9253	389	799	PQFLIPSVTPCMFIHPLDAK/AR DLRRGDVKVKVSVSRGEVISIVE TRGRNRPQQGLVYMPFFDAAQ LVNKLTLDATDPLSKETDFKKC AVKLEKACPYDTLKLATLASG LSAGTPYFVARDIPCEMCEDIPC AKVCPSS

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9195	39563	A	9254	588	1500	RHPPIPAKIGLJHAVAQDRA\NN MQAGPNINEERMPGWRDRPRNF IIVSDPYPTVSAALAADLTPEVSK FPGSELAEQLNDESRELGFYLN QKGLFEELYAWFGRGHGHDLAP FDDYHKARGRLRWPVNNGKET QWRYSEGNDPYVKAGEGYKF YGKPDGKAVIFALPEPEAAEAP DEEYDLWLSTGRVLLEHWHTGS MTLRVP*LHRAFPDQAGLFVYPL DAKARDLRRGDVKVVSRRGE VISIVETRGRNRPPQGLVYMPFF DAAQLVNKLTDATDPLSKET DWPHFSSTYNGPLLQGANKGIL VQQH
9196	39564	A	9255	1	1698	MEREQDSIJIMDAATRNRLEITQ NLAGGAENTLASVLDCTVTPM GSRMLKRWLHMPVRDTRVLLE RQQTIGALQDFTAGLQPVLRQV GDLERILARLALRTARPRLAR MRHAQQQLPELRAQLETVDSA PVQALREKMGEFAELRDLLER AIIDTPPVLSWMMSGARWLARP IICNYEVDRDTIRHTKMNVGDVQ RLSVAVVVNVYKTLPDGKPLPLS NEQMKQIEDLTREAMGFSEKR GDSLNVVNSPNFNSDESG
9197	39565	A	9256	590	910	SCSIQLSPWILPRTVMCVPFGTC ELLST*WLAKERPLKTVSWITIRS FTAETSTFGPTMTASMTFLPTY CSIASSLSSFKLAAAILNSLPQI GRYITIGSGVRRNA
9198	39566	A	9257	1	854	MANRMILNETAWFGGRGAvgA LTDEVKRRGYQKALIVTDKTL VQCGVVAKVTDKMDAAGLAF AIYDGVVANQHYCRQDSSEDF AEMSLLIEGRRLRRLPWEFEI DTARQQLNLQFGTRDLVGFV ENAPRGLCAAGCLLQYAKDTQ RTTLPHIRSITMEREQDSIJMDA ATTRNLEITQNLAGGAENTLAS VLDCTVTPMGSRMLKRWLHM PVRD/DPRVA*APANYWRIAGF HRRATAGTASGRPGTYSGTSG FTNCSPTRSGPYAPRFPATAGA ACAVRNCR
9199	39567	B	9258	I22	868	

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9200	39568	A	9259	2610	2897	PNLYLRFCCCCRLQESHSVTQA GVQWCNLSSLQPLPPGFKQFSH LTGALPKCWDYRSKRPRPANQT SILDVKEDPY*LHWPRSNDIK LNLVANP
9201	39569	A	9260	2166	2426	VQPAGCCGL*RQHGGSYRPESRTA GGRHRG*RRLRRAFIDGGANSS GTGICRDCAFNRISHWTGRTGRP DVSDEHRKTAEQRRDGAVR
9202	39570	A	9261	846	1022	
9203	39571	A	9262	1	1339	MNALSKARQYVEEFDGNIASFIFSGKPGTGNHLAAACNELL RERNLGESEIHTTSDHMVATL PGETQTWPEDFRDVEQRQQVVI FQHLVGCVKVDGKYIQLQVCTFT VGGNYGGTCLRGDESILVIKKES DIEPLIVVTVQQFHIGNGYVV TITPSEGERYQQGVVGLEGRIRRT RRIRHKQSARCYNLRFKPTCAIT QTTPTEVSPVKKQLVLVPNPH YPGNKPNFKRVSVKIIGESASRR LQLSRGDIDIAADALSDRFVSEAI TAKVEEAIKN*LSQYQILPEEW GGESQFVHSKAAGTGIDE\LL DAILLQAEVLELKAVRKGMAS GAVIEFPSLDKGIRGPVVTVLV REGLTHKDIDIVLCGFYGRVRA MRNELGQEVLLEAGPSIPIVEILG SGVPAAGDEVTVVRDEKKARE VALYRQGKFREVKLARQQKSKE LENMFANMTEGEVHEVNIVLK ADVQGSVEAISDSLLKLSTDEV KVKIIGSGVGGIETDATALAAAS NAILEGLFTLTSQDEFVIAPGFS TDPLEEQHSVSVSGLLHKYIINR ALLLVKGGAVNCRYCFRRHF PYAENQGNKRNWQTALEYVA AHPELDEMIIFSGGDPMAKDH ELDWLLTQVHVHQHDVGRRVQ RLPFIHDALFHQQFFNQHQTTF GQVHLARFFVHREVDISILFRRIS VLKKMMSPHRVKDRCYCAQFI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9204	39572	A	9263	922	2357	GKGNDDEKKI.VSDQ*MGTA*RQRIHPIPSIPLLW/YPEGPSVSRPEAGGYNSSLMWTHGKVINGGRGLLIESDIEPGDAR*SSGSCARHGLVFWLCSCRRCMPQTIEAIQHPNA/VAVNKIDRPEADPDRVVKVVLSQYGILPEEWVGESQFVHGSAKAGTGIDELLDAILLQAEELEKLAVRKGMSGAVIESFLDKGRGPVATVLRREGTLHKGDIVLGF EYGRVRAZRNLGQEVELEAGPSIPVEILGLSGVPAAGDEVTVRDEKKAREVALYRQGKFREVKLARQQKSKLENMFANMTEGEVHEVNIVLKADVQGSVEAISDSSLKLSTDEVKVKIIIGSGVGVIEAESLDLRYYSVIYNLIDEVKAAMSGMLSPELKQQIIGLAEVRDVFKSPKFGAIAGCMVTEGVVKRHNPIRVLRDNVVIYEGELESLRRFKDDVNEVRNGMECGIGVKKNYNDVR TGDVIEVFEEIIORTIA
9205	39573	A	9264	1	748	
9206	39574	A	9265	923	1387	PPNLLARCSPSAMARQSPIRSPRPLAPSPALRAPSAPPAPHARLA VPRQA*GLLLLALIAVSTHIEMISNTLAMGWNSPLTTVALLACGFACFIEMGKIPFDVAASWIIMIWSQSSTCTAPTLKPLRSVTLMRUTPVSAARDLVGYFATAVRLP
9207	39575	A	9266	352	478	CDPTQRKPILYWQLQARRGLPIWRNQRFRKAVR*MAMAPMFS
9208	39576	A	9267	54	811	HTTGGGNPPLYGI/SRQIARY*QSRV/GPGFCQDYRDIIHLKFKRQEVP TSSGLMFRLMPWPVLISSMLVLA MALPLFITVSPFAGGGDLITLIYLLALFRFFFALSGLDTGSPFAGVGASRELTLGLILVEPMILSLLVL ALIAGSTHIEMISNTLAMGWNSPLITVLALLACGFACFIEMGKIPFDVAEEAEQELQEGPLTEYSGAGLALAKWGLGLKQVVMASLFVDI.FLPFGRAQELSI\ACLLTSVVTLLKRLL

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9209	39577	A	9268	2	627	CGSIIAL/VAIFKSF ^G HGYLGTLE GLNGLVLKFGYKGDKTKVSLG KLN ^T ISI ^M IGSTWVVAYANP NILD ^L I ^E AMGAPIIASLCLLP ^M YAIRKAPSLAKYRGRLDNVPIH AITRVDLKEDGKG ^L KIVRQSLP YGTASGTHG ^L YPCAYCARLHN ^I EQQLLSMFGD ^T DAIKAYQSFLA RSAFAVSQ ^C IPVNTV ^R AYSVI QNWI ^A ITIRHV
9210	39578	A	9269	2648	3072	LSRTGKT ^T FAIT/LEYAA ^I I ^A VAIFKSF ^G HGYLGTLEG ^L NGLV LKFGYKGDKTKVSLGKLN ^T IS M ^I FIMG ^S TWVVAYANP ^N ILD ^L I EAMGAPIIASLCLLP ^M YAIRK APSLAKYRGRLDNVFVT ^V IGLL TILNIVYKLF
9211	39579	A	9270	467	614	VPLAVPYGRLWRTI ^F SP ^L PSSFR STR ^E *YESMLGRFFERTACLQQ KQF
9212	39580	A	9271	1	846	MSYLWVPPFIASLVLISL ^S LYW NSAVIDQV ^D LGS ^L ALTGH ^D GIL ^I TVWG ^G I ^S TKW ^V PLN ^F PPNVFSF GIVSKRK ^K KDFGRDFTERKC SQIISRASMLMVAVVMFFAFSC LFTLSPANMAEAKAQNIPVLSH LANHFASMTG ^T KTTFSITLEYA ASII ^A LVAIFKSF ^G HGYLGTLEG LNGLVLKFGYKGDKTKVSLGK LNT ^T ISI ^M IGSTWVVAYANP ^N NLD ^L I ^E AMGAPIIASLCLLP ^M YAIRKAPSLAKYRGRLDNVFSTV IGLLTILNIVYQLF
9213	39581	A	9272	95	456	RAISM ^S FRMER ^P CC ^L SLPSSL ^C IS STRVTASSPLSGCSS ^C TL ^L WISW GRMVRNC ^S NT/MQI.QD ^L LLRA HLRP ^K PPMAKLLEPAEG ^F PGTS C ^L LEAE ^P STIRDVV ^L IASQPASQ PASQQGSQI
9214	39582	A	9273	1	1241	

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9215	39583	A	9274	3	1608	SRGFPRREFSGPSIKKKVDAPIQ AQWPVHAVITNSTYDGILLYNT DWIKQTLDVPSIHLDSWVPT HFHPIVQGKSGMSGERGAGKVII FEPQ*AHRLAALSQGSLILIKG EYDQEAFSEAFMRHSPSSPSYPI GG S VETAAAMLRGNPGKRLIN RSVERALHFRKEVQRLREESDG WFFDIWQPPQVDEAECPVAP GEQWHGFNDADAHMFLDPV KVTILTGMDEQGNMSEEGIPA ALVAKFLDERGIVVEKTGPYNL LFLFSIGIDKTKAMGLRGLTEF KRSYDNLRIKNMLPDLYAEDP DFYRNMRIQDLAQGIHSRRVTA SVSSGSQANQQVNFIGDQSTAA LTLSVPSPGDITVNTATQYMTA TLQDKNGNPLKDKEITFSPVND VASKFSISNGGKGMTDSNGVAI ASLTGTLAGTHMIMARLANSN VSDAQPMTFVADKDRAVVVLQ TSKAEIIGNGVDETTLTATVKD PSNHPVAGITVNFTMPQEGVYA MSLEYIILTIALNGSRMWNSA REKRTRQRND
9216	39584	A	9275	106	709	LRSAEDNDTREKNKQTNRSDS KLRLVETSGSPPTSSQTPDPAF RYPKKYCVEDCSYRPE*PRITP DNRLLYGGGVVYGARDPDVVE RLVVPKLLKTFPQLKGVKIDYR WTGNFLLTLSRMPQYGRLDTN YYMQGYSGHGVTCHLAGRLI AELLRGDAERFDAFANLPHYPF PGGRTLVRPFITKSAAYYSLR DRLGV
9217	39585	A	9276	140	558	RKPIIRQGEKAGRNRSDVGCC EKAMSVIIVGGGMAGATLALAI SRLSHGALPVHLIEATAPESHA HPGFDRGAIALAAGTCQQLARI GVWQSLADCATAITTVHVSDR GHAGFGTLSRKITTWGL*QRSW ARWIWYPFAKNYHGLALTIV ELQMGKRLF
9218	39586	A	9277	3799	4086	
9219	39587	A	9278	3017	3184	
9220	39588	B	9279	1	1050	
9221	39589	B	9280	1	1455	
9222	39590	A	9281	374	506	RCIALIAWLTLPVLRVTLK*RW RVARR*RAACW*S*WHISALAP
9223	39591	C	9282	47	406	

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9224	39592	A	9283	1	4749	
9225	39593	B	9284	507	3568	
9226	39594	A	9285	101	638	RQKYSDWSSALVPTAGEPTRHTQTTRAGIAHA/EADFAADILFLLCGKDISTAGGSFV*LADNKQHLMPVCFANHLLTVKM/PHQSPVPDH/QALISHRIRSSRGCSRYSADNSVSRTPLSPTPGRSTMVKCSPICCRKRKGSRVQAATSLTGDTPANRALQRLLFPAPVLPMMPI TGS
9227	39595	A	9286	271	532	
9228	39596	A	9287	643	768	
9229	39597	A	9288	1	1948	MCSHAAGCTIPDVEHWTRINKKVPRLVSVLPNGPDYHPTVRAFLAGGVPEVMLHRLDLGLLHLDAMTVTGTVGENLEWRPEPGA/FRQCLREQDGVEPDDVILPPEKA/AKAKGLTSTVCEPTGNIAPEGSVIKATAIDPSVVGEDGVYHHTGRVRVFVSEAQAIIKAIRVVIVACGFSPTRTAHAASDIDITNTVDLRNRRSQLRGEIVQF//PANKYRTSA*GS*LAHPTGSLCD*VGRLDIPLAANFVQR*SPPGISPTV
9230	39598	A	9289	2166	2426	VQPGGCGL*RQHGSYRPESRTA GGRHRG*RRLRRAFIDGGANSS GTGICRDAFNRISSHWTGRTGRP DVDSGEHRKTAEQR RDGA VR
9231	39599	A	9290	846	1022	

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9232	39600	A	9291	I	1336	MNALS KARQY VEEFD GNI ASFI FSGK PGTG KHN LAA ICN ELL RER NLGE SEI HTT SDHM VTATL PGET QTWP ED FDR DVE QRQQV VVI FQHL VGC V KVDG KYI QV CTFT VGG NYGG T CLR GDES LVI KKES DIEPL I VTV VVQ FHI GNG YV VI TIT PSEG ERY YQGV VV GLE GR IRRT RRIR HKQS A R CYN LRF KPT CAIT QTTP TEV SPV PLKK QLV LPN PH YPGN KPN FK RV SV KJ IGE SAS RR LQL SRG D DIA DAS DRF VSE AI TAK VEA A IKN * LSQ YG IL PEE W GGES QF VHV SAK AGT GID ELL \/ DA II LQAE V LE LKA VR KG MAS GA VIE SFL DKG RGP V AT VL VRE GTL HKG D IVLC GFE YGR V RAM RN EL GQ E VLE A G P S IPE V IL GLS GV PAAG D E VTV VR DE KK A RE V AL YR QG K F REV KLA RQQ KSK L EN MFA NMTE GE VHE VN VNL KA DV QGS V EA IS DS LL K L ST D E KV VKII GS GV GG I TET D T LA A ASN A ILE GL FT L TS Q D E F V IAP GF ST D P LEE QHS VV SGL LHK YH N RA LLL V KGG CAV NC RY C FRR H FP YA EN QGN KRN W QTALEY VAA HPEL DEM IF SG GD PL MA KDH EL DW LL TQ VV H QHD V GRR V QRL PFI H DAL F H QFF N QH QT FF GQ VHL AR FF V H RE V D S I L F R RIS VL KKM MSP HR V K DRC CYCA QF IC P
9233	39601	B	9292	I	2890	
9234	39602	A	9293	I	822	ITQY CDS FTIC LSK GL GT PV GSL LV GNR DY I KRA I WR KMT GGG MR QG IL AA AG I Y AL KN VAR LQED HDNA A WMA EQ \ L RET G \/ AID VMR QDT NML FVR VGEEN AA AL GE IT * KPR NVL IN A SPIV RLER DV PQR IL VL GAS GY JG QH LVRT LS QG GH QI LA A ARH VD R LA KL QL AN VS CH KV DL SW PD N LP AL LQ DID T VY FL VH SM GE AA IY RSSA G VAS VSS VFR V CL RPS Y D P R VFP C FLC R ALL VLP C R LI Y SPL SF AL VLS L API K
9235	39603	A	9294	1565	1825	SRMC VAI RS RN QRS CE IT IA QPG NSS RA FSS A R RV SIS R LS V GSS S S SML PCT CSS F A R CR PR SP PESS PTR LP * STPL K L KR PT

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met no	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, -=possible nucleotide deletion, + =possible nucleotide insertion)
9236	39604	A	9295	236	742	VATRCRSRSPSPSLSPSLSLRVMP TTSAYSFMITAKSSPAVLKLSN A SERVN VSGTISVLRIC TPLFSA RLWL AS ITRFSRSL E STP* PMMWS ISSLQ TRN LECGCSATLFFRLCS SSWR SN/TNDVFTA/VTLITERDG IPAQR RFQSAR VPVYVTRPPAH RLPLPRRCHQK
9237	39605	B	9296	1	951	
9238	39606	B	9297	1	666	
9239	39607	A	9298	761	1162	IILGSMIAIFTI LPIHEQGMFFHL FVTFSILLSSGL*FSLKRSFTSLV SCIPRYFILFVAIVNGSSLVIWLS VFLLFVYRNAACDFC TLILY PETL LKLLISLRRFWAETLGFSKYTIM SSANRDNLNTSSFPN
9240	39608	A	9299	82	160	
9241	39609	B	9300	64	477	
9242	39610	A	9301	408	507	LLPLFQNLLLVYSGI*LLPGLVW KGCMHPGIYP
9243	39611	A	9302	1	3141	MLLGLHSLAAFLQRESFGKQS WGCQLAALLQRRITKMTTEAMK ITLSTQPADARWG EKATYSINN DGITLH LNGADDLGLI QRAARK IDGLGIKHVQLSGEGWDADRC WAFWQGYKAPKGTRKVVWPD LDDAQ RQELDNRLMI DWVRD TINA PAEELGPSQLAQR AVDLIS NVAGDRV TYRITKGEDLREQQ YMG LHTVGRGSERSPVLLA LD YNPTGDK EAPVYACLLGDIITY RN GKKVEVMNTDAEGRVLV
9244	39612	A	9303	1	983	MVRASG YLQLTLD DFN HVL K SE NGVPV YL RDAVKV QIG PEM RRGIA ELN GEGEV AGGV VIL RS GKNARE VI AVKDK LETL KSS L PEG VEIV TT YDRSQL IDRAID NL SGK LLEEF IVVA VVC ALFL WHV RSALV AII SLP GLC IA FIV MHF Q GLN ANIM SLGG IAI A VGAM VD AAIV MIENA/R *TAGR VAA PAS * RHAG * NALAG QEG RLF GPL AL HQNV CDGG CGA AGD RSD DPDD GLL DPW QNSAG KQ *PA QSL FD S CLSSA VAE STALA ENHA AGGG AFGAD GS LA A Q *SPG EFL PQ IN EGD LY MPC DA A QGIP Q RRR
9245	39613	A	9304	362	436	
9246	39614	A	9305	101	208	
9247	39615	C	9306	1	882	
9248	39616	B	9307	1	822	

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9249	39617	A	9308	668	826	VNSHSQQLQRE*NT*ESNLQGM *RTSSRRTTNHCSRK*KRIQTNG RTFHAHG
9250	39618	A	9309	497	1042	LPRIPTVLTSGVRRDGWYRRFG RRPSG*PGNWSSSPVEKSATRT LRITGTSA PSEAITGSSAVVR VPAGKTTAPTEIKSTPVANSRS VLSVTL PDTSSALPLVRLTASR ICSVSKLSSMMISAPAFRASSSS SRFSTSTGASGCSQAFSTA WRTEPEAIIWFSLIRKASESPRR
9251	39619	C	9310	1	3447	
9252	39620	A	9311	570	647	
9253	39621	A	9312	1071	1323	RPPPHRLSGCYHPSHRRPVHGF HHA RQRQFRR*TVDTLPADAP LPSPHAHFRPL/TSIFCPVSTM DNASM*RNSCCRLLSARG
9254	39622	B	9313	1	2585	
9255	39623	A	9314	133	357	SSFFQFCEEIHW*LDGGDIESIN YLREQGHFKIDPSYP*AWNVL PFVCVLFHFIEQWFVVLEEV HIPCKLYS

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9256	39624	A	9315	1	2680	MLVLPLFQPFMRILDHDDSSIDHRPDGNRNTAQRHNIGIQSLEVHDNKSNTQPQRQRNRRHQRAHMPEKQRTDYRRDPLESPKAAACCLFPFAIADPNTPPVFTPPASLPTTGM/FDSPPFNRDA*MVMRSLIRSMVTARAVIGVAICNKGLPATMMALAAQHNIATVLPVCGATLPAKDGEVNGKVQTIGARFANGELSLQDARRAGCKACASSVRRSCQFLGTAGTSQVVAEGLGLAIPHSA LAPSGEPVWREJARASARAALNLSQLKGITTRLEITDKAIENAMTVHAAFGGSTNPLHHIPAIHQAGCHIPTVDDWIRINKRVPRLVSLVLPNGPVYHPTVNAFMAGGVPEVMLHLSLRLGGLLHEDVMVTGSTLKENLDWWEHSSERRQRFQKOLLLDQEIQINADEVIMSPQQAKARGLTSTTIFPWQYAWILHPDLDPETLKLNLISLRLFWAETPVGKNRITQMTNARHRTGFQGVTIHHTGVQFMGFI TRDANSGVKQWTLFQQTTHRFRHHIQRSTFARFQHFPLPGFNNGRQLDVASFVMEFTTG LMSLDTA NEMLSRVTPLAQETLPLVQCFGRILASDVVSPLDVPGFDNSAMDGYAVRLADIASGQPLPVAGKSFAGQPYHGEWPAGTCIRIMTGA PVPEGCEAVVMQEQT EQMDNGVRFTAEVRSQNI RRRGEDISAGAVV
9257	39625	B	9316	1	2577	
9258	39626	A	9317	2	772	AFGASLAQDKPN TGTG*KSPSHPLLRLVIDGKICH LARKVGAVSVVDNPPIRPALQNP LALRADLV LHSCTKYLN GHSDVVAGV VIA KDPDVVTE LAWANNI GTVG GAFDSYLLRGLRTL VPRMELA QRNAQAIVKYLQTQPLVKKLYHPSL PENQGHEIAARQ QKGFGA MLSFELDGDEQ TLRRFLGGSL FTLAESLGGVEKLISHAATMTHAGMAPKARAAGISETLRLISTGIENGENLIADLENGFP A
9259	39627	B	9318	68	1895	
9260	39628	A	9319	I	636	
9261	39629	A	9320	I	942	

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9262	39630	A	9321	479	969	MPSTSQ*I/ISEDFVELNARYR DEEIQRTPQRYSSRRPTQRHIIIV RFTKVEIKEKMLRAAREKGGV AHKRKPIRLTADLSAETLQARR EWGPTIFNLKEKNFQPRISYPITK LSFISEGETKSFTDKQMLRDFGT TRPPLKELLKEALNMERNNRY QPQQKHTKL
9263	39631	A	9322	1	652	MGKKQSRKTGNSNQASPPP KERSSSRAMEQSWTENDFDEL REEGFRRSNYSELKEEVQTHGK EDKNLEKKLDLDEWLARIINAEEKS LKDLMEALKTAKARELCDECTSLS SRFDQLEDGVSMEDEMNEMEK SEGKFPRFKRKRNEQSLOEIID YVKKPNLCLIGVPESDRKNGTK LENTLQDIIQENFPNLGGQANIH IQEIVQRTQPQRYSLRRAATPRHLI VRFTKVEMKEKIMLRAAREKG RIVTHKGKPIRLTTADLSAETLQ AR/RTEWGPIMFNILKEKNFQPRI SYPAKLFSISEGEIKYFIDKQML RDFCHHQGLPLKELLERKALK HGKGNNQ*PPPKERSSSRAMEQ SWTENDFDELREEGFRRSNYE LKEEVQTHGKEDKNLEKKLDL WLARIINAEEKSLKDLMELKTKA RELCDECTSLSRRFDQLEDGV S VMEDEMNEMKSEGKFREKRICK RNEQLSLQEIWVDYVKKPNLCLIG VPESDRKNGTKLENTLQDIIQE NFPNLSGQANIHQEIPEPATKIL
9264	39632	A	9323	403	410	VFLIRWGGKPLKRKLYFLHCSI TQALV*ACQGKYLG*IVGAKNI KYIDFFITASRYLRMLAQVFE*I LLLREVTRYS
9265	39633	A	9324	174	1252	

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9266	39634	A	9326	1	1049	MHRSDMCPDKVDIILTTAFRI AINEVKHSKLTSTVTVTKVLDMF ISRSSLPIDDGGLDDGHSDQVG VLNSPTCYSAHQNGERIERFSR KVFGVGLPPDIDEDEITASFRRF GPLVVWDWPHKAESKS^YPPKG YAFLLFQEESSVQALIDACIEED GKLYLCVS*PLLSKDPKSSKYV PNWLSDSDFVMDGSQPLDPRK TIFVGGVPRPLRAVELAMIMDR LYGGVCYAGIDTDPELKYPKA PGRVAFSNQSQSYIAAISARFVQ LQHGDIDKRVEVKPVYLLDDQM CDECQGARCGGKFAPPFCANV TCLQYYCEFCWANIHSRAGRE VHILPLTESAVAAPRIHIPWT
9267	39635	A	9327	2	126	
9268	39636	A	9328	1	1327	IASNSWNASSSPGEAREDGPEG LDKGLDNDAEGVWSPLDIEQS QEALAIYPPCGRRKIIILSDEGKM YGRNELIARYIKLRTGKTRTRK QVSSHQVQLARKKVREYQVGIK AMNLQDVSKDKALQSMASMS SAQIVSASVLQNKFSPSPSLPQA VFSTSSRFWSSPPLLGGQQPGPSQ DIKPFAQPAYPIQPPLPPTLSSYE PLAPLPSAAASVPVWQDRTIAS SRRLRLLEYSAFMEVQRDP*TRT SKHLFVIIHRTDRNPRFFRTTP LGPVVDVRIQIYDPNEPEKKGGL KELYEKGPNAFLVFKFWADL NSTIQEGPGAFYGVSSQYSSAD SMTISVSTKVCSPGKQVVEKVE TEYARLENGRFVYRIRHSPMCE YMINFIHKLKLPEKYMMSNV LENFTILQVVTSDSQETLLVIA FVFEVSTSEHGAQHHVYKLVK
9269	39637	A	9329	2	339	
9270	39638	A	9330	1505	1876	TYGCASPSRKPRVMPLVTAQVP ITALRVNSSSIPAQSVAETTSNR PPTTGVPAFRPVRAAV*AVISPO ISADPTTGGRA*LISAIPSQSVRH GSYSPRLML*RLDSEILLSSQPL TPVKHQRR
9271	39639	A	9331	1	1710	
9272	39640	A	9332	1	1191	

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9273	39641	A	9333	838	1365	STETLSPPLPATPGEVTLRHLDV VSAEQQMFSGLVEKIQVTGSEG ELGIYGPGHAPLLTAIKPGMIRIV KQHGHHEEFLYLSGGILEVQPGN VTVLADTAIRGQDLDEARAME AKRKAAEEIISSSHGDVDYAQAS AELAKAIAQLRVIELTTKAM*H RLEKHKSQSQRNLRAFFCACDPS
9274	39642	A	9334	3	601	MLSAVGYQP/TLAEEMGVHQ RIPSTKTGSITSVQAVVVPADDL TDPSPATTFAHLDATVLSRQI ASLGIVPAVDPLDSTSRLQDPL VVGQEHYDTARGGQFILARYQ ELESLLAIGMNDLSEEDKLVV ARARKIQRFLSQPFFFVAEVFTGS PGKVYVSLKDTRGFKGIMEGEY DHLPEQAFYMVGSIEEAVEKA
9275	39643	B	9335	681	1071	
9276	39644	A	9336	203	2189	VASSARRGLPVHGPAPLQPGPN SQDRL/ESGTNRGCRGLRGLVKG GKGGGRFPSARLIQTVKGGTPS RDHAIEPSGYSVSAGVGE&RTR KGSVFAHEMPDCNVIDKVSLSV YGQMTEPPGNCMRVALSGLTM AEKFDRDEGRDVLLFVDNIYRYA LAG*ERFATVGR*ASN/AVGIQP TLAEKMGVLQERITSTKTGSITS VQAVVYPANDLTDPSPATTFA HLDATVVLSRQIASLGIYPAVD PLDSTSRLQDPLVVGQEHYDTA RGG*SIQLQRFQELKDFMAL/G LSDELSEEDKLVVVARARKIQRF LSQPFFVAEVFTGSPGKVYVSLK DTIRGFKGIMEGEYDHLPFQAF YMGDMAMTYHLDVVSAEQQ MFSGLVVEKIQVTGSEGELGIYS GHAPLLTAIKPGMIRIVKQHGH EEFIYLSGGILEVQPGNVTVLAD TAIRGQDLDEARAMEAKRASG KVKPSIMQSLTPEKIAAILPLQF FPQPADFTGPVVMLTSRRNNRA LSRCDDQTLMPLGAIRGIRHRH QQAGVRILLNNAIIEHVVDGEK VELTLQSGDTLQADVVYIYGIGIS ADEPLAREANLTDANGIVIDEA CRTCDPAIFAGGDVPISSLINV VDEIIHDILLTQPVATRYCIVKVI FEAVMILRDSGGAPFCNSGMAT

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9277	39645	A	9337	905	2319	SRQAQWKGPSTFSVINYHSLQ KRRTNLTHRQLNNLLSTVLYCS CPSIQKLLMLQTPGSVGLV DLPLKAMSRPALPNATAALPTG TRTQPPTPLTRLPSSHRLLLH SGF*AAALLGVSEMTIRRDLNN HSAPVVLLGGYIVLEPRSASHY LLSDQKSRLVEEKRRAKLA TLVEPDQTLFFDCGTTPWIIEA IDNEIPTAVCVSLSNLTFLAKEK PHCRAFP CGATPFSNPSIFS KRV NNFCRDIAFYY SAGVHVSKGV TCFNLRWPKQWAMSAQK HVL VVDHSKFGEVGPVCMGDL KRF DIVVRECCPEDEYVKYAQ QRIPDKVS RHPVJIRLREPGL PVMEFHHPVLPQRTTESA VVHI AHTRKSWRPEHSA PVLI QTSPV ERGPOYIQCQYQLSLTSEENNQP DTQTTKPAQYSILFLSKYKP IVDAPDRSTQRGWSSGLATQSN EQACTTKCNSCTANWHQNNTT FNSTANPSTFKPPTSAALRVLSL WTGNHCDWC FIRYWR LTPNW QRFR RVGRTERATTHNRLQAF GGHTQGLSPGP RRWLHEQRFPT TS DTGGHTADDFRKLDP CICGP YGSHRHHSV KSEVNFK EKRYAF APAASFR YTVLIRFCAPPNTGRF LLTGTPPLPMLSYRHSFHAGHN A DVLKHTVQSLIIESLKEKD KPFL YLDTHAGAGRYQLGSEHAERT
9278	39646	A	9338	98	596	YSGII MAQSKLYPPVVMAGGS RLWPLSRVLYPKQFLCLKGDLT MLQTTICRLNGVECESPVVICN EQPRFIVAHQMRLQNLSENIIL EPAGRITAPTIAPAAALAANRHS PESAPLMLVLTADHVIANEDAV RAPVKINAIPYPKKGKLVTFGIG LDGRV PRYNM
9279	39647	A	9339	2	437	LECPGRSTANCSPRARATSLLL LTHVHGESRDRDAQEMV DLLAQ YEQHGLQLNSREL PDHPLYLE YLAQLPQSEAVEGLKDIAPL LSARLQQRESRYA VLF DLLLKL ANTAIDS DKVAEKA /VRSAR*Y AAGAGCCLGRAG
9280	39648	A	9340	152	334	HLSPQYGSIPR V ISR MGK GLIIM DHFHYGRDS ILLSME*TLALDA NLQFLYVVLLPNYYL
9281	39649	B	9341	I	1401	

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9282	39650	A	9342	86	2063	
9283	39651	B	9343	1	885	
9284	39652	A	9344	1	101	MDDNITYITFCNPNLNSPQRR MLIUTGPNCMGGKSTYMRQTALI ALMAYIGSYVPAQKVIEGPIIDRI FTRVGAADDLASGRSTFMVEM TETANILHNATEYSLVLMDEIG RGTSYTDGLSLAWACAENLAN KIKALTFLFATHYFELTQLPEKM EGVANVHLDLEHGDTMAMF HSVQDGAASKSYGLAAVLAG VPKEVIRRQKLRLELESISPNA AATQVQDGTQMSLSSVPEETSPA VEALENLDDPSLTPRQALEWIY RLKSLGKTMPSRYQKINAHH YRHIIWVVDIHGEYQLLQSRL HQLSFFPKIDLISVGDNIDRGP ESLDVLRLNNQPWFTSVKGNH EAMALEAFETGDNMWLASG GDWFFDLNSEHQEADLLLKF HHLPHIIJEITNDNIJYAITTCVGN ARRAHAVHFCGDVARLLTCQI NIYRGQFRRLPRTFHRRLLTKL RDLILRLSAGNLQCCPDRAWRD NIHPNTFLRDLFCQATAVVQNRL RLRSRIDRFLGAVERRFGNDL PSSPVWLTNGSCYRANETRQ FARMLGLEPKNTAVRSPESNGI AESFVKTIKRDYISIMPKPGLT AAKNLAEAFEHYNEWPHPRAN PITYQAVCANHYRTLNNNGMT NTGQYNVYHIYLQPAESVAA APHVDHHRSEHGR
9285	39653	A	9345	1062	1179	PRFPILAPYAPVRSVCLR*V*T DLPEYGHILFQPADR
9286	39654	B	9346	1	2439	
9287	39655	A	9347	136	629	RSVTPVTIDIVKLLEFTRLRLPGY TKSIE*TNITFQCAAAA*KNSVS TPRGGGTGNTGQALNQGIIVD MSRHMNRIIEINPEEGVWRVEA GVIKDQLNQYLKPGYFFAPEL STSNRATLGGMINTDASGQGS/ LGVRAVVLLGGDILDQTQLPVEL AETLGKSAE
9288	39656	B	9348	1	4653	
9289	39657	C	9349	584	819	

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9290	39658	A	9350	1	765	MQEWGRY蒂SGCCNSALKGD VCLLYGFRVAGRQASELQELT IGYRAQKNRVS ^W CYCHFRQM AKAQH ^I KGFLNRLRKTAKK*GF QLVLLPFSANGK\AQH ^I KGFLN RLRKTAKKTRDFL ^T RMPKLG ^M TMVGVDPA ^L VLCYDEYKLAL GEERGEFNVL ^N L ^E WLA ^S ALES QPVATVSGESWYFFGHCTEV ^T ALPGAP ^A QWA ^I IFARFGAKLE NVSVGCCGMAGTYGHEAKNH ENSLGI ^E LSWHQAMQRLPRN RCLATGYSCRSQVKRVEGTGV RHPVQALLEIIK
9291	39659	A	9351	1	1710	
9292	39660	A	9352	1377	1712	IFRASLNQ ^I LF ^C G ^I LAGRNHRQ RSVRALSQRKMVP ^T DRK*RC ^A RRA ^R *PSARVL*SGE*TDRQH AD*PTIR*RRSWYL ^R PAYAVS ^V RQSDR ^L YSDEYHW*PVRLQRY VRR
9293	39661	A	9353	203	1293	VASSARRGLPVHG ^P APLQGP ^G N SQDRL ^E SGTNRCG ^I .R ^G PLVK ^G GKGG ^R PSARL ^I QT ^V KGGTP ^S RDHA ^I E ^P SGY ^S V ^A G ^V GE\TR ^R EGNDFYHEMTDSNV ^I D ^K V ^S LV YQQMNEPPGNRLR ^V ALTGLTM AEKF ^R DEGRDV ^L L ^F V ^D NIY ^R Y ^T LAG*ERFATVGR*ASN/AVGYQ ^Y PTLAEMGV ^L QERITSTKTGSIT SVQAVVV ^V PADDLTDPSATTFA HLDATV ^V L ^S RQ ^I A ^S LG ^I YPAVD ^V PLDSTRQLDPLVV ^G QEHYHTA ^R RGG* ^S \L ^R Q ^F A ^Q ELKDFMALP/G ^G LSDELSEEDKLV ^V VAR ^A R ^K IQRF ^L LSQPFVAEVFTGSPGKV ^V SLK ^K DTIRGFKGIMEGEYDH ^L PEQAF ^A YMG ^S I ^E EAVEKAKKL
9294	39662	B	9354	1	505	
9295	39663	A	9355	604	789	TMVASGSRRMTST*SRGSVNG CRTILRWKRHSSPLKIKRKQKS ^L *TMPSF*RLPAENS ^L FEI

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9296	39664	A	9356	1	1514	SVAVLRE*APKIRIQLATMPLEA DASSDQQDNGAEMNLVYDRDTMARLGI DVLAAANSLLNNAFGQRQISTIYQPMNQYKV VMEVDPRYTQDISALEKMFVINNEGKA IPLSVFAKWQPANAPLSVNHQGLWRA LTIWFTLPTGKSLC\DPSAAIDRAMTQLGV PSTVRGSFAGTAQVFQETMNSQVIIIAIAT VYIVLGILYESYVHPLTILSTLPSAGVGALL ALELFNAPFSLIALIGIMLLIGIVVK KNAIMMVDFALEAQRHGNLTPQEAI FQACLLRFRPIMMTLAALFGALPLVLSGGD SELRQP\LGITIVGGLVMSQLLTLYT TPPVYLVFFDRLRLRFSRKPKQT VTDTWRQLWIVAFGFFMQSLDTTIVNT ALPSMAQSLGESPLHMHMVIVSYVLT AVMLPASGWLA DKVGVRNIFFT AIVLFTLGSLFC ALSSTIRIILRF VSLLHMRWQ FRDLTFWQMRF RTNTPTISGS DSSLMNQSHQR SVSSSI
9297	39665	A	9357	3218	3337	
9298	39666	A	9358	252	771	RRCOILLSGSLHSSWR LPGHV*QLASAH RPRF^R*LPGLE PGELEV HVNANV LVIHTD LNCLSV QYAVDV LEVEH IIICGHY CGCG VQA AVENPE LGLINN WLLH IRD IIHGWA YGIHD GILR LDLV TAT NRET LEQY RHR GISNL KRD VHF TTGRFI QQR TNR QR LRF FAQ A
9299	39667	B	9359	604	831	
9300	39668	B	9360	1	1104	
9301	39669	A	9361	242	337	LT VIIIGV SAKTV ILSSA VPIQ^K TVRR VSRR

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9302	39670	A	9362	2208	3411	LAADHRRRNAVQRPCNGGSV QSTDDEAAGRLSHADTHPGRPA RALPGDCRCPETLLRTAGVAE*T KALYTLRSEKTRERPMDKQQA SDEKHRRFHDKESDFLA/FVNL WN/Y/LGEQQKAKLSSNAFRRLCR TDYLNYLVRVREWQDIYTQLRQ VVKELGLIPVNNEPAEYREIHAL LTGLLSHIGMKDADKQEYTG RNARFSIFPGSGGLFKKKPKWVM VAELVETSRLWGRIAARIDPEW VEPVQAHLIKRTYSEPHWERAQ GAVMATEKVTVYGLPIVAARK VNYSQIDPALLHDITIELGTSPAF LITRWGFGGRNLSRTGGPRQEP RRKEIAMELVLKDQAQSALTVE TTFGRDFNEALVHVQVVVYAA GARQGTRAPKTRAAVTGGMPT LYAVGRLSRIPMDT
9303	39671	A	9363	79	559	TLSPGSIINPFKEKPN*DSVPMTL/ RRFIEVRFVQQIHHRMRQRPAHW
9304	39672	A	9364	1	655	THWER/A/QGAVMATEKVTVY GFRIVAARKVNYSQIDPALCRE LFIRHALVEGDWQTRHAFFREN LKLRAEEVEELEHKSRDDILVD DETLFEFYDQRISHDVISARHFD SWWKVSRRETDPDLLNNFEKSMLI KEGAEKISKLDYPNFWHQGNL KLRLSYQFEPGADADGVTVHIP LPLLNQVEESGEWFQIPGL/RRE LVMPD*SCQTVTEFVPANSHSY

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9305	39673	A	9365	1	2082	MDIQEFPDLKGTTSLIEITLTRA GIRLLPSGMCMQQLPRLRVLELS HNQIEELPSLHRCQKLEELGLQH NRIWEIGADTFSQLSSLQALDLS WNPAIRSHHPEAFSTLHSVLVKL.DL TTSQTLPLAGLGGLMHLKL KGNLALSQAFSKDSFPKLRILE VPYAYQCCPYGMCAASFFKASG QWEAEIDLHLDDEESSKRPLGLL ARQAENHYDQDQLDELQLEMED SKPVTPSVQ(CSPTCPFKPCYEYL FESWGIRLAVVVAIVLSSLVLCNG LVLLTVFAGGPAPLPPVKFVVG AIAGANTLTGISCGLLASVDAL TFGQFSEY/GLARWETGLGCRA TGFLAVLGEASVLLTAAVQ CSVSVSCVRAYGKSPSLGSVRA GVLGCLALAGLAAAALPLASVG EYGASPLCLPYAPP EGQPAALG FTVALVMMKLLFWFVGPLP YHQNWYCDLPRGDFEAVWDC AHGEATWAWPHLRKTGLLYCP VAFLSFASMLGLFPVTPAVEVKS VLLVVLPLPACLNPLLYLLFNP HFRDDLRLRRTPRRRRTQGPP*PL CCGREDAGERASC(DSYQPQALV APSLSMWFCEAS*SWAGPLEL ETYGFPSVTLISCCQQPGAPRLEG THCVEPEGNHFGNPQPSLDGEL LLRAEGSTPASGGLSGGWRLSA LWLGLWLHTCKYPSPFFSSPLF PFLSPPSVNDGCF
9306	39674	B	9366	1	510	
9307	39675	A	9367	88	246	TPMRPMKSPMPPTPVSRSGSSSK MG*SSASL*RSIPGLDAKTPW PAGRSGTW
9308	39676	A	9368	693	1041	AEGYSQCPNAREGHVDEENED SAPAAQKIP*!*ED*SPHVSQPV EGEEECVKKQ/GRFSWNTSTS* RQT/TARKKLLADQÆARRSKT KEAHKSYEEHLQAKKEEIKTL SKEEETKK
9309	39677	A	9369	1	1911	

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9310	39678	A	9370	1	921	MWRSIFLDSRYLLSSRRKILILLI HVTFSGIRALAVPFRLPVKEKMS FIFMGDVIIHRLTATQVAPL MANFNPGYSDNSTVYYFDNGQ QIRKLKDGLIIRKPVTVHSRAR CRKNLTLARRKGRIIMGIEACFC CVFLTPALICMVCAVRLLTDRP YLASGDQPLERATGEHASMHE Y PGEGLG QPPGLYPSSHPPGRA GTLRALSQRQDTFDADTPGSRNS AYTEL* DSCVDMETDPSSEGPGL GDPCEA GTPPARQGSWEDEEED YEEELTDNRNRRGRNKARYCAE GWGPVLGRNNELEGWGRGV
9311	39679	A	9371	3	740	ELFPFAAAAAMSMRLQKRL ASSVLRMWQRTNGL*TPMRP M*SPMPTPRQQPIEAHQRWAD HP/LSLVTPGPFGSMPEKTPLA\ AGEGAQGHGALGKAGRGTQS MPGMPGEGQHGLRRIEDFGAG LLQKDTGEI RRSRDRPHVFTAC YLEGEGGMLFQKQGFFMGT PQG RQDKGPQRSFLADQA*RP QGLRTKESTESASEERLPGQRK EEINQRLYSKEGRRPRNKNLPL GSVHTWPLVIT
9312	39680	A	9372	1	2229	
9313	39681	A	9373	3	1560	SGPNSLKFYDWGETVPQPWPB GLSPAFIGFPLCPRGRLGETFSSR PHIR/RNYPELQKRLNGWLSSA LKTARILTVCVAVMLLLSAWG LFDFWNWLQNGAGQKNP*NIP D/LRIRNSILFL/LSAVGWTVLA\ S LIENRLASDIHGRPLPSARTR TLLTLFRNALAVIITITIMIVLS EIGVNIAPLLAGAGALGLAISFG SQTLVKDIIITGVFIQFENGMTG DLVTIGPLTGTVERMISRSVG RQDTGAYHIIPWSSITTFAN FV RGIGSVGAN YDVDRHEDADKA NQALRDAVEDDETRFTSESSPIL RCCOREGLGLKAVVQILSHGR NGLPGEPASSQQLSAASSTPVF HLALQIDSAPDNIDWVEMLFNK NMVTERLQNVMVLEQCFSDSS SLYRFITYSYLLAFNVWLLAP VTLCYDWQVGSIPLVETIWD RNLATIFLAVVMALLSLHCLAA FKSRVTASIPGCKAHAVENVL TTKS KTRIYPEVVVQSGLQKQK GKG SVMFIEAAGL

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9314	39682	A	9374	3	276	VRQYR/LGN/MHQQRMAEMID ARQQQAFGEEGACWGCGPKHR VMLDASGKPGLNLDLACAGYQRD VRHLPRYLYKAMADLLAIIHGRPA SDIMHAHILV
9315	39683	A	9375	102	916	RSLLAIFNHW*KRDLGKFVLW NIK/W/AFAKFCRSAQGTSGRSVI VEHNGEIYACDHVVYPQYRLG NMHRQRMAEMIDSRSQQQAFGE DKFKQLPAQCRSCNVLKACWG GCPKHRFMGLDASGKPGNLNYLC AGYQRVFRHLPPYLKAMADLL AHGRPASDIMAHKKVFKRG ACSGFQKGGLPFRSRITGYCPTL RKKACPCKTGLLGKWTQRR NSSGKSCAKRRGDPLLENRFN GSRVQRKPQWNNSCTGHPEENN FPNYGGTPYQPQRMWP
9316	39684	A	9376	338	1155	SIFISIGNLAANDLSPSPRIARLQK ILHSVYPEEIRDGQNVVRTSWD GRKWGELEGDTYDRVLVDVPC TTDRHSLHEEEENNIFKRSRKKE RQILPVQLVQQLLAAGLLATKPG GHVVYSTSLSHLQNHEYVVQG AIELLIPINTASRYRWK*LTSEG FSWTHFVSSSQSCPGWGAGNTK TSLA LALCTSAKCVGWT*YP QSLKQEYQRVYSVGCTRNWKL GPVAEMHSRSCLHPVRFQFS AIRSRRAVILSNCGASA WPFT SLINPYPI
9317	39685	C	9377	157	453	
9318	39686	A	9378	486	1195	ARPQQYEQVPGKAEASEWERG SSAAPTGGHAAAAAGGVGGG EGSPPALHGRGARAG/GAGICM GLRQQLNR*AMDLTGAGGPAR AGAAGAVARGGGRHQQPGAG GRGRGLGFAAGTAEPRAPGHR PLQRALPPIRREPGERHRAPRAG AAPQCGSARPROPRAPQOSLRAG ALPEAHAQQQGPARTIHPAEPGP AARRAQQSCLRHW*GRGRPG PPDALRGGAASDFRLSARTPICR
9319	39687	A	9379	10	1278	

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9320	39688	A	9380	1	1305	MECVCVKEKEREKEGKEEEE EDEAVAERGGKGERRGERRGE RKREKETYTEKNRYRTDKRDR DREKKEPYEIPSSLIGHGDPKDE LDRNLALKQVKTYWVIQFSKSI EVIEKRMAVLNEQVKAEAGSS AEYKKEIEELKELLPEITEKTED AKESQTTGNVAELALKATLGG GSSVS/SIA SRKPTDGA SSSNCV TDISHFVRKKRKPEEQSPWPKDD AKKVVKQLEVNNGGSDAVPSG NEVLENMEEEAENRVESRAAV EGTVEAGATAESTAYMYDIPA MYQENTAVSKTDEVSDLIHKL AQTDLLAQRAGKRASPQDGG SAEQQAQS DRQEATKQRHKQE AGDRHYDKQMLLEYQGAHELY SSREKRKEKKKKPPHGRLLPPTP VALHGAKRRLLT KRLFNASPN KPKGHISTQFSVMSQAEQQPV
9321	39689	A	9381	67	458	WDMANSGCKDVTPDEEFSFLY FAYGSNLLTERIHLRNPSAAFFC VARLQ/QEGVKSGMVYVVIEVK VATQEGKEITCRSYLMTNYESA PPSPQYKKIIICMGAKENGPLE YQEKLKAIEPNDYTGKGEENE
9322	39690	A	9382	139	710	WDMANSGCKDVTPDEEFSFLY FAYGSNLLTERIHLRNPSAAFFC VARLQDFKLDFGNSQGIKTSQT WHGGIATIFQSPGDEVWGVVV KMNKSNLSNLD EQEGVKSGMY VVIEVKVATQEGKEITCRSYLM TNYESAPPSPQYKKIIICMGAKE NGLPLEYQEKLKAIEPNDYTGK VSEEIEDIIKKGETQL
9323	39691	A	9383	1	731	MANS GCKDVTPD EEF SFLYFA YGSNLLTERIHLRNPSAAFFCV ARLQLLIESPRMSRLAKFWPRT HAVILSKTERTSFWPLKPQKW SGSDTPYSQTRKDFKLDFGNSQ GKTSQLWHGGIATIFQSPGDEV WGVVVWKMNKSNLNSLDEQEG VKSGMYVVIEVKVATQEGKEIT CRSYLMTNYESA PPSPQYKKII MGAKENGULRLKYQEKLKAIEP NDYTGKVSEEIEDIIKKGTITKL
9324	39692	A	9384	41	333	MFCNTDLGT/LLCTDVARGLD IPQVNWIVHYDHDPDDPKEYIHR VVPAFDVLNVNGNEGKQKRG GGGGFDYQKIKKVEKS KIFKH SKKSSDSRQLSH

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9325	39693	A	9385	3	1852	SKQKPMNVGLSETQNGGMSQE AVGNIKVTKSPQKSTVLTNGEA AMQSSNSESKKKKKKRKMV NDAEPDTKKAKTENKGKSEE SAETTKETENNVEKPDPNDEDES EVPSLPLGLTGAFEDTSFASLCN LVNENTLKAKEMGFTNMTEIQ HKSIRPLPLEGRDLAAAKTGSG KTLAFLIPAVELIVKLRFMPRNG TGVILISPRTRELAMOTFGVLFKE LMTHIIVHTYGLIMGGGSNRSAE AQKLNGNGINIIIVATPGRLLDHM QNTPGFMYKNLQLCVIDEADRI LDVGFEEELKQIQLLFTRRQTM LFSATQTRKVEDLARISLKKPEPL YVGVDSDKANATVDGLEQGY VVCPSKRFLLLFTFLKKNRKK KLMVFFSSCMHSVKYHYELLNYI DLPVLAIHGKQKQNKRRTTFQQ FCNADSGTLLCTDVAARGLDIP EVDWIVQYDPPDPDKKEYIHRVG RTARGLNNGRGHALLIIRPEELG FLRYLKQSKVPLSEFDWSWKIS DIQSQLEKLIKINYFLHKSACQ EAYKSYIRAYDHSLSKQIFNVN NLNLNPQVALSFGFKVPPFVDLN VNSNEGKQKRGGGGGFGYQ KTKKVEKSIFKHISKKSSDSQ

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9326	39694	A	9386	1	2703	MAQQATLCSMKGCMRALVAQ LKSESDLQQTVQAKREVPKSK VPAAEKRESGPQAAVNAAVQ RVQVLVDVTLLHFATESTPDG FSCSSSLALSDEPFIQKDVEL RIMPYVQENDNGNETESEQPEE SNENQDKEVEKPDKSEKDLLDD DDDDIEILEECIIAMPTKSSRK AKKLAQTASKLPPPVARKPSQL PVYKLPPAQNRLQAQKHVSFTP GDDVPRVYCVEGTPINSTATS LSDLTIESPPNELATGD/GVRA/S I QSGKSHKPFRVKK/IMDQVQQ ASSTSSGANKNQVDTKKKKPSTS PVKPMQPQNTHEYRTRLPNNEDR VRGSFALDSPHYTPIEGTPYCF SRNDSLSSLDFDDDDVDSLREK AELRKGKESKDSEAKVTCRPEP NSSQQAAKSQSQASIKHPANRAQ SKPVLKQOPTFPQSSKDPDRG AATDEKLQNFIAENTPVCFSRN SSLSSLDIIDQENNKKNESEPIK EAEPANSQGEPSRQLSQQLNLTK QASLSKNASSIPRSESASAGLNLQ MSNGNGSNKKVELSRMRSSTKS SGSESDRSERPALVRQSTFIKEA PSPLRRKLEESASFESLSPSSRP DSPTRSQAQTPVLSPSLPDMSLS THPSVQAESSEKAKSEDERHRVS SMPAPRQMKENQVPTKGTWR KIKESDIISPTGMASQASSGAAS GAESKPLIYQMAPPVSKTEDV
9327	39695	A	9387	2	193	QSSE*NIQGPCNVWSSR*RWER SKGRHLSSASRPLSALSTLRFT SVSQHAAKRVVVIRPQGQ
9328	39696	A	9388	395	761	SMQKKPRPIAHQRQRAAMAA/ GQQPQIPTTGTGVVYPGAITM ATTTPSPQMTSDCSSTSASPEPS LPVIQSTYGMKTDGGSLAGNQ MINGEDEMAMYDDYEDDPKS DYSSENAAPEAVSAN
9329	39697	B	9389	1	477	

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9330	39698	A	9390	167	890	LSGARSSQGRLPWGRGDAVSTS TSRRNPRTGASDERNNHEPGKN SPYLQAQVIRIGGKGATARRKKK VVHRTATA/DDDKLQF/SLKLL GVNHISGIEEVNM/FTNQGTSG STFNNP*KVQAIWAANTFHPL PGPCWRPKPADKKWL.PQPSI.N PSLGAG*S*LRFKGRLARSFLPP NNP/VDGKATHLPTG\KDDDD\K KVPRLSLWRILMRLPKNEGKLEL RSTS*R*NLEEVTGSRYFKIMT AF
9331	39699	A	9391	2	315	GAASLLRAGPGSSGSDP/PLSSR FVERRGALYRSPMNQENPPPYP GPGPTAPYPQYGWQGGPQEPP KTTVYVVEDQRRDELGPSTCLT ACWTALCCCLWDMLT
9332	39700	A	9392	263	680	LLLPAVLTSAPlPPGALATCPCP RLAQLGIGRAAPQKRSPRRRN EASRGRPPDGVRAPLVR/VPPT PRETEPQRRGDGPGLRNPCLSQA SPGAPQFSGP/PPGSPGTRPVRA* SPPGPSWVPGPGLHLTSPLPNRL DNGRV
9333	39701	A	9393	2	537	SGARLLLTCSSETGAASSLLRAGP GSSGSDP/PLSSRFVESRGALYR SPMNQENPPPYPGPGPTAPYP YPPQPMGPGPPIGGPYPPQQGYP YPRIPTVRLAGWTSGSLLKTTV LLWVGRPKREAMKLGTIHLPSQP AGTGLCLLSSLGWTWFTRTRP RPFLFLASSAANLLTGVPCPHLF
9334	39702	A	9394	3	470	PKAKKEAAPPKAEAKAKALK AKKAVLKGVHNHTQQKKIHTP LTFQRPKSLRLRRQPKYPRKSA PRRNKLDHYAIIKPFLTTESAM KKIEDNNNTLVFIVDVKANKHQI KQAVQKLYDIDVAKVNTLIRD GEKKAYVRLAPDYDALDVA KIGII

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9335	39703	A	9395	1	1144	MLYQVLMVDTCGTRGEGAKL YRKpacPTALGFMPRSHGLTA DTVLVSSLSRwFLWRRLLLLL LLLLNLPLQKA/VHRKATPESAI ADCSCPRDCAPWVKFAMLELH SFKCPAGEYWSKDVCCKNSA GTFVKAPCEIPTQGQCEKCHP GTFTEKDNYLDACILCSTDKG DFYGKKTAVHEALCDNIDTRT VMEEMRALV\$QCNLYMAARK AERRRPNRALLENIAMYLTHM LKIFGAJEEESPLGFPVGGPGTN LNPIENGGMDKFLLTVSVLRKT HRVSNQNQNSCRSVSYWKPKC TFCSLTHITYIRYLELRLTESTV MPYQLVLFSEFREGVRKIAREKK VLEVQLSDLALRVTSCSLSGG LKTMKEPCLLF
9336	39704	A	9396	1	639	MDGDEKTSFICAVHNGIFREWK QTGTCSPIKKQQLLRLVECHGK IKAQGGQMYIKAALFTRAKTW NQPKCP\$MIDWIKKMWVHYI// TCEYYTAIKKKIMSSVETWMEL EAIILSKLTQEQKSFKRTFSLYSS RVFORTQDVPLYHNKLNEEADK PTTNKKGLILNRLVNTPIGRK NTGKLSAIKEKLKRPKRKHLSS KIYTLKNDSDLIKDKNI
9337	39705	B	9397	1	825	
9338	39706	A	9398	2	285	HEENRPFVCEH/AGCGKT/FAN KPSLTSDAVVH/DPGKKKML KVKKSRERKRSRSLASHLSGYIPPK RKQQQGLSLCQNGESPNVCED KMLSAVPVLTG
9339	39707	A	9399	2003	2344	PFVGVFVFLFFFSSVFVFTFVPP EYYVLPAPPFRHSVFLVFGKRV VFFFPLPC/CDFRSRLTPPFVCAP PPPPLPFVSVCVPSSLSCGDVC AADKKNNKKFLNTTRWKKKT
9340	39708	B	9400	3	113	
9341	39709	C	9401	48	182	

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9342	39710	A	9402	2	752	VWWNSRRRPVKRRRLASPY ACSGRSAGFLDNCAMCARLA AAAAAQSVYAFSARPLAGEP VSLGSLRGKVLLIENVASL*GTT VRDYTMELQRLRGPRGLVV LGFPICNQFGHQENAKNEEILNS LKYYVRPGGGIEPNFMLFHKSE VNGAGAHPLFAFLREALPAPS DDATALMTDPKLITWSPV/CRK DPGKIKFFLGPGNFFEEKFLGP CTVLPLRRYSRRFQTIDIEPDIE ALLSQGPSCA
9343	39711	A	9403	1	1128	
9344	39712	A	9404	7	378	ARCDHPTAfvvcyrfypwpag HVDAAVH*YVCARATDSIAV WRTLKGTHIIHLHESSIHDFNFLT SQKLWAfVPNKAPrTSgiiCWP EIQSAFQGGGNLYFTIPIVDRNS TNYVLRQVRLLGN
9345	39713	A	9405	318	616	DPAGFPGCWKPLFYDLHYRSQ LHQLCLQAGRTPGQFGHQHRF WWQFCT*El.PSALQPLPEGNLV SCNEQSFGAPATGTNPGEPVHP AALGTWLYLLPPC
9346	39714	A	9406	1	145	MEYYAVIKKDEFMSAGTWM KLETIILSKLTQE\QKPTPLMFSL ISGS

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9347	39715	A	9407	1	2052	MVLVVVAVVVVVLVVAVVV VVVVVAVVVGAVVVVVVV MVVVVVVVVVVEEDNQHKTGA INNNNTAKNPQQSPFHPSATST GAEATQMRNNQKTPHNIMTST QVSLTPPKITLAHQWQIQTKKK YIYLKKHSGVNKIPRNPTYEG CEGPFQGELQTTAQQNKGHHK QTEDHSMLMDRKNNQYCENGH TAQAVPNPYTLLSQPIPEDAEWF TVLDPKHAVFPCIPVHDPSQFLT AFEDPSNPMSQLWTVLPQGFR NSPHLFGQALAQDLSQSFSYLDT LVRLYMDDLLLATHSETLCHQ ATQALNNFLATCGYKVSKPKA QLCSQQVKYGLKLSKGTRTLS EERJOPILGYPHPKTLKLQTLAFL GITGFCQIWIPRYSKIARPLNTRI KETQKANTHLVRWTPEAEVAF QALKKALTHAPVLSLPVQGNFNS LYVTEKIGIALGVLT/PGTSAQ LAELIAITRAPELGEKGKRVNIY ANSIGEREFILTSKGTLVKHQE AIKRLLLAQPKKEVAVLHCHW GHQKGKEREIEENRQADIEARR AARQDPPLMTELGPLAFELA MATARAELSIAIHCCLPPPPQ TRCWLPSPRLIRQGVCCIPDPR AITLTAWPKIPFLGIRKAKNPRS EKTRLATIACCHFGSPPPS WELWEQGPPVTQTHILRSHL
9348	39716	A	9408	2	350	YKVSFKPKAQLCSQQVKYLWLK LSKGTRALSEERIQPILAYPHPK TLKQLRGILGIGTCFRCIWP* SPTGQE/FSLYVTEETGIALGILT QVQGTSLQPMEYLNKEIDELDQ GRTH
9349	39717	A	9409	1	749	MNQSDQEMTGAFVHMKSYTG LISGVAVKMERHIYQDRRIAEIK EFNSCRTGCMGDWSFTTQIRL LENTGIVFKDNLVEEAETFTV LDLMDAFFFICPVHPDSQFLFAFE DPSNPASQLTWTVLQPRFKNSP HLFGQALAQDLSQSFSYDLTQL RYMDDLLLAAAYSETLCHQATE ALLNFLATCGYKVSKPKAQLCS QQVKYGLKLSKGTRDLTTFLP VNEEKIE/P*LSTSNC SKLRC SRG TSRGSLG
9350	39718	A	9410	118	174	
9351	39719	A	9411	577	3018	

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9352	39720	A	9412	310	1964	TFRLTEPTQMRRNQKTNPHNM TKQGSSIPPQKHNTHSSPAMDPN QEEIPDLPIEKNSGVNPKIPRNPT YEGCEGPFGELQTTAQQNKG GHKQTEDHSMLMDRKQNQYCE NGHTAQAVPNPYTLLSQIPEDA EWFTVLDPKHAVFCIPVHPDSQ FLFAFEDPSNPMSQLIWTVLPQ GFRNSPHLFGQALAQDLSQFSY LDITLVLRYMDLLLATHSETLC HQATQALLNFLATCGYKVSKP KAQLCSQQVKYLGKLKSGTR TLSEERIQPILGYPHPKTLKQLT AFLGITGFCQIWIPSILTAKGDL WLSDNHLLKYQVLLLEGPVLQ LRTCATLNPATFLPDNEEIKIEH NCQQVIAQTYATRGDILLEVPLT DPDLNLYTDGSSFVQKGLQKA GYAVVSDNGILESNPFTPGTST QLAELVALTWALEFGEGKRVN INTGSKYAYLVLAHASIWRER EFLTSEGTPIKHQEAIRLLLVV QKPEEVAVLHCWGHPKGKERE IEGNQCADIEAKRASRQDPPLE MLIERHLVWGNPLWEWTNPQYS
9353	39721	A	9413	3	370	RCCPCPRVHHMHISARAERIPPP RPPPFLLVLFQTPGCPCHPGC SPPPAHPSCSSWPQWP/CSSPV SVLLAKPAACLIAAAAVSANPRL LFKPCCRRTASNWAHRQVTLCQ WSELSSCFWPE
9354	39722	A	9414	191	1375	EWPEGGGGRYSSVPSSAVHHART CLAAELS GTSRPQEPRALPPETG VATAAEKSNQPAAI SK/PNGQ GAPLQR/RSPRLSPSPGAAQVPA LPMQDMSEGSSSPSPGGHIWL ASLTPCSLALWNNSCCQSPGSQP RGRDEGDCLVRATEPSATGPDP RRTRLCSISASL VVRNTDPGIS DRRP G ISDRRPGTSDRRPGTSDR RPGISDRRPGTSDR RPGTSDR RPP GTSDR RPGTSDR RPGTSDR RPPGT SDRRPGISDRRPGTSDRRPGISD RRPGTSDR RPGTSDR RPGTISRLP RDWIPAAAASRENSNSADARN RCSSPSRK CQTPTSHRMGRGSA SVGSSAGHTAGGTGLPTPSRC QALQVFPAVLGKRGFLSWERS LKQRDIRGPDFSSTALI
9355	39723	A	9415	3	523	

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9356	39724	A	9416	1	846	MLCDFQDGSTSRRHVNEPSNNPS PQPWSEDQQQASAATVPCAKSV MHRLKKFTIEYLVMKFLKA HAIQM E MLAPKGPSPIP E DASV KEENICRAFS D ALLYKIED I DNK DWNNPQLCSDY/VKD N AYTSF QIQEMET V LKE L KFEVGGPLPL HFLRQA S KGAKAD V EQHTLAK YLM E LT L IDYDMMHYHPSKAA TAASCLSQV L GG G WN L KQQ CYTG T QNEV L EV M QHVAKN VLKV N EN L TKFIA I KNKYASNK FLK I SM P QLNSKA I DKL A FPLM GGS
9357	39725	A	9417	72	I340	CPPFSVRVPPWAGLALLPSPSL MALLRRPTVSSDLNIDTGVNS KVKSHVTIRRTVLEEIGNRVTT RAAQVAKKAQ N TKV P V Q PT K T TNVN K QLKPTASVKPV Q MEKL APKGPSPTPEDVSMKEENLCQA FSDALLC I ED I D N ED W ENPQL CSDYVKD I YQ Y LRQ L EV L QSIN PHFLDGRDINGRMRAILVDWL VQVHSKF R LLQ Q ETLYMCVGIM DRFLQVQPV S RKKLQLVGITAL LLAPK Y E K MF S PN I ED F V Y ITD NA Y PS S Q I RE M ET L IL K EL K FL GRPLPLHFLRASKAGE E VD V EQ HTLAKY \ LM E LT L IDYDMVHY HPSKVA AA ASCLSQV L GG G WN L KQQ Y H K DT Q EN E V L MQHMA K N V V K V N EN L TKFIA I KNKYASS K LL K ISM P QLNSKA VKDLASPLIGRS

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, a=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
9358	39726	A	9418	1	1875	EPEKQQLYDIPASPKAGLHP DSQASGQGVPLISVTLRRGGY STLPNPQKSEWIYDTPVSPGKA SVRNTPLTSFAEESRPHALPSSS STFYNPPSGRSRSLTPQLNNNP MQKKLISLPEIPISYGFLVPRGTFP LDEDVSYKVPSFLIPRVEQQN TKPNIYDIPKATSSVSQAGKELE KAKEVSENSAGQIPHGPDG/ RSPSPEDPDRLSGSSSDRASIVSS CSTTSTDSSSSSEESAKELSL DLDVAKETVMALQIKVSSVA GLMLFVSRKWRFRDYLEANID AIHRSTDHIEEVREFLDFARGV HGTACNLTDNSNLQNRI RDQM TISNSYRILLETKESLDNRNWPL EVLVTDHSVNSPPDLERFVMV ARMLPEDIKRFA SIVANGRLLF KRNC EKEETVQLTPNAEFKCEK YIOPPQRETESHQKSTPSTKQRE DEHSSSELLKKRNANICGGQTLPN LEEKDKPILEQRLLDENKDLGTM NPGLPLIQPSSQQTPERKPRLSE HCRLYFGALFKAIASFHGSSLSS QPAEIITQS KL VIMVGQKLVD LCMETQERDVRNEILRGSSHLC SLLKDVALATKNAVLTVPSAA LGHLQAEAEKLEHQTRQFRGT

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9359	39727	A	9419	1	2013	MGLKSWGGMGLGTAFGKGLR GEKAWCVSGRYHWRYSQWSG TLTQGPWVWRVHSSLDRVYDV PTQHRGPVLKEPEKQQLYDIP ASPKKAGLHPPDSQASGQGVPL ISVTTLRRGGYSTLPNPQKSEWI YDTPVSPGKASVRNTPLTSFAE ESRPHALPSSSSTFYNPPSGRSR SLTPQLNNNVPMQKKLSLPEIPS YGFLVPRGTFLPLDEDVSYKVPS SFLIPRVEQQNTKPNIYDIPKAT SSVSQAGKELEAKEVSENSAG QIPHGSYPDQ RSPSPEDPDRSG SSSDSRASIVSSCSTTSTDSSSS SSEESAKELSLLDVAKETVMA LQHKVVSSVAGLMLFVSRKWR FRDYLEANIDAIHRSTHDIEESV REFLDFARGVHGTACNLTDNSL QNRIRDQMOTISNSYRILLETKE SLDNRNWPLEVLVTDSVQNSP DDLERFVMVARMLPEDIKRFAAS IVIANGRLLFKRNCEKEETVQL TPNAEFCKEKYIQPPQRETESH QKSTPSTKQREDEHSSELLKKN RANICCGQNPGPLIPQPSQQQTPE RKPRLSEHCRLYFGALFKAISAF HGSLSSSQPAEIITQSKLVIMVG QKLVDLTCMETQERDVNEILR GSSHLCSSLKDVALATKNAVLT YPSPAALGHLQAEAEKLEQHTR
9360	39728	A	9420	3	645	DFHTN/K/RVCEEIPIISSKLLHN RRAGCVTHLTNQIQRGPVRGISI KLQEEEKERRDNYYVPKVSALD QEIEVDPDTKEMLKLLDFGSLS NLQQQKATRVYAVVQISAPMF LIWALPLSVAPLITDFKMFVTT SYLISFLIINSSANPIIYFFVGSL RKKRLKESLRVILQRALADKPE VGRNKKAAGIDPMEQPHSTQH VENLLPREHDRVET
9361	39729	A	9421	312	694	LTPAPRKNVTEKYYMCLGNDF HTN/K/RVCEEIPIISSKLLHNRR AGCVTHLTNQIQRGPVRGISIKL QEEEKERRDNYYVPKVSALDQEI IEVDPDTKEMLKLLDFGSLSNL QVTRPTVGMNFKMPRGAV
9362	39730	A	9422	3	383	

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9363	39731	A	9423	304	1862	RMILEATSKMRKGVPSSIQ/SSQ GNSVTLIPSAAKSDNLSDSSHSEI SSRSIVSNCSVDMSAALQDE RCSSQALAVPESTGALEKTEHA SGIGDHQSQHGPGBTLLKPSLIK CLAVSSSVSNEEISQE/IHEAAD SGSWEVGTSRSSSHDNFQSLP NPKSWDFLNSYRHTHLDDPIAE VEPTDSEPYSCSKCSRCTCGQC KGSLERKSWTSSSSLSDTYPEPN YGTVKRRVLESTPAESSEGGLDP KDATDPVYKTVTSTEKGLIVY CVTSPKKDDRYREPPPTEPGYL GISLADLKKEGPHTHLKPPDYSV AVQRSKMMHMNSLSRIPPAASLSS NLVACVPSKIVTQPQRHNLPF HPKLGDVTDADSEAATLGNK CKLLYMSDVRNPVPAVKDVLV QKYTSFNFFHPQEALDRRREEL ALPEGASGEACLSTRSLKRSGV QALAQQTHSRNFLPEKQPFSAQ AAGILHGSIHNTRGPCLLEG KMMTGVLRYAYLLCIAYSRDLI VDEQIMNGLRKA

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9364	39732	A	9424	1	1335	MTFKNPKYPFVSNLAQKQGMS VIKVNGKLQQSNPNRRTNGPDP SGMKVWVSPQGKNPQPTEVLA EGKGNTEWVEEEDTRNFGFGI QKHTDIGIKYDSSTGIYDLDFN VVLDRRASEEGITLTAAALADR ETPSENCLPSPVNPTAQGEEGH PDIIVLVEQEDPTTAPHPCRQCQ QQQCQRPLCRLQPVWPVHIVDLT PLTEIGSEEPVGELNFKHIFRFEV SEDNMTFDASDQGPFFENYWQ LVLSATPGDTWNGALGLHTP KSSSPDTCSAQQAQSCWELSPG GRRIGTLLLPQESGASWLPPGV TSSLAAVRVIMNCGDKATPRN GGVRTLKKLSSLPLSKAGGKVL YGEINPEQEVTQASLSFAALLS YGIFMETEFLVACLIQSGGQLR NQDFSSSIYSLAPGLDPSSVRA GAQRTAPPWGSPRSCP/PVKVN GKLQQSNPNRTTNGPDPGSMK VVVSPQGKNPQPTEVIAEGKG NTEWVVEEEDTRNFGFGIQKHT DIGIKYDSSTGIYDLDFNVVLDR RASEEGITLTAAALADR/TPSE NCLPSPVNPTAQGEEGHIPDPII VLEQEDPTTAPHPCRQCQQQC QRPLCRLQPVWPVHIVDLTPLTEI GSEEPVGELNFKHIFRFEVSEDN MTFDASDQGPFFENYWQLVLS ATPGDTWNGALGLHTPKSSSP DTCSAQQAQSCWELSPGRRIG
9365	39733	A	9425	56	235	
9366	39734	A	9426	1	515	
9367	39735	A	9427	138	830	AWAQLPSALGSTRVSPPSARS QPPWRRRH/CILLETEPLQGTD EDAVASADFSSMLSEEKEELK AELVQLEDEITTLRQVLSAKER HLVEIKQKLGMNLNMELK\QNF SKSWHD\DMQTTAYKRTHDTL SHAGQKATAAFSNVGTAIISKKF GDMSYSIRHSISMPAMRNSPTF KSFEERVETTVTSLTKVGGTN PNGGSFEEVLSSTAHASAQS LA GGSRTKEEEELQC
9368	39736	A	9428	3	381	LLETEPLQGTDÉDALASADFSS MLYEEEKEEVKAELVQLEDEIT TLRQVLSAKERHLVIEIKQKL G MNLMNELKQ\NFSKSWHDMQT TTAYKKTHTLSSHAGQKATAVA FSNVGTAISKKFGDMRRK

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9369	39737	B	9429	79	426	
9370	39738	A	9430	1	570	
9371	39739	A	9431	1	1677	MLESVNVRLLEDLITGPCWEAG WNAGYAFLVVAVEDFTIGKLF DKLEGTKLCLKNALPRVTQTE SHRQLRQEAAANWHISWLKV QKMKA VIAEIWPVADATRIKRALEQQ MELSGSSMAPIMTVQSKTAPP TFNRTNKFTAGFQNIVDAYGV GSYREINPAPYTIITFPFLFAVMF GDCGHGTVMMLAALWMILNER RLLSQKTDNEIWNTFFFHGRYLI LLMGIFSIYTGLIYNDCFSSKSLNI FGSSWSVQPMFRNGTWKTGTH DPHLAVLFKMGHVEGRDCVLR IVLAKIGYRNGLRKIWNLASN KLTFLNSYKMKMSVLGIVQM VFGVILSLFNHIYFRRRTLNIILQF IPEMIFILCLFGYLVFMIIFKWCC FDVHVSQHAPSJLIIHFNMFNLN YSDSSNAPLYKHQFNFGDVFV HQAIHTIEYCLGCISNTASYRL WALSLAHAQLSEVLWTMVMN SGLQTRGWGGIVGVFIIAVF VLTVAILLIMEGLSAFLHALRL HWVEFQNKFVYVGDGYKFKSPFS FKHILDGTAEE
9372	39740	A	9432	3	933	GTWPVSSAACIYAGTGGLG(SQI SMSCTSFWGGLGSGGLATEM AGGLAEMGGIQNEKETMQSLN DHLDYLDVRVNLETEMWRLES KIQEYILEKRPHVRDWGHYFKTI KELRAQIFANTVDNVHILQIDN AQSSMRQELAMRQSVEINSIHG LCKVIDDTNVTLQLETEMGAL KEELLMKKNHEEEVKGLQVQ IANSGLA EQLNRLILYLESKLAQNWAEQ QRKVQEYKDLLNIRVKEAEIA TYRRLLEDSEGLNLGDALDSSN SMQTIQKTTTRQIVDSKVSEIS DTKVLRH
9373	39741	A	9433	3	698	

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9374	39742	A	9434	2	479	PRVRESTIVVTQSAEVGAAET TLTELLRRTVQSLEIDLDSMRNL KASLENSLREVEARYALQMEQ LNGILLHLESELAQTRAEGQRQ AQEYEALLNIKVKEAIA/TVY RRLLEDGEDFNLGDAALDSSNS MQTIQKTTTTRRIVDGKVVSETN DTKVLRH
9375	39743	A	9435	1	618	AEHLLKPLPADKQIETGPFL EA VSHPDPFFDCLGSPVFTPKADIS GNITKIKAGYDTN QPRFRTLKT ILEGEKEMYGAKGPVKVATLA LMWLKRGRLRFIQVFLQSCIDGE RDENHPNLIRVNATKAYEMAL KKYHGWIVQKIFQAALYAAPY KSDFLKALSKGQNVTEECLEK IRLFVNNTATIDVYEMYTQM NAELNYKV
9376	39744	A	9436	1	1569	
9377	39745	A	9437	211	368	ERNSSLSQLQWDNPATPPA TRRPS HSSLRGEHAQ*GLLSFFERLSCT LSRFMPI
9378	39746	A	9438	1435	1703	
9379	39747	A	9439	1	913	MKNYNCWRRVFLFVVTPIMG HIKHRQGPNKQQRGQKRDEQR MRKENRGHRKGCTWCGGTE GTGWGKYEKEVERGLVRYER KRRAYSIGIQQYAAAALPTVYN QNLLTQQSIGAAGSQKEACAY AVMSLASRAPVYRSFDSEKAG DREVQRTMLELLNQLDGFQPN TQVKVIAATNRVDILDPALLRS GRIDRKIEFPMPNEEARVARIMQ IHRSRKMNVS/TDTLVALQML NVYNGKQAPYASCHIFELYQE DNGFLLLEHTGFVSYDNPVAQ AAIQSMNGFQIGMKRLKVQLK RSKNDSKPY
9380	39748	A	9440	3	438	
9381	39749	A	9441	1	247	AIAAIDSDDSGSRQSEWKFWK GFTILDIAKNIYDSWEEVKMST LTEVWKKLIPTLMDSFEDFEE VTVDVWECTVLQQTQI

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9382	39750	A	9442	93	726	TSLGLSLCPRQCKRCPLHLSQQ EEPDPANLEVDHDFFQDKVWP HLALRVPAAFETLKVQSAWAGY WDYNTFDQNGVVGPHPLVVN MYFATAFSGHGLQQA/P/GIGRA VAEMVLKGRFQTIDLSPFLFTR FYLG/EKIQ/ENNIJLRHVCSGIG LPLACNPWLCLKSLVCWLPIFP KVLCPGLLSPSPVSSSQAGHW HPIWAGQGTGSEAEQG
9383	39751	A	9443	1	849	MSGALDVQLQMKEEDVLKFHA AGTHLGGTNLDQFMEQYIYKR KSDGIYIINLKRTWEKFLLAAR AVVAIENPADVSNSGNTGQR AVLKFAAATGATPIAGHFTPGBT FTNQIQAAFREPRLLVVTDPRA DHQPLTESSYVNLPTIALCNTDS PLRYVD/ICNNKGAHSDPSEEIE KEEQA/AAEKAVTKEEFQGEWT APAPEFTATQPEVADLSEGQVQ PSVPIQQFPTDDWSTQPATENW SAAPTAQATEWKMQQQSTILE AESSHQTPNLPAPWSRTSQPP
9384	39752	A	9444	1	1575	
9385	39753	A	9445	1	2325	
9386	39754	A	9446	1	1149	
9387	39755	A	9447	85	1041	REIVTMMSGALDVQLQMKEEDVL KFLAAAGTHLGGTNLDQFMEQ YIYKRKSDFGIYIINLKRTWEKL LLAA/RAIVAIENPADVSNSGNTGQR ILGQKGKAESFAAATGATPICW ARFTPWNLSLTQIQQGSPSGEPR AFLLVTDPQGLNHQPSHGGNL NV*PTPLALVNPD/SPLRRYVD IAIPCCNNQSSLQWGMLWW/M IASGSFCAMRG/TISREHP/WEV/ MPDLYFYRDPEEIEKEEPGCCL RSQVTKEEFQGEWTAPAPEFT/ VTQPEVADWSEGVQ/VPSIVPIQ QFP/TTEDWSAQPATEDWSAAP TAQATEWVGATTDW

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9388	39756	A	9448	1	762	MGKVKVGVNGFGCIGRLVIRT ACNSGKVDIIAINDPFIDLSYMW YMFQYDPTHGKFHGTVAENG KLVINGNPITIFQEPDPSKIKWG DAGTEYVMESTGIFTTMENAG AHLQWGAKRPQGLQNIIPIATT/ GAAKAVRKVIPELNGKLTGMA LRVPTANVSVDLTYHLEKPA KYDDIKKVVVKQASEGPLKGILG YTGHQVVSDFNSDTHSSTFNA GAGTALNDHFVVKLISWYDNEF GYNNRVRVVDLMAHAMASKE
9389	39757	A	9449	93	660	DTMGKVKVGVNGFGRIGRLVT RA\AFNSGKVDIVAINDPFIDL YMVYMFQYDSTHGKFHGTVK AENGKLVINGNPITIFQERDPSK IKWDAGIAEYVVESTGIVFTT MEK/ALGAHLQGGSQKGHSSL APSLMLPPMFVMGVN\HEKDD NSLK\IISNASCTTNCLAPLAK\ VIHDTLVSGEGLKDHDRALP
9390	39758	C	9450	554	715	
9391	39759	A	9451	193	472	RRVGVWRRPQFQQSRSCHGPN QGSAPWLNPTEGFKETDLL\ DDSLVSIFGKRL\KFRSMVG/D RMASKNALNAQPDPGLTCSL APNIQS
9392	39760	A	9452	1	864	GTRMGLAGVCALRRSAGYILV GGAG\WSVLAPRAAAARRCSE GEWASGGVRSFSRAAAAMAPI KVGDAIPAVEV\FEGEPEGNKVK PGKSLFKGKKGVLFGVPGGPPP LGCS\KTHLAKGLWEQG*RLCK AKGKSRRVVALF*VNNDALCDW AQWGQAPQGGKARFGLLAESP LGPFGK\ETDLL\LDSELVSHLL GIRRLK\RFS\MVVQDGIV\KAL\ INVEPDGTGLHAAWAPNIIFTA LEALGPDLPLPPPYSSPCPALC LGPLQFGNVGQISAINTLWVLR PKQKKKKKS
9393	39761	A	9453	1	239	QCCSGGTHGNPAIGDR\MQKQI LPWAPAPAQMCKIRFMAPPERKYS VWIAAPILASLSTSSRNMWISKQE YDESGPSIVHRKCF

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9394	39762	A	9454	2	801	ASAPRAQS LAFA DPPP VHRRQ LTMD DDI AAL VVD NGSGMCKA GFAG DDDA PRAV FPSI VGRPRHQ GVMV GMG QKDS VY GDEAQSK RGIL TLK YPIEH GIV TNWDDME KIW HHTF YNELR VAP EHPV LL TEAP LNP KAN REK M TQIM FETF NTP AMY VAQ A VLS YAS GR TT GIV MDS GDGV TH TPV IEG Y AL PHAIL RL DL AGR DL T DYL MKIL TER GSFT TTA ERE I VR DIK /EE AVL RRP GL RARD GHG VASS S EKS YEL PDG QVIT GNER FRC PE ALFO PSFL G/MESCG HI ETTF NSI MKCD VDIR KDL YANT VLS GG T HQFL PCR PG C*KK ITA LE PV AT MKI RI A VPEA QST PL WNR GA P IL VASL VHL PAK MW DOKS REY D ESGPL P FV HRK I CFQL L PGE EL R
9395	39763	A	9455	3	108	
9396	39764	A	9456	1	1430	MKF LI FAFFGGV VHLL SICSGKAI CKNG ISKR T FEE I KEE I ASCGD V AKA I INLA VY GKA QNRS YER LA LLV DT VG PRL SG SKN LEK A I QI MY QNL QOD GLE KV HLE PV RIP H WER GEESA VM LE PR IH KIA IL GLGS SIT PP EGITA E VL VV TSF DEL QRRA SE ARG KIV VV NQPY I NY SR TV QY RT QG AVE A KVG A LASL IR SV ASFSI YSP HTG I QEY Q DGVP KI PT ACT VEDA EMM S RM ASHG IKI VI QL KM GAK T YPD TD SF NTVA EIT GS K YP E QV VL VSG HLD SWD VQ Q GAM DD GGG FA FIS WE AL SI K DL G LRP KRT L RL VL WT AE EQ GGG V GAF QY YOL HKV NIS N YSL VM ESD AGT F LPT GL Q FTG SE KAR AIM EEV MSL L QPL NIT QV LSH GEG TD INF WI QAG V PG A SLL D DLY KY FF V HHS HG D TMT V HGI QT QM ECL L L FW AV VSY VV AD M B E M L PR S
9397	39765	A	9457	2	631	
9398	39766	A	9458	1	406	PTV CERE LCV FA F QT L GVM NE AA DEI ATGA QV VD L VSM CR S ALE SP RK VV IFEP YPSV VDP NPD P QML AFN P RQL KFM I HTPH QF LL LSS PPA KE SNF RA AKKL FG ST AF /HL HG AM YG SG I YL SPM MSS IS FG YSA
9399	39767	A	9459	7	257	

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9400	39768	A	9460	2	649	
9401	39769	B	9461	50	607	
9402	39770	A	9462	627	1665	EQAGQALSTAPVGDGHELLCE VGSSSFRDVVLGTSMGLCGGY/G GAS/GMGGITAATVNQNQVLSPL NLEVDPNMQGMHTQEKEQVK TLNKSASFVDKVLFLQQQNKM LETNWSLQQQKPAQSNDM MFESYINNLQGLEILGQEKLK LEAELGNMKGLCMFVKEDFK KKYEDEINKPTEMENEFVLIK DVDDAYMNKVELEFRLEG LTD EINFLRQLYEEEIPELQSQI.DTS VVLSMDNSRSLDMDSIIAEIKY EELQTLAGKHWDERRLTKTIS EMNRNISRLQAEIEGLPQRPEQ RASLESVIADAERQGELAIKDA KTKLSELEAAQQRAKQDMAHG
9403	39771	A	9463	2237	2656	LSCSLFSGFACTRFFGTTSILRLPL MYCPVNDSGTAIHASSGPSATTS PP*TPAAGPMSTIWSAARIASSS CSTTITVLPRSRRLWISVPNRSSL SRWCRPIDGSSTTITPTRPAPI WLARRIRCASPESVAERESV
9404	39772	A	9464	3	2790	EFVLIKKDIDVDEAYINKVELESR LEGLTDEINFLRQLYEEEIRELQ SWISDTSVLSMDNSRSLDMDNS VIAEVKAQYEEIANRSQAEAES MYQIKDEELQSLAGKHGDNLRC CTTKTISMEMNRNISRLQAENEG LKGQRAFLEAAIAADEACQCGELA IKDANAKL/SELEAALQRAKQD MAWQLRILMNVRALADIEIATY KKLLEGEESRLESGMQNMMSIHT KTTSGYASGLSSACGGLTSPGL SYGLGASSFSRT

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9405	39773	A	9465	2	1516	SAIPTSTPASTMSIRVTQKSYKV STSGPRAFSSRSYTSGPGSRISSS SFSRVGSSNFRGGLGCGGYGGAS GMGGITAVTVNQSLLSPLVLE VDPNIQAVRTQEKEQIKTLNNK FASFIDKVRFLEQQNKMLETK WSLLQQQKTAARSNDMNFESY INNLRRQLETLGOEKLKLETIE LGNMQQLVEDFKNYEDEINK RTEMENEFVLIKKDVPDVEAY MNKVELESRLEGILTDEINFRLR QLYEEEIRELQSQISDTSVVLSM DNSRSRSLMDSDIIAEVKAQYEDI ANRSRAEAESMYQIKYEEQLSQL AGKHGDDLRRTKT*DLR*TRN ISRLQAIEGLKGQRASL\EAII ADAEQRGIELAIK DANAKL\SE LEAALQRAKQDMARHLR*VTR ELD*TFKLGPGTFF*ATYRKLL EGEERSRL\ESGMQNMSIHTKTT GGYAGGLSSAYGGLTSPGLSYS LGSSIFGSGAGGSSFSRTSSRAV VVKKIETRDGKLVSESSDVLPK
9406	39774	A	9466	1410	3244	PPCRSHPRPPLRGEQKPRPSQP PFAVPAAPAPQV*IPQMIDLNV GFQFYRSLEHFGGKPKVQEPK PSAVWPQPTPTPFLPTPYPPYYPK VHPGLMFPPFVPSSSPFPSRHT FLPKQPPEPLLPRKAEPQESEET KQKVERVDVNQVJDDSY\YDV GGSQKRWQCPTCEKSYTSKYN LVTHILGHSGIKPHACTHCGKL FKQLSHLHTHMLTHQGTRPHK CQVCKHAFTQTSHLKRHMMQ HSEVKPHNCRVCGRGFAYPSL KAHEAKHASGRENICVECLDF PTLAQLKRHL1THRGPQIYNCS ECDKTFQYPSQLQNHMMKHK DIRPYCSECMEFVQPHHLKQ HSLTHKVLRGLWWGGRGLGK RSGALSRALGSRTPVPLCTLPR GGLQGEIQAQSEFSPVCNHSP GVIQAEALKQGPSGVPEILPQLNS CPTKGTCRYYPEGSRLPSAGTI NKGPRLGFSRKGDHSLTSGAPL YVGKESKVHFRAYEDPGVKEH KCGICCREFTLLANMKRHVLH TNIRAYQCHLCYKSFVQKQPLK AHMIVHSDVVKPFCKLCLGKFEF NRMHNLMGHMRLA\RNKGPLK RLYCPSKFTLKGNLTRHMKVK

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9407	39775	A	9467	1	1309	MRIQQLCGHLWQQKKISLELM SSFHKILKNKMCGCAGVTPDSKEL LKYLSSYCNSYPLTGSQEAAPVS DVPLPVSKCSHCSVQLIMCLRP EHIIPNSPGIKGQGKIQHEEKHPT LLHLDASHLMTCFVEMTLVY LIAGIFKSLCSIHSYPPRTLRLHC EKVWDSSLNEERKHEKRGPN FLHRLPAEHQWGVIVQSSNIMAG LSARLQLFLEHRPFVPELTAN GCPTKGLQGEIQAQESEFSPPVC NHSPGVIQAEALKQGPSPGVPEILP QLNSCPTKGTCRYYPEGSRLPS AGTINKGPRLLGFSRKGDHSLTS GAPLYVGKESKVHFRAVEDPG VKEHKCGICGREFTLLANMKR HVLHTNIRAYQCHLCYKSFVQ KQTLKAHMIVHSDVKPFKCKK SFTAQGNsapQEDAGSQGE/PV CLL/CPNWGQRKGRAWRHLRH
9408	39776	A	9468	3	4804	KRLENIQKTLFVAFSEA VWMQ PSVVLDDDLIAGLPAVPEHE HSPDAVQSQRALAHNDMIKE FISMGSLVALIATSQSQSQLHPL LVAQGVHIFOCVQHJQPPNQE QRCEILCNVIKKNLDCDINKFT DLDLQHVAKETGGFVARDFTV LVDRAlHSRRLSRQSISTREKLV TTLDfqKALRGLPASLRSVNL HKPRD LGWDKIGGLHEVRQIL MDTIQLPAKYPELFANLPIRQRT GILLYGPPGTGKTL
9409	39777	A	9469	2	1844	
9410	39778	A	9470	3	772	VPNPYTLLSQIPEEEA EWFVLD LKDVF CIPVHPDSQFLFAFEDP LNPM SQLTCTVLPQGFRDSPHL FGQALAQDLSQLSYLDTLVLQ YVDDLLAACSETLCHQATQA LLNFLATCGYKVSKEAKLCS QQVKYLGKLSKGTKALSEECI QPILAYPHLTKQLREFLGITG FCRIW/NFQALLLERPVLQLCTC ATLNPVTFLPDNE/E EYNCCQII SQTYATRGDLLEVPLTPDPLNL YTDGSSFVEKGPKA

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9411	39779	A	9471	1	6504	MWGSDRLAGAGGGGAATVAFTNARDCLHLPRRLVAQLHLLQNQAEVWWSHOPAFLSWVEGRHFSDQGENVAEINRQVGQKLIGLSNNGQELHAVSLEQHLLDQIRIVFPKAIFPVWVVDQQTYIFIQIVALIPAASYGRLETTDKLLIQPKTRRAKENTFSKADAEVKKLHSYGRDQKGMMKELOQTQKQLQSNTVGITESNEENESEIPVDDSSVASLWTMIGSIFSQSEKKQETSWGLTEINAFKNMQSKVVP
9412	39780	A	9472	2	1658	
9413	39781	A	9473	1	617	MCSWTAPVSSILTHPNWPVLRMAGLTGCASVAMKKKIEHNQCQVIAQTFTTRGDLLIEPLTDPGNLNYTDGSSFVEKGLRKAGYAVVSDNGILESNPLTPGTSQAQLAELIALTWAPELEEGKRVKRKKAIWRERFLTSEGTPIKHQAIRLLLAVQKPKEVAVLHCRGH/QEGNCQVDIEAKRATRSQVARGHKICDFPSCSYR
9414	39782	C	9474	587	715	
9415	39783	A	9475	96	269	
9416	39784	A	9476	1	1398	
9417	39785	B	9477	1	1152	
9418	39786	A	9478	3	241	
9419	39787	C	9479	202	534	
9420	39788	A	9480	108	199	
9421	39789	A	9481	125	352	
9422	39790	A	9482	2	325	RRSLALSPRPDCGLQWHNLGSLQAPLPGFTPFSCSLSPSSWDYRPPR PANFLYFLVETGFHLVSO/SGLDLLTSIDPPASAQSAGITGVSHRARPQNLFFKVRCPF
9423	39791	A	9483	184	383	LGLQWRNLGSLQAPLPGFTPFSCLSLPSSWDYRPPR PANFFFVFFLVKTGFHLVSQGIGLDLLTS*SHPASAQSAGIJGVSRRPAITLQF
9424	39792	A	9484	1	416	MGRSFLGGGSTLMLIIGGGQLHILTPSFPSWTETGNYTCFCGKQYKYYTPTYQEHVLAIPRNSAKDDHRSASILSENRGSHQ/ShASCHHHYCHYYHQHHHCLHHHSYHHIIHCHIIHRGMWRNWDTVLWIHQTTQPVQD

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9425	39793	A	9485	3	534	GRRQRRSRHLHRRQDRQSAP GSGSKIPQKVKVLAADEDDDD DDEEDDFDDEETEEA/PVKKSIQ DTPARNAQKSDQNGKVSKPSS TPRSKGQESFKQEKTPKTPKG PRSVEDIKTKM/QASIEKAHGT I.GTTVGNIPLRGGNQEKFHGAA GVWFKGFGVQRKIQQQQLQKD VTSGS
9426	39794	B	9486	44	924	
9427	39795	B	9487	41	2197	
9428	39796	B	9488	67	1507	
9429	39797	A	9489	134	311	
9430	39798	A	9490	5	1545	EKIQINTI/KNDKGILPLDPTEIQ! TIREYYEHLYAHKLENLEEIDK FLDIYTLPRLNQEELSNRKPN TACSNLRDGSSLGGDHGHGSSIQ AAIEVVGAGSVATKGRGRQDD TDPSNRHYHRPPYSQEKEQCITL LLSWCLGDSQGPQCRPQLSLQE LRREFTVSLHLARKLILSEVRGQ AHRFVSPPNAAAGAGDGGTNPFP WPPLTDLAPQAESHLPGVNLYL LPLGEQLPDVSLTFQAWRRLSV KCTAVRAYQTTRVVETSSCR HVKGASNASTHRSPKEVTQGT NKSERRTRETQRAIRERNAMGC CTCATDVVLVTQLSQLMEGLALQ PQRTRALLLGGSASIKASCAVTII LMSENLGKGSKKSEGVMVRYY AKHKKQEIKPYYQRKSPSLERG QEKKVVGREDREGSENQYLYG PSNISEARNRLPECGRMGLGYV ARLFLGDRRSSTPSFASYDPPSSL VTYGHRRSCRVSDIRVPRLGPN VGGPCKGTCIDLQCEREKKNEE
9431	39799	A	9491	32	2123	
9432	39800	A	9492	1	911	MSTLKGIIKIIISVMIASEFILEE RIKTGLNAAKHCFAPAQSQAASH TISRPIPMPIRSASACSTPTHTPQ DSLTVGGDVQEFAQQSRRN LRNDLLVAADSITNTMSSLVKE LNSEVGSETESNVDSEFARTQF EDLVPSPTSEKAFLAQIHARKP GYIHSGATTSTMRGDMVTGIDA NPVQPEDENYENDSVRQLEN ELQMEEYLQKLQDQEAYQML VPTKKEIHMEDFLSSLPEGAAQ CPRTFIPDCRRKGASYSQTDDEES NMKTDGDDGEPCGHTEEEDSSL AAASPKRGTTTSSS

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9433	39801	A	9493	2	2233	
9434	39802	C	9494	477	737	
9435	39803	A	9495	2	746	GQATHFMAKEV*QWAHAGIH WSYRVPHPPEAAGLIEWWDCL LKSRLQCQLGDNTLQAAGWKVL QKAVYALNQCPPIYGTVSPIDRI HGSRNQRVEVEVEVAPLTITPS DPLAKFLPPGLTTLCSAGLQVL VPEGGMLPPGDTTIPLNRKLR LPPGHFGLFLPLSKQAKMRVTA LA VVIDLQYQDEISLPLHNGDK EEYARSTGDPLERLLVLPCCVIE VNGKLQQHNLGRRTTNPDPPLG MKVWVSPPG
9436	39804	A	9496	70	532	HVALLMPLQNSRSFSGYGFAYP ARNTFSKTTIHGLKECLIIHHGI PSSIASDQGTRFLPKEV/RKWAH AHGIHWSYHVPHYPEAASP/HS DPLAKFLPPVPTTLCASAGLAVL VPEGGMLPPGDATMIPNLSSR SHLGMPPTSLKVVRMCSKDKY
9437	39805	A	9497	51	408	CVPEPRTPSLGFQT/HPAAHAPG AQAPGSAH/DRLSSAGPGSRAA PRAPWRPWTIGYSESQPTVLRP GQPWIGRGVGSSAPSVPALAR GPPRSSRPSCCTWWCLWRCRH RDLGRDINFIL
9438	39806	A	9498	3	618	SSCAFSHRSSRPSRCHTVRSTA PCAAS*HSSRAPKRHWALPGSS G*S/WRETPSTHW**TLPRWRT ALRPSQ*PRPRVFRVRKPCSSRP PTITRCALASAQ*SCAA/PTSSLA QRKSSRSRPRRTATTWGTARRSR AHAVPAGRSPAPSAPPAQPQAP RAWSSAAAAPASPSRLSSAGRGRQ AAPRAPWRLRGPPRSCRPTCCT WWCP
9439	39807	B	9499	215	293	
9440	39808	C	9500	1	1170	
9441	39809	C	9501	25	481	
9442	39810	A	9502	27	265	
9443	39811	A	9503	2	326	GRVGGGRVGSDLGRGDMAKRT KKVGIVGKYGTRYGA/SRVRK MVKKIEISQHAKYTCSF/CGKT KMKRRAVGIWCCGSCMKTVA GGAWTYNTTSAVIVKSAIRRL KELKDQ

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9444	39812	A	9504	2	1125	RVGRRPLPPRPTTHPRRKPLPPNN VTGKPGSAGIISSGPITTTPRLST PRPTGTPLERIETDIKQOPTVPA GEELENITDFSSSPTRTDPGLK PRFKGPHVRYIQKPDNSPCSITD SVKRPKEEATEGNATSPQQNP PTNLTVVTVEGCPSFVILDWEK PLNDTVTVEVVISRENGFSGK NKSIQMTNQTFTVENLKPNTS YEFQVKPKNPLGEGPVNTVAF STESADPRVSEPVSAQRDA!WT ERPFNSDSYSECKGKQVVKRT WYKKFVGVQLCNSLRYKIYLS DFLTGKFYNIDQRGHGEDHC QFVDSFLDGRTGQLTSDQLPI KEGYFRAVRQEPVQFGEIGGHT QINYVQWYECGTTIPGKWW
9445	39813	A	9505	2	385	REAGSGGNNDNFARRRNFS\RG G\FGGSRGGVWIWAVVGDGY NGF\GNDGSNFG\GGGSY\NDF WENTNKSGL\QNFGPHEGGEIFG GQKLLAPYGGWRPNTFAKPTK PQGGIVYGG\SSSS\SSYQKWPEDF
9446	39814	A	9506	945	2313	TRVLLESRAGSQQQSEGAEASWQ RGYARPSQAAISFPEHRRALR ALWAGDCRVADAGPGSSSSTPP SPPSLPKTSVSLGFLCFKKLSSA SCASGRERQLEA*VWAQPLSP TQWSEGQLGVRVWAQPLSPT QWSEGO/PGGPSVGISTSLYTVP EGRT/GWGPECYVFMLHLRPE QHDCTFDHMGRGRREEAIMKM VKLDRKVGRSCQRIGEGGQED DVVASILVSMQPSPRTPSHILP YSKFKDFSSNCARQGWKEMG ACVQRPSAVLGGTRPVSVQAK QPLPCFLLGASALGSGCTGLGV KDRDIDRIVVMMSVMKILRGNQR PSGDEQARGQRAREGLGGLV RRACREQWA\LCPLVHRNWV CVSSFLIASQSNSPQQQHINCCY ANNSPQEEGMVGRQAETFL GGVRNRKPWVGVRGLQGSH QHQHQGAVSSSPKKGVSKRE
9447	39815	A	9507	3	684	

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9448	39816	A	9508	15	513	RIRLEGLWGSSKTMNLCSKCFA DFQKKQPDDDSAPSTSNSQSDL FSEETTSNDNNNTSITTPTLSPSQ QPLPTELNVTSPSKEEYSQSENE ASPVKRPRLLENTERSEETSRSK QKSRRRCFQCQTKLELVQQEL GIMCRCGYVFCLMLHRLPEQHD CTFDPHGAVAGR
9449	39817	A	9509	818	1455	SDYITRDGASFTKALLTWKNPV PNFFWKDKDTFLWGEVIRSTM WKT/DQSPSAAWMGFFGAQPP QQQAPPVIPPNOAGYGMASY QTQILPSPHILAVFMLPERGPNP DPKRKGFLDLARKNLGNWVSTT FLSRFPGVQVLQEFGVPPGTML LRPLELPMHFNFHSTALASLIA DELYLILPQLSVSQMGEFPSFD MMAICAQASTNRLLWMP
9450	39818	A	9510	1	1132	MMEDDGQPRTLVVGNLSRDV EVLILOLFSQIQGPCKSCCKMITEH TSNDPYCFVEFYEHRAAAAL AAMNGRKILGKEVKVNWATT SSQKKDTSNHFHVFVGDLSPEI TTEDIKSAFAPFGKISDARVVK DMATGSKGKYGFGVSYNKLDA ENAIVHMGGQWLGGRQIRTNW ATRKPPAPKSTQENNNTKQLRFE DVVNQSPKNCTVYCGGIASGL TDQLMRQTFSPPFGQIMEIRVFP KGYSFVRFSTHESAAHAIVSVN GTTIEGHVVKCYWGKESPDMT KNFQQVDYSSQWGQWSQVLGN PKPSDRYMANGWQVPPYELY GQPWNQOAFGV\QOSPSAAWM SGFGA\QPP\QGQAPPP\VIPPPN QAGYGMASYQTQ
9451	39819	B	9511	1	1212	
9452	39820	A	9512	1	1032	

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9453	39821	A	9513	17	976	SGRP/GGPGPGMKGPRCF/RGE VFGIVIRGPGFPPGGRRGRVGR GARGKKGPRIKGLGCPSTKLG\RLVKDH*RSKFPWRRSIYSYSG PLKESEUIDDFLGLLSSKDEVFE RLCQVQEPEPVPGQRHQGSRHF VATGNYQWPPTVGSGVLKCSQE /VWPTAHPVGPILAKLLLHSSPC AEGYWGEQSIGKAP/HTVPCQ/ VWTGRGCGSVLVRPHPWHRGGS GIVSAPVA\KKLMMAGIDDCY TSARCGTATLG\NFAKATFDAI SKTYSYLTPDLWKETVFTKSPY QEFTDHLVKTTHTRVSVQQTQA PAVAYNIGFLYKKNKVN
9454	39822	A	9514	1	866	
9455	39823	A	9515	1	1793	MAAAA VSGALGRAGWRLQL RCLPVARCRQALVPRAFHASA VGLRSSDEQKQQPPNSFSQHQHS ETQGAEKDPPESSHSPRYTDQ GGEEEEDYESEEQLQHRLTAA LEFVPAHGWTAEAIAGAQSLG LSSAAASMFGKDGSIELLHFVT QCNTLRTLVEEEQKLVQLGQ AEKRKTDQFLRDAVETRLRMLI PYIEHWPRALSILMLPHNIPSSL SLLTSMVDDMWHYAGDQSTD FNWYTRRAMLAIAINYNTTELVM MQDSSPDFEDTWRFLENRVND AMNMGHTAKQVKSTGEALVQ GLMGAAVTSPRSRGWWPLG EMPYANQPTVRITELTDENVKF IIENTDLAVANSIRRVIIEVPII AIDWVQIDANSVLLHDEFIAHR LGLIPLISDDIVDKLQYSDCTC EEFCPECSVEFTLDVRCNEDQT RHVTSDLISNSPRVIPVTSRNR DNDPNDYVEQDDILIVKLRLKGQ ELRLRAYAKKGFGKEHAKWNP TAGVAFYEYDPNALRHTVYP KPEEWPKSEYSELDEDEDESQAP YDPNGKPERFYNNVESCGSLRP ETIVLSALSGLKKLSDLQTQLS HEIQSDVLTIN
9456	39824	A	9516	3	176	FFFFFAETNSK*ITYQNIIHMVEI FQNSIFWDLYTKDKQIRGQEAA RREKRGGLRPL
9457	39825	A	9517	1485	1679	RVGDAGHDDPGKPGPPGAGHR PEG*TGAHSLRAGLPACRAEPA GPGRAREGSKAPGHCAEELLQ

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9458	39826	A	9518	1	232	FFFFETECSVVAQAGVQWCDLG SLQTLPTG/SSRHSPASAFRVARITGARYHVRLLFVFLVQTGLHLHGQADFDLLT
9459	39827	A	9519	1	2408	GTLVTKVAPVSAPPVKVSSGPRL PAPOIVAVKAPNTTTIQFPANLQLPPGTVLIKNSNSGPLMLVSPQQT VTRAETTSNITSRPAVPANPQT VKICITVPNSSSQLIKKVVATPVKKLAQIGTTVVITVPKSSVQS VAVPTSVTVTPGKPLNTVTLLKPSSLGASSTPSNEPNLKAENSA AVQINLSPTMLENVKKCKNFLAMLIKLAACSGSQSPEMQCNVKK LVEQLLDAKIEAEEFTRKLYVE LKSSPQPHLVPFLLKSVVALRQ LLPNSQSFIQQCVQQTSSDMVI ATCTTTTVPVTTSPVTTVSSQSE KSIIVSGATAAPRTVSVQTLNPLA GPVGAKAGVVTLHSVGVPTAAT GGTTAGTGLLQTSKPLVTSVAN TVTTVSLQPEKPVVSGTAVTLS LPATVFGETSGAACICLPSVKPV VSFCWDHNCKPVIGTPVQIKLA QPGPVLSQLPAGIPTGSSSIKQLFS LFHVVQQPSGGNEKQVTTISHS STLTIQKCGQKTMVPTNIIPTSQ FPPASILKQITLPGNKLISLQASP TQKNRIKENVTSCFRDEDDIND VTSMAGVNNEENA CILA TNSE LVGTLIQSCKDEPFLFIGALQKR ILDIGKKHDITELNSDAVNLISQ ATQERLRLGLEKLTAAQHRMT TYKASENEYILCSDTSQLKFLE KLDQLEKQRKDLEEREMLKA AKSRSNKEDEPQLRLIKQAKE
9460	39828	A	9520	1	637	MLSNVKRGGRKLPNGTWAHDL VTPPTASLLLLLTEPAMPSV AFC HSILIVTKGGVKRTRVPPPNNSS GARTGNPLKVKHISFKTGDELIF LDPHTTQTFVDTTEENG TGNDQT FHCLQSPQRIMNILNLDPSVALG FFCKEEKDFDNWCSDLVQEIKL ENLRMFEVQKHPSHWPFPVPP AKPQEVT TTGAEFIRDSTEQLAEF DLEEDFEILSV
9461	39829	A	9521	3	176	
9462	39830	B	9522	1	792	

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9463	39831	A	9523	2	486	NGHVGLGVKCSKEVATAIRGA ILAKLSIVPVRRGYWGNGKIGKP HTVPCKVTRGRCGSVLVRLIPAP RGTIVSAPVPKKLMMAGIDD CYTSARGCTATLGNFAKATFD AISKTYSY TPDLLKE TVFTKS P *QEL TDHLVKTHTRVSQRT QAPAVATT
9464	39832	B	9524	1	2991	
9465	39833	A	9525	3	263	KHENWSTARQLHACSRVTWQ NRLRLSNKWMPSHVLCLLPS/H MTLQPANLSSLLTTPPEFGPKIA SPICHTCSVNPRTLJSPFSHC
9466	39834	A	9526	1022	1201	
9467	39835	C	9527	1	924	
9468	39836	A	9528	2	837	WKNCLEKRSM TMHRILES*D* RQE ILERHDAKYHSPKAEEKQ MKHKAGSQIVKKEEAKLAL EGFCRFRNHHQTFGSPAGATOR GPLVAISPGPGECQSAVARLT GEKKNNHPGQAQYANRLSPRVGR FINAAGTTGFPTGKRAWPPFRL FLPHKGFADWGPTINQDFRLLG QPSVARFLNFSQGPAGEGQS ARLPGHPFITQPYPILPGYAAG MQALARRPILMFDSLSNFCH SSAYYHLFRRSNQAFKGTNNCL KKITPRPATHRSTVVIH
9469	39837	A	9529	3	1137	APAPSVPGSGLCSSLHMFHPPS RANRAFV D YAPMDEIQAENI SQVRRYLEGTLDEIDVRNPSVT TMLSQPGPPSPGHTPTTHALLAS EPHVNGCKTVSTVHEDYSGSSE SSNDESSEDTSDDSSIPRNRL QSVVAVPKNSTLPMEETSPCSS RSSQSYRHYSDHWEDERLESRR HLYEEKFESIASKACPQTDKFFL HKGTEKNPEISFTQSSRKQIDNR LPELSHPQSDGVDSHTDVKS DPLGHIPNSEETVKAKIPSRRQEQ ELPIYSSDFEDVPNKSWQQTIF QNRPDSRLGKTELFSSSCEIPH VDGLHSSEEELRNLGWDFSQEK STTYQQPDSSYGACGGHKYQQ NAEQYGGTRDYWQANGLGS
9470	39838	A	9530	1	1857	

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9471	39839	A	9531	1	989	MEDWKVRGHQEKTIAFEVQSF SCSERETTLVLLRSPAVPQLL HGLCGPDLSKAAQCHFKAIW QSLGNTLGAWSQATPGHVKS LPPGALISRQGRGQFCSDAVF LLHDSPELPSSLPHGASPLASS DKQAEQTWLGAVGSVQCTSIT ACPRDLEDRPHLTTEHPPAGVHC GQNPCPCHLIFTLYSKSPLLDLA CRIWDVFCRDGEELFRFTALGI LKLFEDELTKMDFIHMAQFLTR LPEDLPAEELFGPSIATIQMOSR NKKWAQEPMHELEWPDRSFRP RVLACPMGSREHRLQACSGST GQGHTKALFPETCCQSPIFQDA
9472	39840	A	9532	2013	2270	
9473	39841	A	9533	3	744	
9474	39842	A	9534	190	991	SVLSNKQNHCQSQTAPPSSAAA SGSRGWVWGLFWGLAAILEGS TGADWSQLPHSCCPSSLVPHVL SVVPLRPPHRDFPVVEDVFTLPV YFSSDWLNEFWDALDVDDYRF VYAGPAGSWSPFHADIFRSFSW SVNVCGRKWWLFPPGQEEAL RDRHGNLPYDVTSPLCDTHL HPRNQLAGPPLIEITQEAGEMVF VPSGWHHQVHNLDTTISINHN WVNGFNLANMWRFQQLELCA VQEEVSEWRDSMPDWHHHCQ VIMRSCSGIKL
9475	39843	A	9535	1	885	MKRRAVMGPPQVQAWKALDL WESSQVMEGKAVVPMGRNPML MRKATQGQLENSPALEKLLPPL QGNVGFRAFTKEDLTEVRDLLL ANKVPAATRAGAIGPCVEVTVA QNTGLGPEKISFFQALGITKIS RGTTIELSDVQLIKTGDRCVGAS EATLNTNPNISPFSGLVIQQVF NNGSIYNPEVLDITEETLYSGFL EGVRNVAISCLQTGYPPVASVP PSII/NGYKGCLALSVETDYTFPP AEKIKTFLADPSAFVAAAPVAT TATAAAPAAAAPTKEESEE LDEDMGFGFLD

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9476	39844	A	9536	65	988	RTAVMPREDRATWKSNSYFLKIIQLLDDYPKCFIVGADNVGSKQMQQIRMSLRGKAVVLMGKNTMMRKAIRGHLENNPALEKLLPHIRGNVGFVFTKEDLTIEIRDMLLANKVPAAAARAGAIAPCETVTPAQNTGLGPEKTSFFQALGITIKISRGTIELSDVQLIKTGDKV GAS EATLNMLNISPFSFGLVIQQVF DNGSIYNPVEVLDVITEETLHSRFLEGVRNVASVCLQIGYPITVASVPHISIINGYKRVLALS VETDVTPLAEKVKAFALDPSAFVAAPVAAATTAAPAAAAAAPAKVEAKE
9477	39845	A	9537	1	993	MREIALTQTROCGKKIGAKVGI RGSEVPAPAYWVAREDVGSSS GLGGGWYVPCAVLVDEPVT MDSLRSGPFGFLIRPTSSLKLIE NADKTFCIDNEALYDIYSRTLK LPPTYGDNMHLLSATMSGVT MCLGPPGQLNADLQKLSVNMV PFPRLHFFMPGFAPLTSRGSQH YQALTV AELTQQMFYAKNMMAARDPRHGRYLTA AAAIFQGRM PMREVDEQMNFNIQDKNNSYYFA DWFPDNVKTAVCIDPPRGILKM SGFIGNNAAIQELFVQCSEQFTAMFRKAIFLHWYTGE\MD E\MEFTVEAESNMNDL\ VSEYQQY QDATAQGGGG
9478	39846	A	9538	231	881	SSLSGTKVGLSPFRLHHWMPVS YSSVITRYYHRAGAEEGKDRII FVTKKDHETPSSAELVADDPNPDYEEHGLLPNGNINWNCPCLG GMASGPCGEQFKSAFSCFHYST FEIKGSDCVQFRAMQCMHK YPDLYPQEDEEEEEERKKPAQ QAEETAPIEATATKEEEEDQVNE GHKALSTSPFGV DLLQKALSSPKKVSFCCPVHYNIQNNLF
9479	39847	A	9539	1	804	

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9480	39848	A	9540	2	3337	SSLLEKMTSSDKDFRFMATSDL MSELQKDSIQLDEDSERKVVK MLLRLLLEDKNGEVQNLAQVWK LGVPLGAFHASLHCLLQLQSS PRLAVRKRAVGALGHILATACS TDLFVELADHLLDRLPGRPVPT SPTAIRTLIQCLGSVGRQAGHRL GAHLDRLVPLVEDFCNLDDDE LRESCLQAFEAFRLRKCPKEMGP HVPNVTSLCLQYIKHDHPNYNY DSDEDEEQMETEDSEFSEQESE DEYSDDDDMSWVKVRAAA
9481	39849	B	9541	1	3178	
9482	39850	A	9542	190	284	LNAQPGTTRLWPAEIRPPRRL GKGGQQVSHHPPISCYCECEE KRLCVNTHVWTK*
9483	39851	A	9543	62	280	
9484	39852	A	9544	1	1452	
9485	39853	A	9545	2	998	ITAGATPEERVICFVEVYLTAFH EGRKGALAKKPYNPIIGETFHC SWEVVKDRVKPKRTASR/LLP AVMNTQWPMTLPKSQYKLRFVA EQVSHIHPPISCFYCECEEKRLCV NTHWVTKSKFMGMSVGVS GEGVLLRLEHGEEYVFTLPSAY ARSILTIPWVVELGGKVINC GYSATVIFHTKPFYGGKVHRV AEVKHNPTNTIVCKAHGEWNG TLEFTYNNGETKVIDITTLPVY PKKIRPLEKQGPMMESRNLWRE TRYMLRLDIDAATEQKRHLEE KQRVEERKRENLRTPWPKQYFI QEGDGWGLQSPLESTMGLLEV
9486	39854	A	9546	12	740	HFFLYKKLIPFVLKNCMFHFS VRGTVVTNDRWGAGSICKHGG FYTCSDRYNPFGHLLPHKWC MTIDKLSWGYRREA GSDYLT EELVQPLVETVVFSA GNPLMDIG PHLDGTISVVFEERL RQMGSW LKVN GEAIYETYT TWRSQNDT VTPDVWYT SKPK EKL VY AIFLK WPTSQLFL GHP KAIL GATEV K LLGH HQPLN WIFFGD KMG IM WELP QLT IHQM PCK WG WAL A LTNV
9487	39855	B	9547	1	627	
9488	39856	B	9548	47	504	

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9489	39857	A	9549	2	379	VDLVREFIERQ/HAKNRYYYYH RQYRRVPDITECKEEDIMCMYE AEMQWKRDYKVQDEIINIMQD RLKAFQQSYRATQQQHGPQAA SGGGSWRPLLQIFS LAASSASV RPGTSWQNCRPPGPDILGKQ
9490	39858	B	9550	49	707	
9491	39859	A	9551	3	1162	
9492	39860	C	9552	342	581	
9493	39861	A	9553	3	513	LLPHKPLAGFFKAYLPSEPPRV YVSSFWPQ/EYKPDTHQELFLQ EEI/S/LLELDLNQVIENRLENKI/A FIRQHAIRVRIHALLLARGLDPF IGPRRDWLVYPAVTGA/VAFGF VEGLDPSPQEHPRFQGTQDNVSK DESTRKEQSVRLVCGADDRK PRDLQILD RDRKGPEL VQ
9494	39862	A	9554	1	1365	
9495	39863	A	9555	771	1536	PRPLSLWSREAGKGVQDCYIDN SQLCRKCDLCPTGSPQLPPYAS IPPTPSPTIK/DPPSTQM/V/QKET DKGVNNNEPKSGNIPQLCRLQAV GGGEGFPARVRVPFSLSDLKQI KIDLGKFSNDPDKGYIDVLQGLG QCFDLTWRDIMALLNQTLTPNE KSAVITAAREFGNLLYLSQLRH WPVTLQPSAVPTPDGSTYDTKE CKIVQSVEMSMEV MIAVMSVQ RQQGKQTQQQPLL VVVRSAEP AEESVPHKSSTRGAS
9496	39864	A	9556	220	249	P*N**PSTLTGTGSTTT*QIRM KVNMGN/DSPQGKNTPKMYS GEFSPV RVHVPFSLSDLKQIKID LGKFSDDPDGYIDVLQ
9497	39865	A	9557	2	385	
9498	39866	A	9558	84	849	PRPLSLWSREAGKGVQDCYIDN SQLCRKCDLCPTGSPQLPPYAS IPPTPSPTIK/DPPSTQM/V/QKET DKGVNNNEPKSGNIPQLCRLQAV GGGEGFPARVRVPFSLSDLKQI KIDLGKFSNDPDKGYIDVLQGLG QCFDLTWRDIMALLNQTLTPNE KSAVITAAREFGNLLYLSQLRH WPVTLQPSAVPTPDGSTYDTKE CKIVQSVEMSMEV MIAVMSVQ RQQGKQTQQQPLL VVVRSAEP AEESVPHKSSTRGAS
9499	39867	A	9559	66	197	RQWKG*KFVFQKM*DLGKYLQ RQLFC LSSLVQPPPWPVPTIEYP
9500	39868	A	9560	1	2340	
9501	39869	B	9561	1	1776	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, - =possible nucleotide deletion, + =possible nucleotide insertion)
9502	39870	A	9562	1	1349	
9503	39871	B	9563	107	769	
9504	39872	A	9564	329	2042	
9505	39873	A	9565	511	1631	HFGNHERTSKVMGNVPRKTKT PLRRILENWEQFDPQTLRKKRLI FFCSAAWPPEGSINYNNTILQLD LFCKRKWKSEVP*VQTFFSLRD NSQLCKKCDLCPTGSLQSLPPY PSIPVTPSPLNKDPPSTQMVKQEI DKRVNSEPKSANIPQI*PLQAV GGREFGPARVHVPFSLPDLKQI KTDLGKFSDNPDGYIGVLQGLG QFFDLTWRDIMSLLNQTLTPNE RSATITAAARELGDLYWLSQVN DRMTTEERERFPTGQQAVPSAD PH*DTESEHGDWCCRHLITCVL EGLRKTRKKA VNF SVM STVTQ GKEENPTAFLERLREALRKHTS LSPDSIEGQLILKIKFIRSAADI RKQTSKVHLRPGAKLKTPY
9506	39874	A	9566	15	178	
9507	39875	A	9567	3	826	RQI.GTRNFLNGTKAKAFELSYL EKVPEGKDTVHKQSLLHHVGT MGGENFPDSSDLYSEIGAITRSA KDDFDQLQDNLCQMERRCIA WDHLKAIAKHEMKPLLKQRMS ELLKDCAERIIILKIVHTRIJNRF HSFLLFMGHIPPYAIREVNINKFC RIISEFALEYRTTRERVLQQKQK RANHRERNKTRGKMITDSGKF SGGSPAPPSPQGQLSYAEDAAE HGEHEGCAENLVPLQESPAHTF SIVSAVFLLIP*HPVY*FKSVTPF LGKEQPL
9508	39876	A	9568	1	670	

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9509	39877	A	9569	1	2426	MPKPSLEAGSCPRLIEFPVDAQ PVIKGEEFTPPPPNSYLALGDIST EEWDLEVQAEYQERMPQRRAA LICVFWSNLGRSLPAPAMRRPC QNFCVALSTFAGDPEPESEAEP EAEAGAGQVADEAGQDIASAH EGAETEVHQALEQEPEPERASLAS EKERQNEGVNEDNCASSVSS SSSTLEREEKEDKLSRDRITGL WPAGVQDAGVNQCGDILTNK RFMLDMLYAHNRKSPDDEKG DGEAGRRTQQEAEAVASLATRIS TLQANSQTQDESVRDVVGCL DNRGSVKAFAAEKFNNSGDLGRV FNAPQGLGWSQVPRGQPTFTK KKKTIRLFWNRN/VGLLTGH/G KNNRRCREFLWSKLEPIKVDTIS RLEHLFESKSKELVSKASKLV RPLFLTSACPFLSFPWKAPLHS STRQLHRLSLQAERWRCSGIRG MECLNGKGPLESRNPAVRKSE GTRQTGAGDMKDGVWQGVPA TPDTPQQMCTVCTVSFAIMDGL NVNSVGPLFHEVAEPLLKE GIDOLDYTLGFFFVSMMLSGGG LLGGSASAKAFELSYLEKPEV KDTVHKQSLLHHVCTMVVENF PDSSDLVSEIGAITRFRHSFLFM GHPPYAIREVNINKFCRIISEFAL EYRTTRERVLQQKQRANHRE RNKTRGKMITNCVRHCVRMFS GSSPAPPSPQGLSYAEDAAEH
9510	39878	B	9570	164	346	
9511	39879	C	9571	160	339	
9512	39880	A	9572	54	212	SFPSVVLWKLQLNLIKQVPGLI LLGVGLISVPGGRI*LLRTGSRK PISQVCP
9513	39881	C	9573	48	185	
9514	39882	A	9574	2	551	ADRRGAVYPRSRDGGGVRGPC AMATSVLCLLRCKDRGTGHIP LKDMILSVHMDTQHMGTDVVI VKNGRKIFGTGCLASAPLHQN KSYFEFKIQSTGIWIGVATQK VNLNQIPLGRDMHSLVMKNDG ALYHNNEEKNRLPANSLPQEG D/VVDDSAILDQFSEFYHTPPP GFEKILFEQQIF
9515	39883	A	9575	3	655	

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9516	39884	A	9576	131	1066	SHSSAAAHPGLLPIAAQSLAVFIEPWQSASSRGQLQV/SAPGIWGIGVATQKVNLNQJPLGRDMHSLVMRNDGALYHNNEEKNRLPANSPLPQEGDVVLWSNNGHSLCKEESLSPILPTSDGEERRRKKRKKRKRKKRKQKQQQQEAAAAPAADAEATAAEAAVEEAARKEEEECEEEGEGNGEEEEEEKA-AAARDGDSQQEKACKSSLQAI LFGHAKLEPGRPLPRTQCRVEATVLVGTSPLDNLPLWSISWLSWQKPVGTSQQQPLGLWTREFPLEGHILTTRNETFTTEATPLIEPGIMLSQMMSEEHII
9517	39885	A	9577	1	2363	ELQRDIKEKHSTGVASVLNCEVLLHDCDACATDAECDISQQATRNLDRRWRNICAMSMERRLKIEETWRLWQKFDDYSRFEDWLKSSERTAAFPSSGVITYTVAEELKKFEAFQRQVHECLTQLELINKQYRRLARENRTDSACSLKQMVHEGNQRWDNLQKRVTSILRRLKHFIGQREEFETARDSILSVWLTEMIDLQLTNIEHFSECDVQAKIKQLKAFQQEISLNHNKIEQIIAQGEQLIKESEPLDAIAIEEELDELRRYCQEVFGRVERYHKKLIRLPLPDDEHDLSDRLELEDSAAALSDLHWHDRSADSLLSPQPSNNLSFASLQPLRSERISGRDTPGSVDSIPLIEWDHDYDLSRDLESAMSRA LPSEDEEGQDDKDFYLRGAVGLSDVMPESPEAYVKLTENAIKNTSGDIISALESQIRQLGKALDDSRFOIQQTENIIRSKTPTGPEDLTSYKGYTMKLLGECSSSIDSVKREHKLKEEEESLPGFVNHLHSTETQTAGVIDRWELLQAQALSKELRMKQNLQKWQQFNSDLNSIWAWLGDTEEELEQLQRIELSTDITQIELQIKKLKELPSCWDHRKAIILSINLCSPEFTQADSKESRDLQDRLSQMNGRWDRVCSELLEWRGLLQDALMQCQQGHEMHSGLLLMLENIDRRKNEIVPIDNSLDAEILQDHHKQLMQIKHELLES

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hnd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, -=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
9518	39886	A	9578	2	3248	ENAVGWSWTDDLTQLSSLKDTL SAYISADDISILNERVELLYLQRQW EELCHQLSLRRQQIGERLNREWA VFSEKNEKECEWLTTQMESKVS QNGDILIEEMIEKLKKDYQEEIA IAQENKIQLQQMGERLAKASHE SKASEIEYKLGKVNDRWQHLL DLIAARVKKLKEIIVAVVQQLD KNMSSLRTWLHIESELAKPIV YDSCNSEEIQRKLNEQQELQRD IEKHSTGVASVNLCEVLLHDC DACATDAECDSIQQA
9519	39887	A	9579	2	194	CSTSLMIREMQIKTTVRYHLTS ARMAIIKSKINSRCWHGCGEH GTLLHCCNLWKERNVSYVA
9520	39888	C	9580	105	215	
9521	39889	A	9581	1	210	MNSHFLKEDIQMANKHMKMEKS \TLLMIREMQIKPTVRYHLTSAR MPIIJKSKINSRCWHGCGEHT LLHC
9522	39890	C	9582	48	182	
9523	39891	A	9583	3	225	
9524	39892	A	9584	1	549	
9525	39893	A	9585	367	971	GVCLLGAPAGRGSLLSGSLR GQGSYLSKNVAVPSEATTVRREL HP**TSLQRPPSDPGGWVVLGF PICNQFGHQENRQ\NEIELNSLK VRSGPGGGFEAQQLHGSSRKCEV \NGISGAHPLFAFLR\REALPVPS DDGPRAL*PTPKLI\WFSGVFA TIVAWNFFEKFLVGPDVPLR RYSR\AFQTIDIEPDIEALLSQGP
9526	39894	A	9586	1	129	
9527	39895	A	9587	1	406	PTVCERELCVFAFQTLGVMNE AADEIATGAQVVDLLVSMCRS ALESPrKVVFEPYPPVDPNPD QMLAFNPRQLKFHMTHPHQFLL LSSPPAKESNFRAAKKLFGSTF AF/HLHGAMYGSGIYLSPMSSIS FGYSA
9528	39896	A	9588	2	634	SSNRSHIVKLPVNRRLFMHTP HQFLLSSPPAKESNFRAAKKL FGSTFAFHGS_HIENWHSLRNGL VVASNTRLQLHGAMYGSGIYL SPMSISFGYSGMNKKQKVSAK DEPASSKSSNTSQSQKKGQQS QFLQSRNLKCVALCEVITSSDL HKHGEIWGCPP/SDHVCTRFFF VYEDGQVG DANINTQEGGIHK EILRVIGNQTATG

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9529	39897	A	9589	3	3623	FGVCARGCLDSAGPWTMSRALRPPLPPLCFFLLLAAAGARAGGYETCPTVQPNMLNVHLLPHTHDDVGWLKTVDQYFYGIKNDI/QHAGVQYIILDSVISALLEDPTRRFIYVEIAFFSRWWHQQTNTAQEVVRDLVRQQRLEFANGGWVMNDEAATHYGAIVDQMTLGLRFLEDTFGNDRPRVAWHIDPGHSREQASLFAQMGMFDGFFFGRLDYQDKWVRMQKLEMEEQVWRASTSLKPPTADLFTGVLPNGYN
9530	39898	B	9590	1	3839	
9531	39899	B	9591	1	513	
9532	39900	A	9592	1	233	KQELNEPPKQSTSFLVLQEILES ENKQDPNPKPSGFRSVKAPVTKA VASIGNAQKLPMCDKGCTVL QQ/ASA/AAFSLSV
9533	39901	A	9593	3	469	LTVARSEHKVWSPLVTGEGKRHPVKMNLASEPQEVLHIIGSAHNRSAMPTNASPASSTTARVITNQYNNPAGLYSSSENISNFNN/ASSL VIDKESEVYKMLQEKEQELNEHPKQSTSFWVLQEILESEEKGDPNKPSGFRSVKAPVTKA VASIGNAQKLPMCDKGCTVLQQ/ASA/AAFSLSV
9534	39902	A	9594	1	1146	MTTQQIDLQGPWPWFRLVGRKDFFQPLAISRVTPGSKAALANLCIGDVITAIDGENTSNMTHLEAQNRIGCTDNLTLTVARSEHKVWSPLVTEEGKRHPVKMNLASEPQEVLHIIGSAHNRSAMPTASPASSTTARVITNQYNNPAGLYSSSENISNFNN/ALESKDWLPA GVEANSRPLDHA/QPSSLVIDKRILKVKMLQEKEQELNE/PPKQSTSFLGFCQEIL/ES/EEKGDPNKP/SGFRSVKAPVTKV AASIGKCSRKFACFVDCWHLGLFLGVFLKLRLDRHRHP*VFMCC\DCGHQT*KQKGPFLLWMQDQIYCEESMAPGSEVNTHPEGYESGSTVFPPSGAQQDPLFLPAGLLLKLFLLKCSGPLSLS
9535	39903	A	9595	65	353	

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9536	39904	A	9596	1	1974	MNGVPVGAQKRVDKKEEVKNG AIAELFSEDWSDCAYKANEVSR IRPLEESELLYILGQSQSKLFVLSG EWSQSSEEASEEVAVTLLYQLA ESPVTICAQIWQGCQAKALEKL EEKRTSQGDPKESPTMLPTFL MNLLSLAGDVAIQQQLVHLEQA VSGELCQRRLVREEQEHEHTKD KEKNTSFETTMEEELGLVGAA DDTEAEILRGFCMELLGDGKT LAAFVPLLLKVYNNNSGLYNSPD LSAAAASPTLGKFCMISTTFCNSQ PHLLFTMLEKSPLPIVRNSLIVA TGDLAIHFPNLVDPWTPHLYAH LQDPAQPVWKTGVLMTHLIL KDMVKVKQGSKAL/RKMLGNF DCFGDKLSDESIFSSFLSVMGKL QHGAKPEGKAIIIDEFEQKLQAC HARGLDGIEELEINQAGSQRAP TAKKPSTVCRHQPLASAASDN DFVTPEPRRTTHRHPNTQQRAS EKKPKVVVFSSDESSIKTVEVGLG YNIKLRAVATQRLSFVWWNMIA EGESAVLVTVAWPECEVAVMG SLGSAARTGTGKRLQGEGLNQL NFVTIATKLEVSWTELGGGCVS ALFASVGTKREKAGFYQGCSF ASNIMKGRGRVKEVEDVQKRLI KMTVEFNLAWSLPPHMAMN GDQGGDRVTHESFRLRCMTLMR
9537	39905	A	9597	785	5049	ACRSRMAPOMYEFHLPLSPEEL LKSGGVNVQYVQEVLSIKHLPP QLRAFQAAFRAQGPMLAQHF DTIYSILHHFRSIDPGLKEDTLEF LIKGVYGSVSVRHSQELPAIL DDTTLGSDRNAHLNALKMCN YALIRLLESFETMASQTNLVDL DLGGKGKKARTKAAIIGFDWE EERQPILQLLTQLLQLDIRHLW NHSIEEEFVSLVTGCCYRLLEN PTINHQKNRPTREATITHLLGVA LTRYNHMLSATVKI
9538	39906	C	9598	134	382	
9539	39907	A	9599	117	235	KIAAPQLHVFLPFLFFCMRPFAF WQPLPPEPLELRPRLSD
9540	39908	B	9600	1	732	
9541	39909	C	9601	1	420	
9542	39910	B	9602	110	928	

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9543	39911	A	9603	1	868	MKLMETLNQCCINAGHEMTKAI AIAQFNDDSPPEAKITRRWRIG EAADLVLGVSLRLSEMPLRKQGD YRTRIWKFEDGLSNVLVIQLNK LIICVMCLDLALKLRLVLLVEG NDPQGTASMYHGWPVLHIA EDTLLPFYLGEKDDVTAYIYFT CWPGLDIIPSCLALHRIETELMG KFDEGKLPTDPHMLRLAIEIV AHDYDVIVIDSAPNLGIQTINSALQ FFDMLRDLLKNVDSLKGFPDD PTGNRTVQLTWQPLPEPLEL\c*
9544	39912	A	9604	1036	1119	
9545	39913	C	9605	1	513	
9546	39914	A	9606	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDESRLSHFEQWGTLTDCVV MRDPNTKRSRGFGFVTYATVE EVDAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEOYGKIE VIEIMTDRGSGKKRGRFAVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSQRGRS GSGNFGGGRRGGFGGNDNFGR GGNFSGRGGFGGSHGGGGGYGG SGDGYNNGFDGNSNFGGGGSY NDFGNYNNQSSNFGPMKGNNF GGRSSGPYGGGGQYFAKPRNO/ GGYGGSSSSSYGSGRRF
9547	39915	A	9607	1	286	
9548	39916	A	9608	1	1674	
9549	39917	B	9609	531	744	
9550	39918	A	9610	1	818	YNRAMFHPHAVNKIALSNNK NPVRSKVLFLELLAAVCLVRRG HKLFYLAEDNFKEVCGEKQRFE KLMEHFRNEDNNNIDFMVASM Q FINIVVHSVEDMNFRVHLQYEF TKLGLDEYLDKLKHTESDKLS\ VQIQAYLDNVFDVGALLEDAE TKNAALERVEELENENISHLSEK LQDTENEAMSKEVLEKQLMQ RNKELDVREIYKDANTQVHT LRKMVKEKEEAIQRQSTLEKKI HELEKQGTIKIHKKGDGDIILP VVASAHCWPWGQKW

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9551	39919	A	9611	1	937	MALLTLKQQQNEDLQDISHFTT TRTPRQGTPVQKEKSEETRLEW ARRMLRRDQHSTKGKVVKRM RGFLVGLVYCDKQSGALESLLC LWNVSGNTTLSSLVEIGSKAAL GLVCGEKQRFKLMIEHRNED NNIDFMVASMQFINIVVHSVED MNFRVHLQYEFKLGDEYLD LLDTKSTDRAKQTLLHYISNVK EQYHQVSLFYNELHYVEKAAA VSLENVLLDVKELQRGMDFTK REYTMHDHNTLLKEFILNNEGK LKKLQDDAKIAQDAFDDVVKY FGENPKTTPPSVFPPVFVRFVKA YKQAEFE/NMELRKKQEQALM EKLLEQEALMEQQDPKSPSHKS KRQQQELIAELRKIRQVKUDNR HVYEOKDGAIEDITVSLENVLL DVKELQRGMDFTKREYTMHD HNTLLKEFILNNEGKLKKLQDD AKIAQDAFDDVVVKYFGENPKT TPPSVFFPVFVRFVKAYKQAEF
9552	39920	C	9612	47	286	
9553	39921	A	9613	1	423	

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9554	39922	A	9614	1	2015	MPSVSKAAAALSGSPQQTEKP THYRLKKEFRTEQCPFLSQHKC AQHRPFTCFHW/HFQTRRRR) PLGRRDGTFNYSVDVYCSKYNE ATGVCPDGDECPCYLHRTTGD ERKVHVRYYKTGTCIHE/TDAR GHCVKNRLHCAFAHGPLDLRP PVCVDVRELQAQEALQNGQLGG GEGVPDLQPGVLASQAMIEKIL SEIDPRWQALLPVALLRHVRVAH FSDANFVLGSYKTEQCPKPPRL CRQGYACPHYJNSRDRRRNPR RFQYRSTPCPSVKHGDEWGEPS RCDGGDGCQYCHSRTEQQFHP EGPVRESGVRGVFCVQSRRPW LQTPVSGTQLKWSWHHVGHRS TINPEGDKPSRLGPAPENIKRGN DFACDGRADAAGMAMPHVCVF IVKSTKNDMRQTGYCPRGPF AFAHEVEKSLGMVNEWGCHDL HLTSPPSTGSGQPGNAKRRDSP AEGGPRGSEQDSKQGVRAHG YVFEQNHLAVFAAVHPPAPSVS SSVASSLASSAGSGSSPTALPA PPARALPLGPASSTVEA/LALE PTPSSPTSSAVQGVAGELMGMS GGQGCCSHVVGALAAVPAWT HSGDLEWDPSITRTRVNVGGGP AARPAMTLAREPQLLVGGCP TRNCSGPAASPOQLIDAGQG GRGERDSSQRPLRPQTTHRQDT
9555	39923	A	9615	2	609	IHSLCVSPCLSPCHCLSLSPASLL VSFFCCFLMLTFPSLCVCGCLP VHLLPSL/HFLSQVLNEYFHNV CELDLVNFYKVECPFLPKSPVV PESKEIGSQVDGQSRMEQRSQA HTNRENDIAREGGSEETHSKPG KGNLEFRFRCSHLQLGECPIPP WQKERTIAQGPEPEARAAVPA GRHDTRHVNAGCALISLRPP WGGA
9556	39924	A	9616	60	277	
9557	39925	B	9617	43	354	
9558	39926	A	9618	3	309	GGGQGRPGAGGQQGRSDGGGQ GSPGGGSQGSPGGSGVGQGS RGGQGKPGGGGGQGSPDGGG PLAGGASGRGSRGQA/Q/CPISV SATHLAF
9559	39927	A	9619	36	363	

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9560	39928	A	9620	1	512	MLMPGLSACVRDCVAFLQAVV LGDPSPAQCQDTWTLAASAD GTCKAVGTEDGSVYFISVYDKE SPQVVKHKAFLSESSVQHVYVD QQGIFLLVGTAEGKVFIIANSS SSFQIIGFT/DGGQRHFTDIHSVS FRNRHSGSDGAFLASRSREKQV GDVHTAYITATSFHNLC
9561	39929	A	9621	1	822	MKLGV/QVVITDHEKLDQIRQR ESDVTKERIQKILATGANVILTT GGIDDMCLKYFVEAGAMAVR VLK/RIAKASGATILSTLANSKA HTSASIILRGANDIMCGEMERSL HDALCVVKRVLESKSMVPGGG AVEAALSIYLENYATSMSGSQE LAIAEFARSLLVIPNLTAVNAA QDSTDLVTKFRAFHNEAQVN EHKNLKWIGLDLNSGERGDNK QAGMFPEITVKVKSLSKFATEAA ITILRIDDLTKLHPESKKDHGG YEDAVHSGALND
9562	39930	B	9622	625	1162	
9563	39931	A	9623	202	402	
9564	39932	A	9624	350	652	SAGGYPDGQGVHPGPPELFAA GRLGHTLREHGHHLRYHRPG HMGRRPLPCRMGHREPGLH* QDCPRAWQWCWPHPRGHLQD VPPPGIHQLRLSQPGP
9565	39933	A	9625	83	1503	SWNTPYNHWATKQ/LSSHYSR GGAKYFGEAVKQSLVESYTHP NSNETERSANIDTMVNWFTE DFDFVTLCYREPDNVGHRFRPE AENRKLMQQIDRTIRPWWDDHR EEETQQQDPLSNYIKFMDLVK FDIVGYGGFGMPLPKLGQEAEAL YQALKNAYPHLHIYKKEGFPHEH FHLAKHDRVLPIVMYANFGYSI NGISLILYFYTHLCDKYFNVHF HEPLSLWRAQTTPSLSHRYISLV RHMDATNLDASEAQLPGSPYP DSAPGPANLDSTQDLPQRRLSW PYPRPRPNAHPGPALQPAPRTL LLTLPGPAPSLPPRTALGPPPL QSRPGFPRPVSRQRCGPAAHFMAP EENAGTELLLQSFERFLAART LRSFPWQGGGGRAERPAAGLAG VQGGTGWVSVLKPPALLPREFL GSPRSGPDRDPVPVPGAWPKSLA PLLPRELAAEDEGVSTALGGQT RARCGVQFTIIFTTF
9566	39934	B	9626	1	1177	

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9567	39935	A	9627	I	283	
9568	39936	A	9628	I	708	MPKGKEAKGKKLALAPAFVKKQEA KVVNPFLFEKRPKNFGIGQDIQP KRDLTCFVKWPRYIRLQWQR SILYQQLK PETKQEKKWRLA QAE/SVGKGDLPMKRLPVFRAG VNTTVDNKKAPLVTTHDMDPIEL TVFLPVLCHKMGA TCC IKGKARLGCLVH RKTYTTVDFTQVN SEDKGALAKLVEAI GTNYNARYDETHCHWDGNVL GPKSVAHIAKLEKAK ELATKL
9569	39937	A	9629	I	836	GTRPKMPKGKAKGKKVAPAP AVVKKQEA KKVVNPLFEKRP NFGIGQD IQPKRDLTRFVKWP YIRL QR QRAILYK RKLKEPPAIN QFTQALIDR QTATQLL KLAHKYR P ETKQE KQRLU LRAEKKAA GKGDV PTKRPV /LFRAGV KQPSPL V NE ESFLV VISH UD VDPIEL VVFLPALCR KMGP VY CIIKG KARLG RLSH KKTCT VTA FTQVN SEDKG ALAKL VEART YNDRY DEIRR HWGN VLP GPKS VARI AKLE KAK ELATKL
9570	39938	A	9630	3	119	
9571	39939	B	9631	I	711	
9572	39940	B	9632	97	942	
9573	39941	A	9633	I	588	
9574	39942	A	9634	I	1029	
9575	39943	A	9635	I	1031	MADQKE ARHSASQW KCFVGFL SFRGH MQVAWEAD RCKGP GRP LLAEAL QDLWPSPR RSQRDP VP ERPC CRP QSQPLPR FGSL SAPLH RENNF KDFP QADGLL V1PLV EEQC RGVL SEPL PDL QLLTGD IR YDEAM GYPMV QQW VR RSNL Y RVK LST ITLA AGFT NV LK I K L T K Q V R S N L Y R K G Q P L T H L V K V I P P Q F S L I C E M G T F I L F C N I N C A W G R G R E Y S Q C

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, <=possible nucleotide insertion)
9576	39944	A	9636	3	4091	FASASAVSAAASSSSFATAATA AAARSTAAPPAMAAGARLSP GPGSGILRGRPRPLCFHGP PPPLLP LLLLFLLLUPPPPLLAGATAAAS REPDSPCRLLKTVTVSTLPA LRES DIGWSGARAGAGAGT GAGAA AAAASP GS PG SAGTA AE SRLL FVRNELPGRIA VQDDL DNTELP FFTLEMSGT AADISL VHW RQQ WLEN G TLY FH VSMSSSG QLAQ ATAP TLO QEP SEI VEE QMHILHIS VMGG LIA LLLL LV
9577	39945	A	9637	2	398	SDARVDALNKIKIWERIKKHLE GHSTNLNSLDIAKLKEQFEASQA HLTLMPGTGVLEGAADRLSAS NP LKWI KTLGSSVISMMIVLLIC VVCLCVVCRCRS*LLREVAH RD KAAFAFIALQIKEGEHVGNST
9578	39946	A	9638	201	495	WKKTLM PG TG VLEGAAN/GLA AINPLK WIKTLGDSVISMIMIVLL IC/VCLC IVCRCRSR LLREVAHC DKATFAFI ISEKMWYFGFCFCN NSLRVIASSCIH
9579	39947	A	9639	3	409	GIYILHQKKKTWEK\LLLAACAIV AIENPADVS VISSRKTKQKATPL FAAVTGATLVAGCFTPTFSNQ ISA AFREPQLL VVTDPRADHQ P LTE ASYINLPTIALC\TDSP LH YV GLAIQCNNKG AHSGG LTCNL S
9580	39948	A	9640	3	438	
9581	39949	A	9641	288	489	SFRPLS VLGDC VVRGPTKPSGK CSPASRSLF VRRHILLHPQGLH NLDQNKA TPPPQPL\GHQTCAC
9582	39950	C	9642	23	411	
9583	39951	A	9643	1	209	SPSTT AVCCPPRPSIDFHSSGSSR VSA ALLIQ/QRFPLPLWIGLKAR HCSCGLRQRQVSWQETEEDGK AG

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9584	39952	A	9644	28	925	PEAGTRS WREPDPEDLRRFLS AACRSFPQWLPGGGGGQVSSC SDTDVPYVLLA V KSE PGRFAER QAV RET RKR KPT S! G I R L F L L G S PVGEA GP D L N S L V A W E S R Y S D L L L W D F L D V P F N Q T L K E P / V L W L P G W A G P C P T G S F V L R A Q D D A F V H T P A L L A H L R A L P P A S A R S L Y L G E V F T Q A M P L R K P C G P F Y V P E S F F E G G Y P A Y A S G G G Y V I A G R L A P W L L R A A A R V A P P F E D V Y T G L C I R A L G L V P Q A H P G F L T A W P A D R T A D H C A F R N L L L V R P L G P Q A S I R L W K Q L Q D P R L Q C
9585	39953	A	9645	I	1612	MIFVVIIILMVVLSP EGG SGL DSS PFLSEANAERIVQTLCTVRGA LKPYPPGTGP NFRYSHGVPPHLF AYFP PG STV SQDN SFIS PQLOHI F E V R Q S A D F M P R W Q M L R V L E E E L G R D W Q A K V A S L E E V P F A A A S I G Q V H Q G L L R D G T E V A V K I Q Y P G I A Q S I Q S D V Q N L L A V L K M S A A L P A G L F A E Q S L Q A L Q Q E L A W E C D Y R E A A C A Q N F R Q L L A N D P F F R V P A V V K E L C T T R V L G M E L A G G V P L D Q C Q G L S Q D L R N Q C F Q L L T I C L R E L F E F R F M Q T D P N W A N F L Y D A S S H Q V T L L D F G A S R E F G T E F T D H Y I E V V K A A A D G D R D C V L Q K S R D L K P L T Q F E T K A F S D A H V E A V M I L G E P F A T Q G P Y D F G S G E T A R R I Q D L I P V L L R H R L V S P I P E G D L W P W H R K L A G A F L A C A H L R D H I A C R D H K P G H L P P L L G Q S P A R R S H C R Q P P H Q R G T P G W I P H D S L H G G F S P Q S R P V P A V V P L I P S P S A L G Q R S P L G L P S L A W L S S L A Q E L R I P G A G E L P T S C P R S C T S P L E S E V S E N
9586	39954	A	9646	930	1123	G V R R D G S S A S V T V G Q P C R D T S L A F E T V A G P Y L A * K T * T S G K P G S D * R A S K V A G G V Q N G T R T T A T
9587	39955	A	9647	719	1346	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met codon	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=-Stop codon, /=-possible nucleotide deletion, +=-possible nucleotide insertion)
9588	39956	A	9648	1	823	MKKVLIAALIAGFSLSATAAETIRFATEASYPPFESIDANNQIVGFDVDLAQALCKEIDATCTFSNQA FDLIPSLKFRRVEAVMAGMDITPEREKQVLFTTPYVDNFALFVGQQGKYTSVDQLEGKKVGVQNGPTHQKFIMDKHPEITVVSDESYQNAKLIDLQNGCAARAAPGSRRYGGWTIQASTARPSDVLLTADSVFAVRSRGAAATAYHRCCLSGVMVNAAATACEHSTASQGRASRTVTDSADPHPKRSVRRRASFRRSGRGFCGTVR
9589	39957	A	9649	583	730	
9590	39958	C	9650	333	439	
9591	39959	A	9651	2	171	
9592	39960	A	9652	1	826	MGGLFWRSALRGLRCGPRAPGPSLLVRHGSNTIMGVFVAVGTPVPSRVPCIEADTLKPQGPSSWTRERTLVAVKPDGVQRRLVGDVIQRFERRGFTLVGMKMLQAPESVLAEHYQDLRRKPFPPCPSSRYMSSGPVVAMVWEGYNVRA SRAMIGHTDSAEAAPGTTIKGVDFSVHISRNVIHASDSEGAQR EINQLWFQSSELVSWAIDIGGQHSSIHPLGLRLRAALTTPSPTQDPYPPLARTPSPTSXPALSPNPLTS PVSPLAPPQAQREF

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
9593	39961	A	9653	144	1650	NCETTKGSAILRNVDPLSTLLPL RRAGSSPGLMPVVEEMEIDEEK QMKGFLDDSERMAFLVSLHLG AAERWFILQMEVGEPLSHENKS FLRRSQQIYDSLSEIDILSAVLC HPKQQKSVRQYATDFLLAR HLSWSDAILRTRFLEGILSEAVT TKMGRIFLKVA GSLKELIDRSL YTECQLAEEKDPSGNSSQVPLT ACKRNNEEAMGNELSSQQQTE EHQHVSKR CYYLKEHGDQEG LHDHLLGQSTGHHQKAHTNNVA ATKKVVQQQLQLEAGLNSVKVS QAATEPQTIIISPNAQLQEPSPGIE WEQFPKAQIPSEPKQENLCPFVST MNSIKGLHEDYQGNAGKVLS VPGRYRYALQNLGTAIVQGEER KQSSLCPGEEGKRHELRSGSHS LVMKHAMVLFNVGFEETKDQIH LPTRLGMAEVETLCIYAKQLPH KLIAKLRLKGTRPLSNNHEHIL THPGLEGWLHTEFRILSINNNKY HLSAYLVQSIVLHVGMGFRHKY
9594	39962	A	9654	8	440	VFERSTPTLETVRSKQEWETR LNGVRIMKKNVRDQFNSHIQL VRNGAKLSSLPQIPTPTLPPPSE TSCFRCFNPVPLWLLGCPSPPLG RQTEDPGEAADPVPTVQ*GPD DQHSSADQDSTYHHGRPDHGG TYPVGCCTTGRT
9595	39963	C	9655	89	389	
9596	39964	A	9656	1	184	
9597	39965	B	9657	1	942	
9598	39966	A	9658	424	614	NDGPDWGRRRRTDVNRKRGF KISKTLTYLSDIYSCHVFYYIG NVCIESLYSNVRK*NYVYY
9599	39967	A	9659	1	717	
9600	39968	A	9660	103	374	
9601	39969	A	9661	1590	2051	SYPVSEERSQAEQPSSNPYSHFT STPIRDRLHASGVSTQSLSGSSD ALLHWAGHNAHYAQCRRSPLL VFPNPECPFPQAQPAFLTTPSWLP WQK*PWLGFPQCPRSTHAPCR LHPTSPGLGGVKASAETPRPQP VD/ETGEDPGEAADPVPTVQ

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, <>=possible nucleotide insertion)
9602	39970	A	9662	1	2912	MAQALPWLLLWMGAGVLPAA GTQHQIRPLRSLGGAPLGLR LPRRETDEEPEPGRRGSPFVEMV DNLRGKSGQQYVYVEMTVGSPP QTNLILVDTGSSNFAVGAAPH FLHRYYQRQLSSTYRDLRKGV YVPVTTQGWEGELGTDLVSIPIH GPNVTVRANIAAITESDKFFING SNWEGILGLAYAEIARPDSSLE PFFDSLVKQTHVPNLFSIQLCG AGFPLNQSEVLASVGGSMIIGG DHSLYTGLSWYPTI
9603	39971	A	9663	1	902	MSAKEKGKFENMAKADKVHY VREMKTYYIPPKQETKKFKDPN APKRPPFS/SEYCPKIKGIEHPGQ STGDVAKKLGEMRTNSAADDK WPYEKKAALKKEKYRKDTAV YRAKCKPDAAKKGDVKAES KKRKNEKDEEDEEEDEEEDEE DDDNEYADNECTGFSGFVYKT FNSPVHNSLFLNVEIHALGFDL LESIFCILLVVVEVFSLQKGVAML EEVVVNNGERSGRSLPWLPAAAPS LPVPPVPLGLRHPPSQSDNHSLO LTFLTAIRLLRPRLGAVALLETV EDGRTKTNLPDENSVPFSPET
9604	39972	A	9664	146	733	LNMGKGDPPKKPRGKMSYYAFF VQTCREEHKKKHPDASVNSEF SKKCSEWRKTMSAKEKGKFED MAKADKARYEREMKTYYIPPKG ED/TKKKFHKDPNAPKRPPSAFF LFICSEY/RAPKIKGIEHPG\LSIG\ DVAEETGEEMWNNTAADDKQ PYEKKAALKKEKYEKDIAAYR AKGKPDAAKKGVVKAEKRSTR PRIPDL
9605	39973	A	9665	30	359	
9606	39974	C	9666	418	555	
9607	39975	B	9667	550	1717	
9608	39976	B	9668	1	1705	
9609	39977	B	9669	328	484	

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9610	39978	A	9670	5	1215	IIVLPKMSMPVSAQLTITSIPP WAVE/WGNVTLSVQGIPQNLIS YNWLRLGATTNQVTRILNFNFFS HGYTLGPAHTGRETGRADGSLI IIDVRASDNGIYTLHLISSGEKV AIMLCYLSLLVAPWHFHKTPR WRFPWGPRASQRASCQSQQS WSSGC SK/VSQAALYIQKIKEQP QKNQDLLLSVGVPDFTQDFN WYLGEETYGGTRLFTYIPGIQR PQRDGSAMQRDIVGFPGNSM LLRRRAQPIIDSGTYQVAITINSE WTMKAKTEVQVAEKNKELPST HLPTNAGILAATIIGLAAGALL ISCIAYLLVTRNWWRGQSHRMAT TEKPELGAHADGDNNIYEVM PSPVLLVSPISDTRSINPARPLPT PPHLQAEPEHNOYQQDNLNPDP APYCQLVPTS
9611	39979	A	9671	I	558	EGGLRITPSNPYHVDISQTKPCH *TNHC1QKEYSKNYGKYEEGNE MFFKEFNQYVLTSALINTLESSIL LQIKHIIRNCLLSVEPAISTKHL \\QSFQLFQDFMVDEELKVWL IEVNGAPACAO*ACTSLCFYKW EVGSAVGIVCGYKCSHFDCCEG GCHSDRRPLGGLYLAGGFAESL PFLFPRV
9612	39980	A	9672	I	534	MVGVDVTFKVISREEROTQRL GSSSPKRCPLEQEFEHEYSSFFG RNCLLSVEPAISTKHL PYQSQL FGDFMVDEELKVWLIEVNGA PACAQSPAKSL/CATSSSLFLSPP PWTCQQHSRQPTALAEILLSCH GWTRAGAQACLWAFVLSVTC VWNPHHHYHHHQPYRGWLL LYQNII
9613	39981	A	9673	624	805	SGGHPGH WLPPNPMA SPGATT PV GEG/ELQYASLSFQMVKPWD SRGQEATDTECSEIKIHR

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9614	39982	A	9674	I	1005	MENRKKVKGEWIAVPQPVKELRGVLNAATTLSK TREILRGKCFQLTSPTGNEPSHLSWTPRKR SRDGHPGCPDPLAASGARPLRSSS AFAAAAADSGSTVQVWDKGV LRVADVVSTIEPVTHVNLGWA AKVGPPISHGSAVISAFSKEGMF RIFSERKTLLAKLRFQNTQLRK LKLSEMEKAAGRSQS QGVSFQKG KGLGDRACEEMSEN P QPKGRKK PKAPQEVSFRENGNW KTPS IFF SPKTPRK KKKSF SKEELMS SSDL EETRWQAPSIPKRKK STPEEET VNDP L EAGHKVSGSKKKRKF S KI EEPV I SSGPEEAAGKSSSSKK KKFHKASQED
9615	39983	A	9675	I	2742	
9616	39984	A	9676	I	405	MADIPQE ARQYRH KQAY A YSI QGEG V E D D D E R I V R F H T R W P L Q N A D G T V A E Y N G Y H V V F A L A G S P K D A D D T S I Y M F Y Q K V G D N S I D S W K N A G R / V L K D S D K F D A N D P I L K D Q T Q E W S G S A T F T G S V F L A F G C Y S K
9617	39985	A	9677	3	642	GKGLF D E D E E S D L F M E A P Q D R Q A G A S V K E E S S S K P G K K I P A G A V S V F L G D T D V F G A A S V P S L K E P Q K P E Q P T P R K S P Y G P P T G L F F F S A P I H S K P S K T R K V Q S T A D I F G D E E G D L F K E K A V A S P E A T V S Q T D E N K A R A E K K V T L S Y S K N L K P S S E T K T Q K G L F S D E E D S E D L F S S Q S A S N L K G A S L L P G K L P T S V S W F D D E E D E D N N L G V Q
9618	39986	B	9678	175	1422	
9619	39987	A	9679	I	3096	MVTHQQPAARKPNMTSKKPKP MGPKAHGIFSGTRKNNNLEIYMD QTRTGIAKTKLSKNNKS GGM TLPDFKLYYKAIVAKIACGGSMY NSDTDEDEETEPSSSSQQQIENSI TMNKMKLKAKMKNMNL SKK HITQVSDEEEDDGCDLFA DSE KEEKDIEDIEENTRPKRSRPTSF ADELAARIKGDAVGRVDEEPTT VS YEDDRRGKQNQDAYTEGGLS TIKTVNCSSSLIPSGEAKL RKT L/ KEKKERRTPS DDE
9620	39988	A	9680	I	2925	
9621	39989	A	9681	2	688	
9622	39990	A	9682	I	1005	
9623	39991	B	9683	I	588	

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9624	39992	A	9684	I	2763	
9625	39993	A	9685	2	1075	NSDEELLFSHKLQKDNDPDVDL FAGTKKTKLLEPSVGSFLGVDDE DDDLFSSAKSQQPLVQEKKRVV KKDHWSVDSFKNQKHPEISIQGSK EKGIWKPETPQIAHQVSLHLKP NEPSTRIGKIQANLAINPAALLP TAASQIS EVKPVLP ELAF PSS EHRRSHGL ESVPVLP PGS EG VSFDLPAQADTLHSANKSRVK MRGKRRPQTRAARRLAACQESS EAEDMSVPRGPIAQWADGAISP NGHV*PQLRAASGEDSTEEALA AAAAPWEGGPVPGVDTSPFAK SLGHRSERGEADLYDSGDIFSRAP GSQ/SVERNPQRQRSRDLPPPGW KQRPRSGKQPRKRSP*QPKHP LPKGRTTSSPW
9626	39994	A	9686	I	4086	VTPRAAWLGLGFGRGSAVLGLC WQPRSPSPSRAAGMMNRITTPDQ ELVPASEPVPWERPWSVEEIRRS SQSWSLAADAGLLQFLQEFSSQ TISRTHIEIKKQVVDGLIRETKATD CRLHNVFNDLMLSNTQFIENR VYDEEVEEPVLAEEAKTEQE KTREQKEVDLIPKVQEAVNYG LQVLDSAFEQLDIKAGNSDSEE DDANGRVELILEPKDLYIDRPLP YLIGSKLFMEQEDVGLGELSE EGSVGSDROSIVDTE
9627	39995	A	9687	1930	5781	RAKSPANIIMTGSNSTHILTLN VNGLNSPIKRHRLASWIKSQDP SVCCIQETHLMCRDTHRLLKIG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDHSHTLIMG DFNTPLSTLDRSTRQKVVKNDTQ ELNSALHQADLIDIYRTLHPKST EYTFPSAPHHSYSKIDHILGSEA LLSKCKRTEIIITNYLSDHSIAKL ELRIKNLTQSR
9628	39996	A	9688	1	3654	
9629	39997	A	9689	1	5127	
9630	39998	A	9690	1	3663	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
9631	39999	A	9691	I	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDHSIIM GDFHTPLSTLDRSTRQKVNLKDI QELNSALHQEDLIDLYRTLHPKS TEYTFSPAPHHTYSKIDHIVGSK ALLSKCKRTEITNCLSDHSAIK LELRIKNLTQNRSSTTWKLNNLL LNDYWVVINEMKAEIKMMPFETN ENKDPTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
9632	40000	A	9692	I	3489	MGDFNTPPLSTLDRSTRQKVNK DTQELNSALHQADLTIDYRTLH PKSTEYTFPSAPHHHTYSKIDHIV GSKALLSKWKRTIEITNYLSDH SAIKLELRIKNPTQSRSTTWKLNN NLLNDYWVHNKMKAEIKMMPFETN ETNENKDPTYQNLWDAFKAVCRGK FIPLNAAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELEKEIETQKTLQKINESR SWFFERINKTDRPLARLIKKKR EKNQIDTIKNDK
9633	40001	A	9693	I	3235	
9634	40002	B	9694	I	3300	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
9635	40003	A	9695	I	2563	MKAECIMIFFETNENKDTTNQN LWDAFKAEVEESLNRPITGAEI GAIDNSLPTKKSPGPDQGFTAEFY QRYKEELVPFLLKLFQSIEKEI LPNSFYEASILIPKPGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHICKKLIIHHDQVGFFPGMKG WFNIRKSINVQHINRAKDKNH MIIISIDAEKAFDKIQQQPFMLKTL NKLIGDGTYFKHIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCP SPLLNFNILEVLARAIRQEKEIK GQLGKEEVKLSLFAADDMIVYL ENPIVSAQNLKLISNSKVSGY KINVQKSQAFLYTSNRQTESQI MSELPTTIA SKRKYLGQLTRD VKDLFKENYKPLLKEIKEDETNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFTELEKTT LKFIFWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYC YQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNQWKGKDS LFNKWCWENWLAIWRKLKD PFLPTYTKINSRWIKDNLVRPKT IKTLEENL GITI QDIGMGKDFMS RTPKAMATKAKIDKWDLKLK SFCTAKETTIRVNRQPTTWEKIF ATYSSDKG LISR IYNE LKQIYKK KTNNPIKKWEKDMNRRHFSKED IYAAKKHMKKCSSSLAIREMOI KTTMRYHLLPVRM AIIKKSGNN
9636	40004	B	9696	I	3420	
9637	40005	A	9697	I	3579	MPGHNLKWKLNRGTVLIETGI QLSTSTILGSASEPPSAPIPKAQV SSTEKLRCIDDLKPFPALASEL SRRAKALQIA G FPPMKVPRDTI SKVCLDKTVGKLCHSGEESRK CTLICNNKHYP IQDNLQGYKTQ NKFLNKEILELSALRRNAERRE RDLMAYKSSLEAKLCQIESKYL ILLQEMKTPVCSEDQGP TREV AQLLEDALQVESQE QEQAFV KPHL VSEYDIYGFRTV P E DDEE EKLVA KV RALDLK
9638	40006	A	9698	I	4371	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, + =possible nucleotide insertion)
9639	40007	A	9699	1	1825	MVKGSIQQEELTILNTYYAHTG APRLIKQVLSLDLQRDLSHTIIM GDFNTPPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFPSAPHIYSKIDHILGSK ALLSKCKRTEITNYLSDHSAIK LELWIKNLTNQHSTTWELNNLL LNDYVVHNEMKAIEKMFETN ENKDITTYIHLWDFTKAVCRGK FIPLNAHKRKQERSKIDTLTSQL KELEKQEQTSHSKASRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKKREKNQI DAIKNDKGDTTDPTEIQITIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLRNPITGA IVAIINSPLTKKSPGPDGFTAKF YQRYKEELVPFLKLKFQSIEKE GILPNSFYEAISIILPKPGDRTTK KENFRPISLMNIDAKILNKKLA KRQQHKKLIHHHDQVGFGFPGM QGWFNRIRKSINVQHINRAKDK NHMIISIDAEEKAFDKIQQPMLK TLNKLIGIKYLGIGHLTRDVKDLF KENYKPLLKEIKEDRNWKWNIP CSWVGRINIVKMAILPKNITL QLLVLPELSTIPLWLPALAGQ
9640	40008	A	9700	1	4449	
9641	40009	A	9701	824	3693	AWKGTTDRSTRQKVNKDTQEL NSALHQADLIDITYRTLHPKSTE YT/FFSAPHIHTYSKIDHIVGSKA LLSKCKRTEITNYLSDHSAIKL ELRIKNTQSRSTTWKLNNLL NDYVVHNEMNAEIKMFETNE NKDTTYQNLWDAFKAVCRGK FIPLNAHKRKQERSKIDTLTSQL KELEKQEQTSHSKASRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDT
9642	40010	B	9702	1	2858	
9643	40011	A	9703	1	3354	
9644	40012	B	9704	288	3301	
9645	40013	A	9705	1	3457	
9646	40014	A	9706	1	4794	
9647	40015	B	9707	1	3384	
9648	40016	A	9708	1	3345	
9649	40017	A	9709	1	3780	
9650	40018	A	9710	1	3720	
9651	40019	A	9711	1	3894	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
9652	40020	A	9712	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKVQLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQEILNSALHQADLIDITYRTLH PKSTEYTFSSAPHHHTYSKIDHV GSKALLSKCKRTEIIITNYLSDHS AIKLERIKNLTSQRSLTWWKLNL NLLNDYWVHNEMKAIEIKMF ETENKDPTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDL TSQKLELKQEQTHSKASRRQE ITKIRAELEKIEETQ
9653	40021	A	9713	1	3780	
9654	40022	B	9714	1	3855	
9655	40023	A	9715	1	3345	
9656	40024	A	9716	965	4362	TWKGTTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDITY RTLHTKSTEYTFSSAPHHHTYSKI DHIVGSKALLSKCERTEITNYL SDHSAMKLELRKLNLTQNCSSTT WKLNLLNDYWVHNEMKAE IKMFETENKDTTNQNLWDA FKAVERGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTHSKA SRRQEITKIRAEI.KEIETKQLTQ KINESRSWFFERINKIDRPLARLI KKKREKNQIDT
9657	40025	A	9717	1	3921	
9658	40026	A	9718	1	3988	MTGSNSHTILTTLNINGLNSAIK RHRLASWIKSQDPSVCICQETH LMCRDTHRKLKGWRKIYQAN GKQKKAGVAILVSDKTDKFPT KIKRDKGEHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSILDR STRQKVNLDTQELNSALHQAD LIDIYRTLHPKSTEYTFSSAPHH TYSKIDHVGSKALLSKCKRTEI ITNYLSDHSAIKLELRKLNLTQS RSTTWKLNNL
9659	40027	A	9719	32	583	GPHGAFTHGR/RFGRDPYEGP RRTGKRKQKSARGCIVDANLSI LNLVIVVKGEKDIPGLTDTMVP CHLGPKRASRICKLFLSSEDDD VHQCVRKALNKEGKPKRTKA PTTKYLVTPHVLQHEWHIAL KKQRIKENKEVAEAYAKLLAK RMKEAKEKHQEQUIAKRRLSSL RASTSKSESSQK
9660	40028	A	9720	318	605	

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9661	40029	A	9721	1	649	MGLKGQGVEGLLRQSGSVL QPLSREDLGRSQSESLGPEFQLG WEWLPPERVERENLSYDCVLG QRPMHLPNMNQLASLGKTN EQ SPHSQIHSTPIRNQVPAQPIQM SPGLLSPQLSPQLVRQQIAAH LINQQIA/S*PAPGS PASSHHQPA VPEPS/IPSPEQLSQSQPTLPWKS LQISTSKSEMS*RGPVCPKLSLQ EWHSTAHRNLKTWKKD
9662	40030	A	9722	15	272	KPQWP GIPSPG PPPG SFKC K*KS GHWAKECLQP RIPP KPC PICAGP HWKSDC STHLAAT PRA PGTLA QGS L TD SFP D L L GLA AEG
9663	40031	A	9723	96	531	VQPADLLRPLHTDTNCIWCQRP GTEGLL RETGPLSS/PLTP/MRRS TYD L RSSD QPK EHL/TDFKSGSC FKCRKSGHWTKECQPRIPPKP CPICAGPHWKSDCPSCPAATPR APGTLA QDSLTD SFTDPKGSLI DYFPD L L CLVAED
9664	40032	A	9724	3	567	GRLQTGA DPAW RVH GTW RSTS AAD AID QM W P V M RTW RLNE RHYGG L TD LGKAETA AKHGEA QVKIWSNI SKDRYADL TDDQL SSCESL KDTIAS ALP FWNKE IVP QIKEGK WVLIAAHGNSLRGIVK HLEGL SEE AIMEL NLL TGIPIVC KL DKSSK PIRCM EFLG DGETLC KAMEAV AAQ GKAKK
9665	40033	A	9725	2	801	GGVPHP QPAAMAAYKVLV IRH GESAWN L ENRFSGWY DADLSP AGHEEA KRG GQAL RDAG YEF D ICFTS V HLY AIRT LW TV LEMPL SEM WL PV VRTW RLNERH YY LTG LNKAETA AKNG EAQVKIW RRSYDV PPPPM EPDH PYFSN ISK DRYAD L TED QLPSC DR LKD TI ATAL PFW NEE I VPQIKE GKR VL AAHGN SLRGIVK HLEG L SEE AI MELUN L PTGIPIVY EL DKNL KPI KPMQFLG DEET VRK AMEA VAA QGKAKK

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
9666	40034	A	9726	3	573	VAPVVQVWKEMHKLLPFSPDS VVTGHDISIDSGIFDQDKLIGRI DVGRVGIAACGCQDVAIVWNYL AACSVDRNTCRIMPRNCRPEVE ETPGLEKEEKSLSQPKEGEATDL KKEVEKISSSEEETVNLKEEEV KIPPPEEETMDLKEEEEIPPPTEL RDQKLHMHVLKDLEPVSAVPHK DSLFIQQLTTVPV
9667	40035	A	9727	2	685	TLYCRVFLLDGTEVSVDLPHKA KGQDLFDQIVYHLDLVETDYF GLQFLDSAQVAHWLDHAKPIK KQMKIGPAYALHFRVKYYSSSEP NNLREEFTRPKITKMDFKKSKL TLVVVEDDDQGREQEHTFVFR LDSARTCKHLWKCAVEHHIAFF RLRTPGNSKSNSRDFIRLGSRFR FSCFS/ERENAHTSTGNSPALRER PGDGSVSREGRWVDEGWQPQR GGRGQNALCSVP
9668	40036	A	9728	1	419	MSKFGRATRGLRKPEVGDVIRT IVRAGLAMPGPPLGPVLGQRRA SINQFCKEFNERTKDIKEGIPLL TKIFLPKDGTIEKIGQPTVSYF VKAAAGIEKGARPT/DLSSEEEFA AFQKEQAIFLAAQKKADLATQE EEAAKK
9669	40037	A	9729	97	826	SQLPRIMSKLGRAARGLRKPEV GGVIRAIIVRAGLAMPGPPLG\N VLGQRGV SINQFCKEFNERTKD IKE\GIPPLPTKIL\VKPDV\RTFEIKI GQPTVSYFLKAAGIEKG\ARQ TGKEVAGLVTLKHYE\ARIKA SGLRAFALQDVPLSSV\VRSIIGS ARSLGTSRGERTSSSEELAAFQ KERAIFL\AAQKIEADFGLPKKE AAKEIDPLPHQLPDFQKEVSLQ KLCPRGGRRSHQYDDGFHDFE
9670	40038	B	9730	273	418	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
9671	40039	A	9731	69	1565	RRRRFQASGAAAMLSSRAEAA MTAADRAIQRFLRTGAAVRYK VMKNWGVIGGIAAAALAAIGIYV JWGPITERKKRKGGLVPGVLNL GNTCFMNSLLQGLSACPAFIRW LEEFITSQYSRDQKEPPSHQYLS LTLHLLKALSQCETVTDDEVLD ASCLLDVLRMYRWQISSFEQP HFQDGLVQLRQVGVVCRHYPEK WEAASWTSQNCGADDAHELF HVITSSLEDERDRQPRVTHLFD VHSLEGHPLTLHDCLHHFVTQSE SVRDVVCDNCTKIEAKGTLNG EKVEHQRITTFVKQLKLGKLPQ CLCILQLRLSMVQPGTPLKRJIE HVQFNEFLMMDIYKYHLLGHK PSQHNPKLNKNPGPTLE/HAGW AGSPHTSSESARGPQNTDFYEW RLLPIFIANAVSADALPSPSCSR LQLLHPLPADGQLSSTMGDMA LWDTLFYIYRSPPSARNPLSTSN QWLWVSDDTVRKASLQEVLSS SAYLLFYERVLSRMQIIQSQEC
9672	40040	A	9732	I	1393	PLQLQPRHIIGAQIQLGPLLQRV QAIRLGFSHMVLSLW/VMQSAR VEILEPPPLRQRMYGAWRISL CPQGLSTVMRSELTASSTPQVQ EILPPQSPPEYLGPKGITERIHKIM HVKGIAKLPANRNQSPGVSG KRLVNCVSASAVIDSEPAVPEP DVCAGIVIKKQCFPVIARCNKT KQVDSPHRAYAKPSPFFPAVV VVTSESKDPRVKQNPTHPLAE GSNAAHFHKTQISQSLKWLPVG YLNSTTYEYRDLTKGLSLLCSL LLGVEADIPSMAGLHVRLHMQ VPQQPCIAFAVSSPLHQGGKET EDAWSFHIPSTIHRWPTSPSQL SSLRASTQLLCLHINLAKCFIWG ILAQVLSCHHHIRTQFVGMLTF VCAGDDSKLSPDIRTLVRLRLTS YLVSASVLLKSQKMA LCSASRI LDVSVSPGDHVASEARCAP DLVAPRPMPHQNQGSLEWTEE
9673	40041	A	9733	44	282	FSCLILHDAFPCLILHDAFPCL CSVTGSI.VLSRVPLRGTHQKSA IATSTKIALSNM/KILKHHHTDAY FKKQQLFFDVSKK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met codon	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, -=possible nucleotide deletion, !=possible nucleotide insertion)
9674	40042	A	9734	3	381	EQQQGQR/SQWWRGAAARVSRTVKRVLCE/VVECPLKSACPDVDMYWAAALQRLASLLKADGNLVTMAALHSHYHMVGSKKKFFGLHPEKETVEKAMQEAGCQVQRCA/ISCSSETCSINDGICFVAACKGPSV
9675	40043	A	9735	2	209	CRHSTQHCVS/HHGHSQYK/DSHQHYSHYHHHHPHHHHQSPYLHHHHYDCHLHHHHHNDHYRHISVYDI
9676	40044	A	9736	197	3348	RVVQTDMIKGMLETSLLKISLDQAFIRICLNSTCFRPKGKLVIK/C EKSINSASLVSTSQRISCRPKTHI SKNYGNNFLNSSLTQKQEVHMREKSFQCNCESGKAFLNYSSSVLR KHQJIIHLGAKQYKCDVCGKVFNQKRYLACHRRCHTGKKPYKC NDCGKTFSQELTLTCHHRLHTGEKHYKCSECCKTFSRNSALVIHKAIHTGEKSYKCNECGKTFSQTSYLVYHRRLLHTGEKPYKCEECDKAFSFKNLERH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
9677	40045	A	9737	1	1665	MAGACWLMAFQYWVLKLLVV KSA/SWPRQSSLKWVNWFKG QDLETWGKKETRKFYGYRNE EAQKYSCKPRKPD^WCHCWQ W**WLMASFQYWVLKLLVVKS AYGLVVKALSNIGISKVAKTW KPGGKKRLENFM ^A EEMKKHR STHVGFPENLNTNGATAGNGDD GLIPRKRSPRTPEQQFPDTENEE YHRDFSKLCLGSAANGVVHVE VKMCVYNGKGERQEEMKGGLI SMNLVVVEEMKKHESNNVGG ENLTNGVTAGNGDNGLIPQRKS RTPENQQFPDNESEEYHSLGDK SKTSFQNSNNNNNKQQEQQQQ NPTFSNTRKLTKLYKAPIPPSII SGCPNINDSNWQEIEHGMQTA GLPTRPLSHGLLQQKGA ^A FRCLG CKCSEPTGSLILQAKATNTQK WQATYPKSQNEQLVPSVGSY RCSTPAQPMKTAVGHKPCKAT GAELPKALGAQPLHPCALDV QGFKKGNFGAVGLNLGLLEF HGVSGVLLVGPDDGLISEGVV REDLMCGVWSAGTWSVGTAE RCLEKPGALHVIEGPLDSWDP VMPNGPVKSRSQSSCLDGPGR CSEILTQSHGNKKPARASSKS SQSINDRPLAVLTNQYQVCEQLA SERQSSNSCSIRDSA
9678	40046	A	9738	1	115	RRTARGPQQTSDGLGLTSPCRN ASEHTADILELSTLIV**RRQ*ICL CLDFLYY/LIPEGRCFCRACDLV HNFDTIILQHQHRTLTSQGVDDF LKAKATFKASDFIDALVLSKVA SPRILIQGGRMGA*DQVSDQAS VYGRCCSSSGAEAAKRPKSAWL LLGYDSDRASGLY*ILYNLTKH D/YRECCQPVMQES*S*RRTAR GPQQTSTDGLGTSPCRNASEHT ADILELSTLIV
9679	40047	A	9739	1	506	MVIVGLAAGVLLVGPDDGLIS EGVVREDLMCVGWSAGTWSV GTAERCLEKPGALHVIEGPLDS WDGPVMPNGPVKNHGEQQE VPSKHPQMALEICLCLDFLYY/L IPEGRCFCRACDLVHNFDTIILQ QHRTLTSGVDDFLKAKATFK ASDFIDALVLSKVAPSGS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met htd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
9680	40048	A	9740	I	380	KFSRPSVNMLRIVKPCITRG/Y/P NLKSVNKLIYKHGRGKINKKRI ALTDTNTLIDQSHGQYGIICIEDLI HELYIWPFKLSSPQSGMKKKT THFVENGAANREGQIHLRLIR MNCGVYRDYFSNLVS
9681	40049	A	9741	3	279	
9682	40050	B	9742	23	197	
9683	40051	A	9743	2	402	CGDRGALRPPSCAGRSGPGP PPRPPRPLPWHPAPPAHGAPLA RPGARARRSEKPKSEPKRLRRSS PRAQEEGPGEPPIPPEALLLPPP PPPPTPAVPRRPRPVPGPGRAAG ALGDVPEAAEAYLERVPPSSC
9684	40052	A	9744	1	660	
9685	40053	A	9745	1	1035	
9686	40054	A	9746	I	2575	MRAAGGAMLCGKQGRWDPEG EGAHPGFIPKLACCSSQGVFRQL HLRTAVTAAVSRHFPQPSWRY DPGPQFLGEKSGFKPRCPGVAV CQFQSMNAFIHWFRNKAASS CDRICKIPVPPPEATFVEPNCLPGEI GQLLRQLQSGRNLKEWLREQF CDHPLEHCEDTRLHDAAVYGD LQTLLRSLLQEESYRSRINEKSV WCCGWLPCPLRIAATAGHGS CVDFLIRKGAEVDLVDVKQGT ALYVAVVNGHLESTQILLEAGA DPNGSRHHRSTPVYHASRVRG ADILKALIRPAACDRSVSITADT HFRLYIKVVPAMFRSRKAIPFLS SCTAWRCADELFQIQPVPLVDT SGSGKTVSNVITESHNNSDNEED DQFVVEAAPQLSEMSEIEMVTA VELEEEEKHGGGLVKKILETKKD YEKLQQSPKPGEKPSATGWHG ECLGTRNRRAQGALVGWGWLY SERHSGMLRAITLKVKGGGRQ GIQA/AWKSETFRSRAAPENPL GRWGFAILLSKII*^RQVL\KLHF SLSPQARVNSRFPGSGKAGLGL WMEGARPSGHVPKERVVAGK RPQVPTKAHHTCVRETAGNQE GNGEALQQEQRQLGVAEAGSN GEGALQQEHRITDCAVEPLKAE LAELEQLIKDQDKICAVKANI LKNEEKIQKMERSLFESAWKE KDIVSKIEKLRTSIQTLCKSAL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
9687	40055	A	9747	2	1739	MKGLYTDAEMKSDNVKDKDA KISFLQKAIDVVVMVSGEPLLA KPARIVAGHEPERTNELLQIIGK CCLNKLSSDDAVRRLVAGEKGK EVKGRLASLTSRSQELDNKNVRE EESRVHKNTEDRGDAEIKERST SRDRKQKEELKEDRKPREKD DKEKAKENGGNRHREGERERA KARARPDRNERQKDRGNRERDR DSERKKETERKSEGGGKEKERLR DRDRERDRDKGKDRDRRRVKN GEHSQLLDREKNREHDKPEKK SASSGEMSKKLSDGTFKDSKAE TETEISTRASKSLTTKTSKRRSK NSVEGDSTSDAEGDAGPAGQD KSEVPETPEIPNELSNIRRIPR GSARPAPPVRVQRQDSMEALQM DRSGSGKTVSNVITESHSNDNE EDDQFVVEAAPQLSEMSEIEMV TAVELEEEEKHGGLVKKILETK KDYEKLQQSPKPGEKERSLFES AWKKEKDIVSKEIEKLRTSITQLT CKSALPLGKIMDYIQEDVADAM QNLQMYHSENQRQHAEALQQ EQRITDCAVEPLKAEIALEQ LIKDIQJDQKICAVKANILKNEE KIQKMVYSINLTSR
9688	40056	A	9748	93	800	RANLP*TQPYCHCGLAPAALTRI VGGSAAGRGEWPWQVQLWLRL RREHRCGAVLVAERWLSSAH CFDVYGDPK/QWAALFLGT/HVP ERRGGAVERVARYKHPFYNL YT/FDYDVALLELAGPVVRT/SL VRPICLPEPA/HATPDGTRCVIT GWG/YGS/TGAQLQKAAVRLLS EQTCAA/LYPVQISSRMLCAGF/ LQGGVDSCSGDAGGPACREPS GAPVPGQPRCTAPARWPRRSA LSPAPL
9689	40057	A	9749	107	378	NLVP*LRSGD/SPLGDQSPVLLIF TP*ERSTYNLKSSD*PAQETS/PP ISNPDTEN/PDCSTHLAATPRA PGTLAQGSLTDSFPDLLSAAE D
9690	40058	A	9750	2	286	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Motif	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=>Stop codon, /=>possible nucleotide deletion, +=>possible nucleotide insertion)
9691	40059	A	9751	215	631	GTQSCNQKVLSANNLQELGIGPKFQMRKLPQLAPMQPNRGRTS LGRSICPPVLCMSRKIHLRPQVLRPTSPRNISPILNRVESDHAGTPALVLHP*RQVPLFWGRGKYPNPFLCLYPPSAFLGGKKHPTPSPSP
9692	40060	B	9752	1	933	
9693	40061	A	9753	1	2283	MLPNRLGSSETITDAELRVTLTVEELNGLRAVQDMFVKQILKAARSLLRVITIPNLKYPGTQTLRKAAAPDPNTTGLIFLEKLCEIAAAIASYVAVPSLEINHRKKANPULLRRSGSGSVSLQLLAEKIWEVGVRPWARVLVWEWLPDQNPLSGLTKSNSTSRRHELPHGRAIQLHLSGWELWSEPSNLLDLVVTGDIENTSLAPEDPTFTLTMPSGSCHPESPSDGPGLSSLVAVWFVLVEDWLSRKRLESEPAELPLGKAGEVFVDTLPLPSRRTHFSGFLGHFCYSFSDGYSTNRAAPDGSSSTKAEKHGSCRKQPPTYTLQCRDKAGLVRHGNSPVSAYGWLFSEERPCKPTRTPFSWEGDPPGLLTADETSLVVHLELPVFPFSFLKRAQNSRHSGMGSPLEAAEAYSTVVVMADVSQYPVNEPLVAAVVCQEPEERAQPDVHFQ/CLRLGGHAGGVaarPLPAAETPPLQRPPSVRA*SAP*SGARAADDPRRTHSVQAEEAQRPEPDILNHVFDDVESF/VSRLQKSAEAARVLEHR/KRGRRSRRRAAGEGLLTTR/AKPPSEAEYTDVLQKIK/HAFSILLARLRGNIADPS/SSELLHFLFGPLQMV/QPSGGPEFASSVRRPHLT/RDAVALLRDNVTPRE/RRLWTSLGDSWTRPGLELSPEEGPPY/IEFFSGWEPPVTDPQSAPGRTRQRNSYSTSGGA
9694	40062	B	9754	1	930	
9695	40063	A	9755	76	247	QLKTDTAQQLPRKLFVESHNYHCSWPGLQSGLPHYSGYHTSS*LYLSDPADIHPISP
9696	40064	C	9756	95	301	
9697	40065	A	9757	352	545	DILNHVFDDVESFVSRLLQKSAERPGCWRRRTRPQKPAQGVAG*RGTRWGI*TPPDLFQMSPLSP
9698	40066	B	9758	406	602	
9699	40067	A	9759	1	543	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9700	40068	A	9760	2	138	LDDFVGRMLTLMGCPPIPEC/PR VPSPLREGRKTQAA1.SVRRGRSHRR
9701	40069	A	9761	1	417	
9702	40070	A	9762	830	1029	YLPHLSLRLPCCPPLPLSKPN LP*LRPSSLQRDYLISIFILINMP SISSTMLLYGGKEISSLH
9703	40071	B	9763	40	980	
9704	40072	C	9764	419	700	
9705	40073	A	9765	271	1185	
9706	40074	A	9766	2	1655	RGRRSRRAAGEGLLTLRAKPP SEAEYTDVLQKIKYAFSLLARL RGNIADPSSPELLHHFLFGPLQMI VNNTGGPFEASSVRRPVLVTSDD AVALLGNNVTPRENELWTSLG DSWTR/LRA/EELSPEEGGPYRP EFFSGWEPPVTDPQSRAWEDPV EKQLQHERRRRQQSAPGRCQ WVTGIDLEPESEPQLESETAGK WVLCNYDFQA\RNNSSEA VRSSS GDV\I\EV\I\DDSR\KWWKVDRP AGQE\YV\PY\N\LT\TV\PG\RL\H SQSPARSHDSTPPPPAPAP/V/ LPPAL\APR\WRDPR\WDSCDSL NGLDPSEKEKFSQMLIVNEELQ ARLAQGRSGPSRAVPGPRAPEP QLSPGSDASEVRAWLQAKGFSS GTVDALGVLTGAQLFSLQKEEL RAVSPEGGIARVYSPTVORSL LEDKRES\SELEAVMEKQKEEG GRRGNGGGHLTCQAPFAKSDE APWENGPPQTLPNSGSRSSEGW PICSGPGLPPLPVDRLNNDPCCCSP SGEDLDWLGVGRAWRQSTESA SRPPR\CSGALSIVILRSPINMP PCLAKKKKK
9707	40075	C	9767	565	762	
9708	40076	A	9768	1	401	SPLRPLLALALASEPCAQQGAC PASADLKHS\DGTRTCAKLYD\IC SDPYYENCCGGAELSLESGADL PYLPSNWANTASSLLVVAPCEL TVWSRQKGAGKTHKFSA GTYP RLEEYRRGILGDWSNAISALYC RCS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asn	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
9709	40077	A	9769	1	1489	MPQILLQNNGIIEAFRRYARTEG NCTALTRGELKRLLEQEFADVI VKPHIDPATVDEVLRLLEDHT GTVEFKEFLVLFVKVAQACFKT LSESAEGACGSQESGSLSIHS GAS QELGEGQRSGTEVGRAGKGQH YEGSSHRSQQGSRGQNRPGV QTQQGATGSAWVSSYDRQAES QSQERISPQIQLSGQTEQTQKAG EGKRNQTTTEMRPERQPOTREQ DRAHQGETVTGSGTQTQAGA TQTVEQDSSHQQTGRTSKQTQEA TNQNQRGTEHGQGRSQT SQA VTGGHAQIQAGTHTQTPTQTE QDSSHQTGSTSTQTQESTNGQN RGTEIHGQGRSQTSQAVTGGHT QIQAGSHTEVEQDRSQT VSHG GAREQGQTQTQPGSGQRWMQ VSNEPEAGETVPGGQAQTGASTE SGRQEWSSTHPRRRCVTEGQGD RQPTVVGEEWVDDHSRETVILR LDQGNLHTSVSSAQGQDAQS EEKRGRITARELYSYLRSTKP
9710	40078	A	9770	2	3031	
9711	40079	A	9771	6288	6584	TAVSLPAPLFDLQIPPRKRSLK ETVMAPENLTN*RAPPQSSARV FQ*EALYVPGP*ALDPPEVCSSY SSVCGLHQLSHSSSESSSTLGSL LGSFQML
9712	40080	A	9772	884	1032	ESRPNTTTRLRKTSSWSFQS*TA TQTKGPDRPGASMTKPGATSER SASG

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9713	40081	A	9773	1	1457	RSAQKEKTAAKEQQQGEKTEVLSSDDDAPDSPVILE PSLPPSTPPSTPTYKKSLRLLSDQIRRLNLQE GANDVVFSVTTQYQGTCRCKATIYLWKGDDKVVISDIDGTTKNSDALGHILPQLGKDWTHQGITS LYHKIQLGQLVMPLDARPERPMDGMKVRAFMERLLFVRRGTDKRWSRMYVTCQSQQNNLNEE IYINQVVIQANMKLQLWAMRTDDARGLSSLGDTESPSCPSVVPGLQPKPAPVCAGDALLQAQIPGVLLGTLFSGAAFYSGLYGGSEQFLDHLLHPARAAPPPPLVGPAPRVPGSAPSAPELAGPAVWRFA AAASRGVVVAASGWGRGGEASQTFQTGKEPGGTRHPTRMLGSTGCIFPGTLEKSQGYERYNAMRADPALCFLEKVGMPDEKSLSAEQGVTDGTSZIPERARQNEEQLTSFGLLWPTPQGSTDHIDNHPRERYPEMRWELDVPLPDIDYMEIPVDWWDA
9714	40082	A	9774	3	4804	KRLENQKTLLEVAFSEAVWMQPSVLLDDLDLIAGLPVPEHEHSPDAVQSQRLLAHALNDMIKEFISMGLSLVALIATSQSQQSLHPLLVSAQGVHIFQCVQHQPNNQEQRCEILCNVIKNKLDCDINKFTDLQLQHVAKEETGGFVARDFTLVVDRAIHRSRSLRSQISTREKLVLTTLDfqKALRGFLPASLRSVNLHKPRDGLWDKIGGLHEVRQILMDTIQLPAKYPELFANLPIRQRTGILLYGPPGTGKTL
9715	40083	A	9775	1	897	
9716	40084	A	9776	486	800	CLQLSWLSLGQAQVHWLGRAVHTACCMD*VLLFGESPGFLVR LTPGILLGLL*P*KQGHCHSVSLEVRJ/CGHS*TFTSWAFSVLQGKASAQPVKVSTQNSRY
9717	40085	C	9777	332	497	

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9718	40086	A	9778	I	6504	MWGSDRLLAGAGGGGAAVTVA FTNARDCLFLHPLRRLVQLHL QNQAIENVVWSHQPAFLSWVEG RHFSDDQGENVAEINRQVGQKL GLSNGGQELHAVSLEQHLLDQI RIVFPKAIFPVWVDQQTYIFIQI VALIPAAASYGRLETDTKLLIQPK TRRAKENTFSKADALEYKKLHS YGRDQKGMMKELQTQKQLQSN TVGITESNEENEIPVDSSSVAS LWTMIGSIFSFSQSEKKQETSWG LTEINAFKNMQSKVVP
9719	40087	A	9779	I	5421	
9720	40088	B	9780	124	273	
9721	40089	A	9781	84	493	IHANNCS*L*KAALNFVLLLLQ KRL*GEKHTLSETGREGNKVG GVGS*VTGTGQETELGSLGRCH SPLSVLHLLPFPS/ILLGRTHLNA LLIRDYFASSCKYL*EVLLSLSD GSG*NLMHSVWMAGNSSAEYVR
9722	40090	A	9782	I	5954	MDGMTEACIKGGIEACYAAVS CVCTLIGALDELDSQGKGILSEQ VQLLLRLEELKDGAESWRDS MEINEADFRWQRRLVSEHTP WESGNERSLDISIVTTDTGQTT LELEGQTTTPEDHSGNHKNSLK SPAPEGKETLSKVLETEAVDQP DVVQRSHITWPYPDITNFLSVD RTRSÝGSÝRÝSESNFSDVDDQDLS RTEFDSLSCDQYSMAAEKDGSRS DVSDIGSDNCSLADEEQTPRDC LGHRSLRTAALS
9723	40091	A	9783	I	2217	
9724	40092	A	9784	I	1360	
9725	40093	A	9785	I	777	MNIKNPPIAQHLDNLPIVKASSI GMTWGLVRNGVSAPTKQKSCIRI HILARCTGAVAFEKLLYFKSPAN QAHARKVGKQVQDCYIGRDIV AKAGAIHLNVGKGTPVCCPLL EEGINSEVWTTEGQYGRAKINA RPVQVKLKDSTSFPYQRQYPLR PKA/LTKGFQKIVKDLKAQGLV KPCSNPCSTPILGVQKPNRQWRJ EALKLQIVLQMEEPQMGSMTKI YHGPLGRPASPSCSDVNIEGPN TKEISTAPPILCPNSAGSS
9726	40094	A	9786	I	415	

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9727	40095	A	9787	1	451	MVHFISRLLYSDGLDPGDPIQ DSSDAALSVSPHCSPDSRVSTT KHLWVSPRLLRVAVRVKNIDIT NFSSSW!NDGLAFCALLHTYLP AHIPYQELNSQDKRRNFMFLAFQ AAESVGKSTLDINEMVRTERP DWQNVMLFVIAIYKVFET
9728	40096	A	9788	3	605	DEWP PERIIQVN EPTTWH/EDGL WGYRTRFYMINQIIW/LQAIIEII TNKTDRALTI LAQQETQMNRNAI NQNRLALDYLPAAEGGICGKF NLTNCLLHVDDQGOVVEDIVR DMIKLSHVPMQVWHGFDPGA MFGKWPVVLGGFKTLIIGVILV1 GTCLLLPCLLPVLLQNMKSFAT LVHQNASEQLYYYMNHYRSVLQ EYMGs
9729	40097	A	9789	3	876	GAGGGFGSPMDIFDMFF/GGGG RMHERRGRKNVHVQLSVTLED LYNSATRKLAQKNAICDKCE DRGGKKGGVEYCPNCRTGM QIRIIQJGPGBKVQQIQSVCVECQ GHGEQISP KDRCESCNGRKILR EKKILEPHIDKGKMYQGQKITFH GEGYQEPGLEGEDIIIVLDQKD DAVFTRQGEDLFMCIVKHGDI KCVINEGMPYPRPYEKGRUIIE FKVNLPENDFLSPDKLSSLKEKL LPKRKEVEETDEM DQVELVDF DPNQERWHHYNGEAYEDDEH
9730	40098	A	9790	199	410	
9731	40099	A	9791	134	1369	KMVKE TYYDVLGVKPNAQE ELKKAYRKLA LKYUHPDKNP EGEKF KQISQAYEVLSDAKKRE LYDKCGGEQAIKEGAGGGFGS PM DI PDMFFF GGGG GRM QRERRG KNVVIQQLS VTL EDLYNGATRK LAQK NVICDKCEGR/SGRFKE QGA VRSACPNCRGTGM QIRIHQ IGPGM VQQIQSVCMECQGHGE RIRPKDRCKSCNGRKIVREKKIL EVHIDKGMDGQKITFHGE GD QEPGLEPGDIIIVLDQKDHA VFT RRGEDLFMCM DQIOLV EAL CGF QKPISTLDNRTIIVITSHPG!QIVK HGD IKCVLNEGMPYIYR PYE K GRL IIEFKVNFPENGFLSPDKL S LLEKLLP E RKE VEETDEM DQV ELVDFDPN I QERRR HYNGE AY EDDEHHPRGGVQCS DLL MGPV

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9732	40100	A	9792	3	337	GYSQAPRKR/GGECSLSQPSFK AQPDAAASLEPPSLETPAGRTPA TLTQGSPAAVREPLSPGHNAK ARLRSRPARPPWIPDPDPGGHFW TDFCAPESLQGETRTSRSFQLL
9733	40101	A	9793	1	346	SGS*QLQMCSCGLPAHTQDETHI SSCGQLDLALPPLLPLPSPLN TLPPQGLCTC
9734	40102	A	9794	1	1110	MEGEEAAGAAGPDPVGHRKKC GFHPVCEREA P STFAAVMILV VQYIGEICRYLLKQPVREAERR HRVRLAVGNGLRPAIWEETTER FGVRQIGEFY GATECNCSIANM DGKVGS CGFNSRILPHVYPIRL VKVNEDTMELLRDAQGLCIPC QAGEPGLLVGQINQQDPLRRA NGYVSESATSTKIAHSVFSKGD SAYLSR DALMMDELGYMYYR DRSGDTFRWRGENVSTTDVEG ELSRLALGQTDVA VYGVAVPGK LGLQGVVLRHGV EGKAGMAA VADPHSLLDPNAIYQELQVKLA PYARPIFLRLLPVQDTTGTFKIQ KTRLQREGFDPRQTSDRFLFD LKQGHYLPLNEAVYTRICSGAF
9735	40103	B	9795	28	376	
9736	40104	A	9796	3	461	VRQC RGI RD PYRFKKRTELFIA AEGI HTGQFVYCGKAQLNIGN VLPV GTMPEG TIVCCLEEKPGD RGKLARAS GNYATVISHNPETK KTRV KLP SGSK KVISSANRAVV G/VVSGSS*MLRAVGEHA VSAG GQPVARLG PWNSITCCSKTWV
9737	40105	A	9797	1	701	MQEVPGMFERN YPHPAITFKPS VPVSRSLDYA PLPGVFRDPY W FKKRTELFIAAE GHGHTGQFVYC GKK AQLNIGSVLPVGTMPEGMI VCCLEEKPGGRSKL WASGNY ATAISHNPETK KTRV KLP SGSK KVVSSANRAVVGVVAGGGRT DKPILKACQAYHKYAKRNW WPRVWDVAMNPMEHIFPGGGN HQHIGIPS A/SRDDPAGCKMGL IAARQTGRLWGTKTVQEKEN

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9738	40106	A	9798	1	910	QCGGIRRTPVAMGRVIRGQR KGAFSVFRAHV/KHRRGAARLR AVDFAERHGYIKGIVK/DAERW PGREGKGRPAUTPHSRLCPDQ IIHDGRIGAPLA RVVFIRDPYRF KKRTELFIAAEGR HTGQF VYC GKKAQQLNIGNVLPVGT MP*G TIVCCLEEKPGD RGRKULARASG NYATVISWNPETTKTTRVKLPS GSKKVISSANRAVVGVVAGGI G RIDKP FEGWPGRYHKYKAKR NC*PRIGV AMNPVEHP GGG NHQHIGKVPT RRDAPAGRKV GLIA ARRTGRLRGTKTVQEKE
9739	40107	A	9799	1	405	LEISIMAASISGYTFSACVCFHSAN NSNADHEGFLGEVRQEETFSIS DSQISNTFLQV K VIGWYRFR RNTQQMSYREQVLHKQLTRI LGVPD VFLFSFISTANNSTHA LEYVLFRPNRRY NQRIISLAIPN
9740	40108	A	9800	1	232	
9741	40109	A	9801	1	420	
9742	40110	A	9802	3	1272	EISIMAASISGYTFSACVCFHSAN SNADHEGFLGEVRQEETFSISD SQISNTFLQVIEHHNHCPCS KL FSFYDYASKVNEESLDRLKDR RKKVIGWYRFRNTQQMSY KIEQVLHKQLTRILGVPPDLVFL LFSFISTANNSTHALEVVLFRPN RRYNQRIISLAIPNLGNTSQQEY KVSSVPNTSQSYAKVIKEHGTDF FFDKDGVMKDIRAIYQVYNAL QEKVQAVCADVEKSERVESC QAEVNKLRQITQRKNEKEQE RRLQQA VLSRQMPSESLDPAFS PRMPSSGAAEGRSTLGDAEAS DPPPPYSDFHPPNNQESTLSHSR MERSVFMPPRQAVG SSNY AS TSAGFEVFLGSGADLPPQRRAA GDSGEDSDDSOYENLIDPTEPS NSEYSHSKDSRPMAHPDEDPRN
9743	40111	A	9803	3	513	GAYGGGGACDNNGYGYGF GSDRFRGDLNYCFCGMSDHKY GDGGSTFQSTTGHCIYVHIEIGP DGRVTGEADVEFA THEDAVA A MSKD KANMQHSYVEFLNCAA GASGTAYGSQMMGGMGLSIQS SYGGPASQLSGGYGGYGGH SSMSGFDQVLQENSCDFQSDIA
9744	40112	B	9804	73	1127	

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9745	40113	A	9805	1	3647	MVRVHVGAALLEPLTSVRESR ATSAFQVSPYEDEPICRCPNCDP VGSSLSSVCIKDDLIHsDLHNGKQ PGQCPCKEGBTGEKCDRCQLG YKDYPPTCVSCGCNPVGASASDEP CTGPCVCKENVEGKACDRCKP GFYNLKEKNPRGCSECFCFGVGS DVCSSLSWPVGQVNMSMGWLW TDLISPRKIPSQDALLGRHRQVS INNTAVMQRLAPKYYWAPEA YLGNKLTAFFGLKTYTSDIP VETVDSNLMSHADVIIK
9746	40114	B	9806	141	236	
9747	40115	B	9807	66	266	
9748	40116	A	9808	1	330	
9749	40117	A	9809	1	792	
9750	40118	A	9810	129	311	
9751	40119	A	9811	3	538	
9752	40120	B	9812	96	536	
9753	40121	A	9813	1	2090	MSSNQKSPITKTSKSPGTANVLD VNNSTLMFVGGLGQQIKKSPA VKVTIFKGCLGEAFLNGKSIGL WNYIEREGKCRGCFGSSQNEDP SFHFDGSGYSVVEKSLPATVTQ IIMLFNTFSPNGLLLYLGLSYGT KDFLSIELFRGRVVKMTDLSG PITLLTDRRYNNGTWYKIAFQR NRKQGVLAVIDAYNTSNKETK QGETPGASSDLNRLDKP1YVG GLPNSRVVRRGVTTKSFVGCIK NLEISRSTFDLLRNNSYGVRKGC LLEPIRSVSFLKGYYIELPPKSL PESEWLVTFATTNNSGIIAALG GDVEKRGDREEAHVPPFSVMLI GGNIEVHVNPQDGTLRKALL HAPTGTCSDGQAHSISLVRNRR IITVQLDENNPVEMKLGALVES RTINVSNLVVGPIPEGETTSLLT MRRSFHGCIKNLJFNLNDHGFD SVEQKRFCGVPSCARESARGRA QAQDTAQELQSESACDKRSQPO PGKGHMYGGVLQPOSFLQKN LLLFYDEVLDLQPNGKEKEFSV GANHNAMFVVHWGVCFCFL PSGEWLASPFCVHPQTIHPPDR FQASVTDLEGYFLAKPTQAPAPA CPLDPIRPPLLGHAAQQPLLTQ HTDAAVTPSSAVTARAANYCA GGRNERKKTGREKRHLTGGPC VALRTFTVLIHSSHHIQVDGIRA GYVQRDGLQPTNRQIVM

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9754	40122	A	9814	1	8705	MRGGVLLVLLLCVAAQCRQRG LFPAILNLASNAHISTNATCGEK GPEMFCKLVEHVPGRPVRNPQ CRICDGNSANPRERHPISHAIDG TNNWWQSPLSQNGREYHWVTI TLDLRQVFQVAYVIKAANAPR PGNWILERSLDTTFSPWQYYA VSDSECLSRYNITPRRGPPTYRA DDEVICTSYYSRLVPLHEGEIHT SLINGRPSADDLSPKLLEFTSAR YIRLRFERIRTLNADMLTLSHRE PKELDPMLPR
9755	40123	A	9815	1	564	MGDLEDKLVLPIGELPRHLDQN SEQLKQVVQRELKELHETCQQ HQLCQASTSGEPKERDKEEGK DSKPRSLRFTWSMKTTSMDPN DMMREIRKVLDANNCDYEQKE RFLLFCVHGNDARQDS/LPCQWG DGKSCQVGPRLSLNGVRFKRI SIGTSCPLKNIAASKIA\NELKP VKKSQIYQVQGRYIHI
9756	40124	A	9816	2	451	ANAHGFMELQDGYSTETGEK GAQLSGGQQKQRVAMARALVR NPPVLILDEATSALDAESEYLIQ QAIHGNL/QKHTVLIJAHRLSTV EHAHLIVVLDKGRRVQQGTHQ QLACPRAGFYGKLVQRQMLGL QPAADFTAGHNEPVANGSHKA
9757	40125	A	9817	1	498	MVKY/YLGQGVLRSSW/DQVV PA/FWQYRNPVQRYLTEDIVH RENOQTMTFTWNINHARPMVV EERCVYCVNSDNSGWTEIRREA WVSSSLCGVSRAVWEFGLAQF KSNVTKTLKGFEYILAKLQGEA ASKTLIKTAREAKEAKETALA ATEKAKDLASKAATKKQQQ
9758	40126	A	9818	3	231	
9759	40127	B	9820	94	375	
9760	40128	A	9821	45	439	

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9761	40129	A	9822	304	1557	DRQNVMEQFNPGRLNLINLGK NYEKAVNAMILAGKAYDGV AKIGEIAATGSPVSTELGHVLIEI SSTHKKLQRESLMMENFKKFHK EIHELEKKIELDVKYMMATLK RYQTEHKNKLESLEKSQAELK KIRRKSQGSRNALKYEHKEIEY VETVTSRQEENQKSIADGCKEA LLERERGASCFPGLNKHCGFA/ NTHIHYYLHQSAELLNSKLPR WQETCVDAIKVP [*] EKIMNMIEEI KTPASTPVSGTPQASPMIERSNV VRKDVTLSKCSKPMPAPSGR AYTSPILDMFNFNPATAAPNSQR VNNSTGTSEDPSLQRSSVSATG LNMMKKQKVKTIFPHTAGSNK TLLSFAQQGDVITLLIPEEKDGWL YGEHDVSKARGWFPSYTKLL EENETEAVTVPPTPSPTVRSFG
9762	40130	B	9823	1	1128	
9763	40131	A	9824	1	434	
9764	40132	A	9825	92	319	SIPPYPIPPPVDRKIED*LEGMQT SGLFQQTSG*EEGVGSMSGR PPHPEPLKADFICKREVRLAFSI ACIWMR
9765	40133	A	9826	1	851	
9766	40134	A	9827	227	305	LVIFSIFNLVG*NISDCIIILICQLK
9767	40135	A	9828	66	808	YCWQSQGAKPRDLGGPDLIPLN HSPRVSHLLCHRHIRKAGGVFV ADEIQVGFGRVGKHFWFQOLQ GKDFPDIVTMGKSINGHGPVA CVAATQPVARAFEATGVYEFN TFGGSPVSCAVGLAVLNVLEK EQLQDHATSVGSFLMQLLGQQ KIKHPIVGDRVGVGLFIGVDLIK DEATRTPELKRHVYLVSLRKE NYVLLSTDGPGGRNILKFKPMMC FSLDNARQVVAKLDAILTDME EKVRSCNR
9768	40136	A	9829	3	597	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hud	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
9769	40137	A	9830	1	3281	MGFHHIVGQAGLKLTSGTPQL LALVQHWVPGARL.VEELPHEL VLVLPYTGAHDGSFATLFRELD TRLAELRLTGYGISDTSEEIFL KVVEEECAADTDMEDG/TLRAA PMHRHCWPRRNPTAQDAATGD SAGIDGEPAGSAPETDQQSGPD AVGRVQGWALTRQLQALLL KRFLLARRSRRGLFAQIVLPA LF VGLALVFSLIVPPFGHYPALRLS PTMYGAQVSFFSEDAPGDPGR ARLLEALLQEAGLEEPP
9770	40138	A	9831	1	684	RTRGPQQSRSGGRRRPIPLYLP TSCIKELVAGGVAVESWPGRD AAQLLLCSCLLSPPPVMTETRE PAETGGYASLEEDDEDLSPGPE HSSDSEYTLSEPDSEEEDEEEE EEETTTDPEYDPGYVKV*RLGG GRGGPSRRAPRVAQQPAQPCQ LCGRSPPLGEAPPGTPRCTGTSCC MPGVRCRQSHTGSLAEGVGW EEGAEEIGVVTVVMGDGLPVC CVVLEV DV
9771	40139	A	9832	1	670	MESDIGRKGGKDPEAGPHEHSSD SEYTLSERPSEEEEEEDEEEEEET TDDPEYDPGYVKVQLRLGGGRG GPSRRAPIAAQPPAQCQLCGR SPLGEAPPGTPPCRLLCPATAPQ EAPAPEGRALGEEEEEPPRAGE GRPAGREKEEEEEEETYHCTE CEDSFNDLGLETGTSCCMPGV RCRQSPTGSLAEGVGWEEGA EEIGVVTVVMGDGLPVCVVL
9772	40140	A	9833	3	512	
9773	40141	A	9834	3	815	MLYSRGQPQMGHGPVLVCGLL GTGCTAGAQELREAYTSSIQQID QAEEERISEIEEDKLNEIKREDKITE KRMKRNEQLQEIWWDYVKRPN LRLIGVPKSVDENGTKLENTLQ DIIQENFPNLARQANVQIQR TPQRYSSRRATPRHIIVRFTKVE MREKUMLRAAREKGRVTHKGK PVRLTADLSAETVQARREWGP FNILKGKNFQPRISYPAKLSFISE GEIKYFTDKQMLKDFVTT/RPA LKELLKEALNMERNNWYQPLQ KHAKL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=-Stop codon, /=-possible nucleotide deletion, +=possible nucleotide insertion)
9774	40142	A	9835	1	561	MVNGRIPQAPSQFSHLARLHPA PSPNSDPSPFLAELLMPMSVIGL TPSYPSRFSSESTFLQEAFPDLC QAEDPVYANGGLNYSYRGYGA LSSNLQPPLSLQTGNHSNGPTD L'SMKGGAFTTSTTPTPSSTST SRPVPTAQLSPTEISAVRQLIAG YRESAAFLRSADELENLILQQ NRPRRHL
9775	40143	A	9836	2	226	KGVQFQFSSYGV*PVFP*PFIK*G VLSPLFVFLRFLKDQMIVVDV*H YF*GLCSVPLVYISVLVLVPCCF FFTVAL
9776	40144	A	9837	2	350	YKVKSKPKAQLCQQVKYLWLK LSKGTRALSEERIQPILAYPHPK TLKQLRGILGITGFCRIWIPR*S SPTGQE/FSLYVTEETGIALGILT QVQGTSLQPMEYLNKEIDELDQ GRTH
9777	40145	C	9838	213	365	
9778	40146	A	9839	1	1923	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met het	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
9779	40147	A	9840	1	2091	MVLVVVAVVVVVLVVAVIVVVVVAAVVVGAVVVVVVVMVVVVVVVVEEDNQHKITGA INNNNTAKNPQQSPFHSPATSTGAEATQMRRNQKTPHNMTKQVSLTPPKITLAHQWQIQTKKK YLIYLUKHSGGVNKIPRNPTEYEGCEGPFGELQTTAAQQNKGHHK QTEDHSMLMDRKKNQYCENGHTAQAVPNPYTLLSQPIPEDAEWF TVLDPKHAFVCPVHPSDQFLAFEDPSNPMSQLIWTVLPQGFR NSPHLFGQALAQDLSQFSYLDTLVLRYMDDILLATHSETLCHQ ATQALLNNFLATCGYKVSKPKAQLCSQQVKYGLKLSKGTRTLS EERIQPILGYPHPKTLKQLTAFLGITGFCQIWIPRYSKIAARPLNTRI KETOAKANTHLVRWTPEAEVAFQALKKALTHAPVLSLPVGQNFSLYVTEKITGALGVL/PGTSAQ LAELIALTRAPELGEGKRVNIYANSIGREREFLTSKGTLVKHQE AIKRLLLAVQPKCEVAVLHCGHQKGKEREIEENRQADIEARR AARQDPPELEMITLEGPALELAMATARAELS LAIHHCCLPPPPQ TRCWLPSSLRIRQGVCCIPDPARAITLTAWPKIPFLGIRKAKNPQV REHEACHHLSGLPPFWKWPITILGALGARTPGNTGSTYTFIGY TYTSPVIFILSWQYVYFHGLYY
9780	40148	A	9841	1	1284	

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9781	40149	A	9842	I	1522	MVAPGHSVTSRLGSVFPLLVLDLQYEGAECGVNADVEKHLERGKKLLAAGQLADALSQFHAAVDGDGDNYIAYYRRATVFLAMGKSKAALPDLTKV1QLKMDFTARLQRGHLLLKQGKLDEAEDDFKKVLKSNSPSENEEKEAQSOLIKSDEMQRRLRSQALNAFGSGDYTAIAIFLDKILEVCVWDAELRELRAECFIKEGEPRKAISDI.KAASKLKNNDTEAFYKISTLYYQLGDHDCHSFSEFRDVLNLNDQDHKRICFAHYKQVKKLNKLIESAELIRDGRYTDAKSAYESVMTKTEPSIAEYTVRSKERICHICFSKDEKIPVVAEAVCSEVLQMEPDVNALKDRAEAYLIEEMYDEAIQDYETAQEHNENDQQIREGLEKAQRLLKQSQKRDYYKILGVKRNAKKQEIIKAYRKLAQWHPDNFQNEEEKKKAEEKKFIDIAAAKEVLSDEMRKKFDDGEGPLDAESQQGGGGNPFHRSWNNSWQGFNPFSSGGPFRKFHFN
9782	40150	A	9843	5	519	LTCQEEHKKKHPDSSVNFEVSKKCLERWKTTSAKEK/SKFEAKAKSDKARCDEIKNYIIPPCKKKGRPPSAFFLFCSEHRPKIKSGHPGLFVETAKKLGEMWSGQSAKDQPYEQKAVKLQERYEKGIAAYRAKGKSEAGKKGSKKNKPEDEEEEEKEDEDDEEEEGEDE
9783	40151	A	9844	I	3140	YSIATVLAEEEKLDPRTDEAKRLRPQRNFNITFTHGTVFRLTLESTFFNSALLFTTIQDQLPLPKTIITNAFHFRRNHHQTGFKLSANQRGPLAATLSPGPGGEQGQSAVARLTGEEKKNHPPGAQYANRLSPRVGRFINAAGTTGFPTGKRARSDSSLAKENNQKAYKETYGVSHITRHDMILQIPKQQQNEKYQVPQFDQSTIKNIESAKGLDVWDSWPLQNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFY

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9784	40152	A	9845	2	604	FLELPPAAAAAVLSASPGALER EARSPRSPQTADTSPRPRAPAC APSRARAMPSDRPFKQRSSFAD RCKEVQQIR DQHPSKIPVIIER YKGKQLPVLDKTKFLVPDFHV NMSELVKIIRRQLNPTQAFFL LVNQHSMVSVSTPIADIYEQEKK DEDGFLYMVYASQETTGF*ASS PCLSAHLPPLTHPRLCPPPGPAHP
9785	40153	A	9846	3	303	RDQHPSKIPVIIERYKGKEQLPV LDKTKFLVPDFHVNMSELVKIIR RRLQLNPTQAFFLLVNQHSMVSV VSTPIADIYEQEKK EDGFLYM VYGLPGKPFGE
9786	40154	A	9847	254	2110	
9787	40155	A	9848	234	1904	
9788	40156	A	9849	5	189	
9789	40157	A	9850	1	1546	MASASSQPSLAVGFFSSFDPGAP SCTASSASGILSPTASEVPYASG MPIKKTGHRGVDSSEGETTYKKT TSTALKGAIQLGITYTVGSLSTK PERDVLQMDDFYVVESIFFPSEGSS NLTPAHHYNAFRFKTYAPVAF RYFRELFGIPPDDYLCSCLCSEPLI ELCSSGAGSGSLFYVSSDELIIK TLQHKEAEFLQKLPGYYLNLS QNPRTLLPKFFGLYCVQTGGKN IRIVVMNNLLPRSVKMHKYDL KGSTYKRRASQKEREKPLPTFK DLDLFLQDIPDGLFLDA(DT)NAL CKTLQRDCLVLQSFKIMDYSL WLSIHNIHDQAQREPLSSDTLQV SIDTQRLAPQKALYSTAMEFIQ GEARLGDTMEADDHMGGIPAQ NSKGERLLLYIGII(DI)LSQSYTFLK KLEHSWKA(VV)HDGDA(VS)VHR PGFYAERFQHFMCNAVFKKIPL KPSPSKKFRSGLSFSLHTGSSGN SCITYQPLVSEEHKSQV(KV)QVE PGVHLGRSDVLPQTSE(PPLEEIT)

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9790	40158	A	9851	233	2051	AGPGAGSTCLREARRGRGGP QNAGSVKRRWEDSIPRRGRTGL KESQAAEFGAAKMASASSGP SSVGFFSSFDPAVPSCTLSSASGI KRPMASEVPYASGMPKIKIGHR SVDSSGETTYKKTTSSALKGAI QLGITHTVGSLSKPERDVLQM DFYVVESIFFPSEGNSLTTPAHHY NDFRFKTYAPAVAFRYFRELFGI RPDDYLYSLCSEPLIELCSSGAS GSLFYVSSDDEFIJKTVQHKEAE FLQKLLPGYYMNLNQNPRTLPP KFYGLYCVQAGGKNIRIVVMN NLLPRSVKMHHKYDLKGSTYK RRASQKEREKPLPTFKDLDFLQ DIPDGFLFDA DMYNALCKTLQ RDCLVLQSFKIMDYSLLMSIHNI DHAQREPLSSETQYSVDTRRPA PQKALYSTAMESIQGEARRGG TMETDDHMGGIPARNSKGERL LLYIGIIDILQS YRFVKKLEHSW KALVHDGDTSVHPRGFYAER FQRFCMCNTVFKKIPLKPSPSKKF RSGSSFSRRAGSSGNCSITYQPS VSGEHKQAQVTTKA EVEPGVHL GRPDVLPQT PPLEEISEGSPIPDP SFSPVGETLQMLTTSTLEKLE
9791	40159	A	9852	30	298	EPFIIFIYLFIYLFETESRPVIQ AGVQWCNLSSLQLPLPTGFQKQFS ICLSPLTSDYRHPPCANFCFS FSRDGVSPCWPGWSQTPDLR
9792	40160	A	9853	3	938	
9793	40161	A	9854	208	870	LGMAGRIFTVNILQSPLN PSTLL AEVCVEQCTLMDSKMKPLWIM YSNEEAGSGGRVSVSLKRDDD LWQDMLTMQTIRLMVDVPTDIA NIQLNNRNMDGGNEEFTLSCA GYCVATVVLGIGDRHSDNIMIR ASGQLFHIDFCHFRQRVPFILTY DFVHVIEQGKTNN/SEKFERFRG YCERAYTILRRHGLLFLHLFAL MQAAGLPELSCSKDIRYKLDSL VHPL

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9794	40162	A	9855	1	790	VEELSKKLAQSDQASKVQQQK LKVGQLGEWVWPLDKGGKLFS KLWGRGGLVYKWFLLIYKISY ATGIVGYMAVMFTLFGLNLLF KIKPEDAMDFGISLLFYLYYG VLERDFAEMCADYSTIGFY SESGMPTKHLSDSVCACVCGQQI FVDVSEE/EDH*EHRC5/CPHEF CIRGWCVGKKQTCPYCKEV DLKRMFSNPYPLLGSLLGVGC KKVLASVTCIWVLLGPSSLLPT RTCQTMNNKKIMKVMMRIRK MMTDTMAS
9795	40163	A	9856	1	1005	FRGRAVKMAAVVEVEVGGA AGERELDEVDMSDLSPPEEQWR VEHARMIAHKHRGHEAMHAEM VLILIALTVVAQLLLVQWKQRH PRSYNMVTLFQMWWVPLVFTV KLHWWRFLVIWILFSAVTAFVT FRATRKPLVQTPPLRVYKWPLL IYKISYATGIVGYMAVMFTLFG LNLLFKIKPEDAMDFGISLLFYG LYYGVLERDFAEMCADYSTIG IFYSESGMPTKHLSDSVCACV GQQIFVDVSEEGDHVETTYRLSC NHVSHEFCIRGWCVGKKQTCP YCEKEVDLKRMFSNPWERPHV MYGQLLDWLRYLVAWQPVIIG VVQGINYILGLE
9796	40164	A	9857	28	267	LNIGKGDSKKPRGKMSSYAFFV QTCREEHKKQHPDASVNFSEFS YKKDIAAY*AKGKPDAAKKGFI KAEKSKKKKEEEEED
9797	40165	A	9858	1	194	MKGKGDPKKLRGKMSSYAFFVQ TCQEEHKKQQPDasvnfsefs KKCserwktmsakeksedma kl
9798	40166	A	9859	241	958	HQIFILFFRKITKHGQRRLSRSPR GKMS*FAFFVQTCREEHKKRH PDASVNFSEFSKKC/SQRGWKT MSISKEKGKF*RYGQKRDKAR YEREMKTYYPISKGGDQKRSF KDPNAPQGGPPFGPSFLFCSEY RPKIKREDHPGLSIGDVAKKLG EMWELTLQ/SDKQPYEKKAA KLKEKYEKDIAAYRAKGKPDA AKKGVVKAEKSKKKKEEEEDE EDEDEEEEEDEDEDEDEDEDEDD

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9799	40167	A	9860	2536	2909	KSGVPGSRFSSSDKSDTGTGTL FSTYFLKSDFQLQLIDISASTAS KSLFSAVLFQEYIILSFGLSEIIISL SSAVCWREAPKLSMVGCLAAG GKLTC*AAGLATDGRTEL DAAPAAAALSAV
9800	40168	A	9861	5	1752	KCTICLRNS/AVCCGGCGQLSG YLNGEGADGAERGGGSQVEC LRAPVCQAASSLAASQLAAG GQAANHAQLRCLSPADCALML FIQVEVLTNSIAMVSVHLKEKQP LKLVLGELGFRSPAGEEQATPV VGGEGLGCIEDSAAVAEGGIAI GGIVGINTALQEVLKPHTIKMQ RNNAQLSSRRKEPKEGLCGERG QDRMSRAKGSSSKGKELPPGCR RVTMKPLLVRRETQEGQAERG AEEQLQTLGPFAVYRDSPSKNF YKRDKMLKGLEAKVNFWWR TNEGFLLEEDAGOQEFQIQKAVTP ALCPSRKAEVPLSCLTLKLSED GKAKKAPYNTGPLGLHLHLSMC SHSRKGFEQLWQLNSGKLLQG PRDSVEGSARRAETA/WHCPAVL HFAPALLAALRCQRDLESAAA PSHTRSCQHPRLLSGAVQTAGF SNPPKKVIQIKWNFLVMILLNFP GSTKLIARLKQQMNYKEMASQ RLTOSMLPHRSRLIGAGPCNR VHPEPVIVTLEQKQVFAARIKKN QTCLLCQSQIWCAHYQQGWICA WLAGFGKIIYIFSTIGVIDTLSSG HIHLQPNCARDASASWESPA
9801	40169	A	9862	1	668	MWRLVIQDAKDENGVLVGNR VLAHSLSAIVSCLALNNRRISG WTP/CGPSGSPPGFMGRRGTST/ RLPTG**CPEGQPPRCPCG*ASG CASSPAECRMPATHLPGNSGRV PFPPGPVNYSPLRLQAPEQVTG S/SPWPFS/RPVLGPLPLEGS/PPP F/RLPPRPPRPAVGVAAGSSWGHS AASVRSPGRRPEGESIHPRPPA SRLPWLRLATREEEAGAPKLGED SYPNF

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9802	40170	A	9863	2	624	FMGRRGTSTPPLADNAPRGSP PGAHVVGGWDPDLRAPVTGF SCSGSCSQRGAADWESPPRSPP CRASCASSPAECRMPATHLPG NSGRVPFPGPVNYSPLRLQAP EQVTGS/SPWPFS/RPVLGPLE GSUPPF/RLPPRPRPAGVAAGSS WGHSAAASVRSPGRPEGEISH PRPPASRLPWLRATREEEAGAP KLGEDSYPNF
9803	40171	A	9864	51	225	
9804	40172	A	9865	1	276	AFAAIPTNTLLEQKALDEPAE TESVSKDNTL*PPVETPTTLPRA AGRETKYANLSSPTSTVSESQ/P D*AWSNSPSTCKIQNITEKRGGSL
9805	40173	A	9866	3	441	QTNFKGCSKVTSKLNMSLLW TPTGR*GCDRKVEQQPGDGLGT AAVRPKSLAISSSLVS/ACASK TQGTDLKTSHPHEMLI:HGMAPQ QKHGQQYKTKSSYKAFASIPYK HIAFGTEDS/STTLPRAAGRETK YANLSSPTSTVSESQAD
9806	40174	A	9867	123	417	SLDDLFVSGLLSLDSGILTR NLEVSAN*WVVGSLLTGVTNV KIRGLASEPPAETVFSKKFLFN KLLFSRFSSSILKENEKERKNER HRGSNSV
9807	40175	A	9868	153	1624	TTRRKSMMPTLSGKYLEDNSDL FSEQALDEPAKTESVSKDNTLE PPVELYFPAQLRQQTEELCATID KVLQDSLMSMAPSLSPKTQASSS LAYMNVERTPSPTLKSNTMLSL LQTSTSSSVGLPPVPPSSSSLLK SKQDGLRGPENPRNIHTYPT LASSALSSLSPPINQRATFSSEK CFHPSPALSSLINRSKRASSQLS GQEELNPSALPSLPVSSADFASLP NLRSSS/APSCQSAHPGAPAQSL SSAFTCGSGTLPSSRLGKSESTTP NHRSPVSTPSLISLTTEELISP CALSMSTGPKNKKSKTPTTLPR AAGRETKYSKSDNYLTNLAGS QGERDQAALKTCSEVQSGTILQE REFEANKLQGMQQSDLFKAEY VLIVDSEGEDEAASRKVEQGPP GGIGTAAVRPKSLAISSSLVSDV VRPKTQGTDLKTSHPHEMLHG MAPQQKHGQASAYKGEESNEE DWTLKSSRMTNPRKLSNDKI
9808	40176	A	9869	1	762	

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9809	40177	A	9870	1	537	
9810	40178	A	9871	490	681	MGLVLLHVGVKLGSWLRNGSQ ETAGQJISPLSSWHDGTGAGAL DFSPGLSCLPVR*GSRAAAPH
9811	40179	C	9872	258	527	
9812	40180	A	9873	1	2865	MLPAFEHQTPSSAFGLLNLQQ WFVGRSGRAFGHRLKAALGSL LLKFSDSDWLPCCSACRGPIVG LHLVIVYVKSHQNAYRHKNIQL KQTLLSCNTTKVRSFIEVSETR NPPAGTNSGHILGTCGPGRYAK GKETGKEIIKGQPQNPQGYRLCPL QAVGGGEFGPTQVHVVPFSLSDL KQIRVDSLGFSDDPDPRQYPLRP EAHEGLQDILRYLKQVQLVRK CSSPCNTRILGVQPKPGQWRLV QDLRFINEAVIPL
9813	40181	A	9874	3	177	
9814	40182	A	9875	255	1299	AAVFPLWCWRTRGKCHSLEWR PCTVCSPDSSPKVSAGQALCG SETLPLTQTPDIQVPATLESQHP ANLLVSAAWKSRSRKSLSIFSTWT GTVISLGPRTPHSEITIIPLPWS HGSSITFQVTFRPHVTTTMEIQ LNVSSPVALENATSSLVKNQS LRFVYVTDSNPPARLSWTWEG QALNLSQLSSESAVALLELPVESC DGGEFVCQAQHPLGSQHVSISL SVQSDSVISIEEGVLQTLGFTLIR GILMGTSCTFICGFTWICCTSPVII PKPGTQSCFSTRDATALPDACG SPGPKRVWMCSESHQPLCAVP DEDEQELHYAVLHFHKVQPQE PKVTDTEYESEIKIH
9815	40183	A	9876	27	385	ASTTSGSTSTAARCTAWSPG PLVTAVEKFEEAAAALGQRIST LQKGSPDPLQVRMLNDQLMLL ERTFLNPRAFPEERYYSHVWLWA /PSHGLRSHIPGILSNACSRADT ASGSEA WAEQ
9816	40184	A	9877	160	480	
9817	40185	A	9878	19	433	GLDHGWAGDRWRTRPVVGAG EGRAPRLNSPSPSGQIRSPGPGDLS IVDNWIRYFNRSRSPVYGLVP/GF SSHQA VARTAGSVILRLSDSFFL PLKVSDYSETLRSFLQAAQQL GALLEQHSISLGPLVTAVEKFE AKAAAL

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9818	40186	A	9879	1	996	MALSKERSTVTRTQWARKTML QGETIQISESVSTYLRPVSGT VLGTMNSKTSARIYPTVHTAFD TFDYVDKFLDPGFSSHQAVART AGSVILRLSDSFFLPLKVSDYSE TLRSFLQAAQQDLGALLEQHSI SLGPLVTAVEKPEAEAALGQR ISTLQKGSPDHVLWA/PSHGLRS HIPGLSNACSRARDTASGSEA WAEVQRQLSIVVTALEGSVEAL HEVLOLPAALRACPLRKLALAV DAAFREGNAARLFRLLQTLPYL PSCAVQCHVGHARREALARFA RAFSTPKGGQTLPGMVNLLA WMDSGKHGTCAERTCPWTER RELCs
9819	40187	A	9880	66	744	RAHEDRERSGVQIRTQSWNNG KREKDFLHQSGILETLLMKGC WRKSCTSARIYPTVHTAFDIFD YVDKFLDPGFSSHQAVARTAG SVILRLSDSFFLPLKVSDYSETL RSFLQAAQQDLGALLEQHSISL GMHSPDPEVRMLNDQMLLER TFLNPRAFPEERYYSHVWLWA/PS HGLRSHIPGLSNACSRARDTAS GSEAWAEVQRQLSIVVTALEG AAATLRPVADL

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9820	40188	A	9881	2	2241	PRVRRMQWTKVLGLGLGAAALLGLGIILGHFAIPKKANSALAPQDLDLEILETVMGQLDAHIRENLRELSREPHLASSPRDEDLVQLLLQRWKDPEGLDSAESTYEVLLSFPSQEQPNVVDIVGPTGGIIHSCHRTEENVTGEQQGPDVQPYAAVAPSGTPQGLLVYANRGAEEDFKELQTQGIKLEGTLTRYGGVGRGAKAVNAAKHGVAGVLVYTDPADINDGLSSPDETFPNSWYLPPSGVERGSYYEYFGDP LTPYLPAPVSSFRVDSLAVNSGFPIPIPTQPIGFQDARDLLCNLNGLT LAPATWQGALGCHYRLGPGRPDGDPFPADSQVNVSVYNRLELRNSSNVLGIIRGAVEPDTRYVLYGNHRDSWVHGAVDPSSTAVL LELSRLVLTLLKKGTWRPRRSIVFASWGAEEFGLGSTEFTEEFFNKLQERTVAYINVNDISVFANATLRVQGTTPVQSVVFSATKEIRSP GPGDLSIYDNWIRYFNRSPPVYGLVPSLGLGAGSDYAPFVHFLGISSMDIAYTYDRSKTSARIYPTYHTAFDTFDYVDKFLDPGFSSSHQAQARTAGSVILRLSDSFLPLK VSDYSETLRSFLQAAQQDLGALLEQHISLGPLVTAKEVKFEAEA AALCQRISTLQKGSPDPLQVRM LNDQLMLLERTFLNPRAFPPEERYYSHVLWAPSHGLRSHIPGILS
9821	40189	A	9882	I	1962	
9822	40190	A	9883	I	166	MEYYAALKKDEFMSFVGWTMKLETILSKVCQGQKVKIIHMFS LTGALLVRGPWA
9823	40191	A	9884	I	378	
9824	40192	A	9885	I	681	
9825	40193	A	9886	I	3174	MEYYAAIKNDEFMSFVGWTMKLETILSKLLQQQKTKHRMFSLIGSIIVKVPSSLQAJIQLQSGKEVDVNSEVHVQEMAEARKDDVV TVTDAEKALDKIQHFLFMVKTLSKIGIQTGYLNVIKAIYDKPTANILNGEKLKAFFPLRNETRQGCPLS PLLFNTVLKVALARAVROQEKEIKGIOQIGKEEVILSLFADDIMVHLENPIVSAQNLLKLIDNFSKVGYKINVQKSQAFLYTNNRQTESQIMSELPTIASER
9826	40194	B	9887	I	352	

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9827	40195	A	9888	3	430	FFFLLPVAGLRRPRPLGPVPPR PRVPPPQDRAATMKKKQQEFKAH DIKFKSAGPGQKLKESVGEKAH KEKPNQPAPRPPRQGPTNEGTD GSRCQPQ/WLEQKQSRRAWGPH IAGHHPKPGEKGTSRSHRQE PRGPRDQRGI
9828	40196	A	9889	1	1062	MKKFFQEFKADIKFKSAGPGQK LKESGVVWGRPNGLMSVKGN CECGNLWLLYPEVAALAAEAE GPEVGSVEDQRRQQGYFVRLG SLSARIRHLAYEHSGVKLRSQSK HRAQDTLAQLQETLELVDHMP CGVTPTAPARGKVHIELWGEW RQRPP/REPPPE/QAELETVLALAR SLTHELQGTVEALEFSVVWGLPA GAQEKAEVRSVSDALQTAFA DARCRFDVPAAALAEGGRGRVA HAHACVDELLELVVQAVPLPW LVGPFAPILVERPEPLPDADLV DEVIGGPDPDRWAHLDWPAQQR AWEAEHRDGSGNGDGRMVG AGDICEQEPETPSCPVKHNPDA RAGLLTHGPVEAG
9829	40197	A	9890	11	285	
9830	40198	A	9891	2	138	FFFLGFHVFSIPLIPRDNSF*GV FSSLDLITAVFVTLAELRSVT